

4318	cg43959472	349	CAAGCCCCCAAA TCATCAGAAAAC A[G/C]CAAGGAG CAGGAGGAGCTT GAGCAG	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
4319	cg43959472	575	TTGGATTAGGAC GTCGCCCGGTTA G[C/gap]ATGCTG CCCCTGAGAGG AGAGCACA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
4320	cg43968894	292	TTTTTTTCTT TGAATGCCAAGT C/GTCTTCTGTA CTTCTTTTATTA ACA	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34040 CGI-45 PROTEIN - HOMO SAPIENS (HUMAN), 370 aa.	7.1E-203	
4321	cg43968894	428	TTAAATTTTACAT TACTCTGCCAAG A/gap/AAAAAAAAA AAATTAATAACTC AAGTT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34040 CGI-45 PROTEIN - HOMO SAPIENS (HUMAN), 370 aa.	7.1E-203	
4322	cg43968894	439	TTACTCTGCCAA GAAAAAATAAA A/gap/AJTAAAG TCAAGTTACTTG AAGCCT	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34040 CGI-45 PROTEIN - HOMO SAPIENS (HUMAN), 370 aa.	7.1E-203	
4323	cg43968894	546	GCTCTATAAGCA GATCCAGGCCCT A[G/A]AAAGATGG GACCAGGGTATA TAATT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34040 CGI-45 PROTEIN - HOMO SAPIENS (HUMAN), 370 aa.	7.1E-203	
4324	cg43918848	1271	GGGAGCGCCC AGAAATTCATGT CTG/TGTCTGA CAACTTCAACA GGACTT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2

4325	cg43918848	1273	GAGGCGCCAG AAATTCATGTCT GTG/TJCTGACA ACTTCAAACAGG ACTTTA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
4326	cg43918848	1386	ACGGGGCTGGC AGTGTGAGAGA AC[G/A]CTCTGGA AGCTCCTAACAG ACGGCT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
4327	cg43918848	1549	CTGGGGGGAGG CAGCACGGGGC GCA[gap/G]CCCT CGGCAGGCGAG CGGGCGGGAT	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
4328	cg43918848	187	CTTTGGTCAAGG TGTCACACAT T[A/C]CCACTGCA GCTCCAGCACAC GCGGC	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
4329	cg43918848	231	CAGCGGCGCAC CATGAACTCGGA CG[C/T]GGAGCC CAAGGAATGGAG ATCGCAC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
4330	cg43916740	1960	AAATCGCGGCC ACAAAGCATCCCC C[C/gap]ATCCCT TGCAGGCTGGG GGCTGGGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P30679 GUANINE NUCLEOTIDE-BINDING PROTEIN, ALPHA-15 SUBUNIT (ALPHA- 16) - Homo sapiens (Human), 374 aa.	8.1E-202	19 (19p13)
4331	cg44128902	1274	AAATACCTCAGC CTCTGGTTTTTC A[C/G]CAGCTTGG GATTGGGGTTAA ACCTTT	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201	1 (1p36.2)



4332	cg43957976	975	CCTGTGTGAGTG CTGCAAGGCCAT C[G/A]ATTGTTCC TGGGAGCTTCTC CAGAC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P28906 HEMATOPOIETIC PROGENITOR CELL ANTIGEN CD34 PRECURSOR - Homo sapiens (Human), 385 aa.	7.3E-201	1 (1q32)
4333	cg43957976	976	CTGTGTGAGTGC TGCAAGGCCATC G[A/G]TTGTTCTC GGGAGCTTCTCC AGACC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P28906 HEMATOPOIETIC PROGENITOR CELL ANTIGEN CD34 PRECURSOR - Homo sapiens (Human), 385 aa.	7.3E-201	1 (1q32)
4334	cg43957976	178	ACCGTCATTGAA ACCAGGATCCCT G[C/T]TCAACCCC TCTGAAAGAAA TCAAC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P28906 HEMATOPOIETIC PROGENITOR CELL ANTIGEN CD34 PRECURSOR - Homo sapiens (Human), 385 aa.	7.3E-201	1 (1q32)
4335	cg42914819	149	ATCCCTGTATGA ATCAAAAAGTGC C[C/A]TTCTTGCA GCTTCTGTGAC AAGGA	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27726 CGI-17 PROTEIN - HOMO SAPIENS (HUMAN), 385 aa.	4E-200	5
4336	cg43981683	1097	AGCCCTGGCTG GGCCTGGGCA GGA[C/gap]CCTA AAGGGTTACTGC AAGTTCTGG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4337	cg43981683	1099	CCCTGGCTGGG CCTGGGGCAGG ACC[C/gap]TAAA GGGTACTGCAA GTTCTGGGC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4338	cg43981683	213	TGGGCTTAGTGT TAAGCGTGAAG G[G/gap]CGAGGC CAGACAGCTGGA GGCCTGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11

4339	cg43981683	219	TAGTGTTAAGGC GTGAAGGGCGA GGC/gap]CAGAC AGCTGGAGGCC TGGTCCTCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4340	cg43981683	291	TCGGAGGCTGAA GGAAGGGCGGC GGC/gap]ACAC AGGGCCCTTCCC CTCTGCTG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4341	cg43981683	348	CTCCTGCTCAGG CTTCTCTCTAG G/A]GCATTGG AGGAATCCTCTT TCCCTG	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4342	cg43981683	390	CTTCCCTGTCG GAAACTCAACAC T[G/A]TACAGAAC TCCAACCATTAAC CCTTC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75133 KIAA0638 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	1.4E-198	11
4343	cg43268635	124	TGTTCAAGCAAT TCTCGTGCCCTTG G[C/gap]CTCCCA AGTAGCTGGGAC TGCAGGT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA06193 SKAP-HOM - HOMO SAPIENS (HUMAN), 359 aa.	3.7E-197	
4344	cg43268635	562	ATCTTCAGCAT CTACCAAAAAA A[A/gap]CTCGCA TGATACACTAAA TTTAAAA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA06193 SKAP-HOM - HOMO SAPIENS (HUMAN), 359 aa.	3.7E-197	

4345	cg44916575	1932	CCCAACCCGTGAG AGGACAAAACA G[A/G]AAGCCCT GTGAGTGTGGG AAAACCTC	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16842 BETA-GALACTOSIDE ALPHA-2,3- SIALYLTRANSFERASE (EC 2.4.99.4) (CMP-N-ACETYLNEURAMINATE-BETA- GALACTOSAMIDE-ALPHA-2,3-SIALYL- TRANSFERASE) - HOMO SAPIENS (HUMAN), 350 aa.	3.7E-197	
4346	cg43114683	1695	TTATGATTATTTA TTAGTTTTTTTTTg ap/TAAATGCTTG TTCTAAGACATTT CTG	gap T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15184 PQ-RICH PROTEIN - HOMO SAPIENS (HUMAN), 400 aa.	2.6E-196	12
4347	cg44015472	115	TTGGACCCAGG TTGCTTGGCGCT G[C/gap]CTGCCA CAGGACCCCGG GACAGACA	gap C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA-TRYPsin INHIBITOR LIGHT CHAIN (IT-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)
4348	cg44015472	116	TTGGACCCAGGT TGCTTGGCGCTG C[C/gap]TGCCAC AGGACCCCGG ACAGACAC	gap C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA-TRYPsin INHIBITOR LIGHT CHAIN (IT-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)

4349	cg44015472	1290	ACAGGCTCGGTC TAGCAACAGAAG G[G]gap]CCACCG CCTCCCTGCAAC AGGGCAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)
4350	cg43951541	825	TTTTTTTTTTTA AGAATAAATCACI C/TITTCACAAA CTAAGACAAACT TTTT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78310 COXSACKIE AND ADENOVIRUS RECEPTOR PROTEIN - HOMO SAPIENS (HUMAN), 365 aa.	6.3E-195	
4351	cg43928808	1419	GTTCATTTCATTC AACGATAGTTTC T[A]CJAACAGTAC TTAAATAGCGGT TGGAA	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16769 GLUTAMINYL-PEPTIDE CYCLOTRANSFERASE PRECURSOR (EC 2.3.2.5) (QC) (GLUTAMINYL-TRNA CYCLOTRANSFERASE) (GLUTAMINYL CYCLASE) - Homo sapiens (Human), 361 aa.	2.7E-194	2
4352	cg43993380	2317	AACTGGTTAAAA AAGGAATAGGG GTT[A]GAGTGTT ACAGAGAGTAGT CTGAAG	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O00623 PEROXIN-12 (PEROXISOME ASSEMBLY FACTOR-3) (PAF-3) - Homo sapiens (Human), 359 aa.	5.6E-194	
4353	cg43993380	2463	TGCTTGCTGCTA AGAGTTTGCTAA A[C]GJTGTCATGA ATTATTCTGGTTA TTAC	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O00623 PEROXIN-12 (PEROXISOME ASSEMBLY FACTOR-3) (PAF-3) - Homo sapiens (Human), 359 aa.	5.6E-194	
4354	cg43993380	2508	TATTACTAAAGTT TCTATGAAACACI T/gap]TAAGTAGA TTTTAAGATAAA TGTT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O00623 PEROXIN-12 (PEROXISOME ASSEMBLY FACTOR-3) (PAF-3) - Homo sapiens (Human), 359 aa.	5.6E-194	

4355	cg43993380	2509	ATTACTAAAGTTT CTATGAACACAT T/gapJAAGTAGAT TTTAAGAATAAAT GTTT	T	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O00623 PEROXIN-12 (PEROXISOME ASSEMBLY FACTOR-3) (PAF-3) - Homo sapiens (Human), 359 aa.	5.6E-194	
4356	cg43993380	2544	TTAAGAATAAAT GTTTCTGGAATA GAGGACTATGTT ATGATTTTGTAG AAATG	A	G			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:O00623 PEROXIN-12 (PEROXISOME ASSEMBLY FACTOR-3) (PAF-3) - Homo sapiens (Human), 359 aa.	5.6E-194	
4357	cg43987823	1470	TTAGCCCTCGCG CCCCCGCCGTT G[G/gap]CTGCGG GAGAGCCCGCG TCCCACTC	G	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P54826 GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1) - Homo sapiens (Human), 345 aa.	1.9E-193	9 (9q21.3)
4358	cg43987823	1520	CCCGTGCTCGC CTCGACCCCGC GCC[G/gap]GGCA CCTGTGGCTTGG GACAGATAG	G	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P54826 GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1) - Homo sapiens (Human), 345 aa.	1.9E-193	9 (9q21.3)
4359	cg43987823	2729	TTGTATTTTATA GACATGTTTTTT gap/TJAAAAATCC TAAGTTTTTAAAT AACT	gap	T			SILENT- NONCODING	UNCLASSIFIED	Human Gene SWISSPROT-ACC:P54826 GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1) - Homo sapiens (Human), 345 aa.	1.9E-193	9 (9q21.3)
4380	cg43970111	889	TGCATATGCCCT CTCCACCTTAAC AT/CJCAAAATGG GGGAGGAGGAG AATTTA	T	C			SILENT- NONCODING	UNCLASSIFIED	Human Gene TREMBL-NEW- ACC:AAD43131 SYLD709613 PROTEIN HOMO SAPIENS (HUMAN), 357 aa.	6.5E-193	14

4361	cg40988719	117	CCAGCGGGGC TGAGCTAGGC GTA[G]CTGTGA TTTCAGGGGCAC CTCTGGC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q11130 ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L- FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 7) (FUCT- VII) (SELECTIN- LIGAND SYNTHASE) - Homo sapiens (Human), 342 aa.	3.6E-192	9
4362	cg40988719	118	CAGCGGGGCT GAGCTAGGGC TAG[C]GTGTGAT TTCAGGGGCACC TCTGGC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q11130 ALPHA-(1,3)-FUCOSYLTRANSFERASE (EC 2.4.1.-) (GALACTOSIDE 3-L- FUCOSYLTRANSFERASE) (FUCOSYLTRANSFERASE 7) (FUCT- VII) (SELECTIN- LIGAND SYNTHASE) - Homo sapiens (Human), 342 aa.	3.6E-192	9
4363	cg43985790	170	TTTTTTTTTTT TTTTTATTTT[C] /TTCTGAAGTG TGAATTTTAATAT TG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O08746 MATRILIN-2 - MUS MUSCULUS (MOUSE), 956 aa.	4.6E-192	8
4364	cg43985790	281	TATACATATATCA AGGTAAGTCCA [G/A]TACAAAAA ACAGCATTTCT ATGG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O08746 MATRILIN-2 - MUS MUSCULUS (MOUSE), 956 aa.	4.6E-192	8
4365	cg43985790	561	ACCAGGTTTCTC AGTACTGATTGT TT[C]TACTTCAC AACATTATTGATT TAAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O08746 MATRILIN-2 - MUS MUSCULUS (MOUSE), 956 aa.	4.6E-192	8
4366	cg43984795	364	CAAAAGTTTCAA ATGAAACAGGT A[C/G]CCCTCTT TCCTGTAGGCTT TCCAG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.8E-192	16

4367	cg43984795	435	AGTACTTCTATTA AGGAGCTGGA A[G/gap]CCCACC CTAGGACTTGAA TGGCACC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.8E-192	16
4368	cg43984795	47	TTTTTTTTTTTT TTTTTTTTTTTTTT CJTCAGGATCTTT AACTTTATTAGC AG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53990 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.8E-192	16
4369	cg43939832	1338	CCACCAGCCAG CAAGCATTAAATG GG[G/gap]CTGGT GCCCACTTTCCA CTCAGCAG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA06754 JM5 PROTEIN - HOMO SAPIENS (HUMAN), 360 aa.	1E-191	
4370	cg44001682	173	TCATTTTATTTT ATTAAGCACTACI A/GJTAACACATT GCATGCTACATA ATAA	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O15541 ZINC FINGER PROTEIN 183 - Homo sapiens (Human), 343 aa.	3.2E-191	X
4371	cg43980381	1253	TCCCAGGCTCTG GCTGGCTGGTA GC[C/gap]AAGCA CTTATGGACCAG AGTGGCCC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03385 GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) - Mus musculus (Mouse), 852 aa.	5.6E-191	9
4372	cg43980381	1628	ACTGCAGTTCTC TCATGCCCCACAG G[C/gap]ACTGGC CTGTGACCTTCG CAGGGGT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03385 GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM A (RALGEF) - Mus musculus (Mouse), 852 aa.	5.6E-191	9
4373	cg43920610	198	AAGAGTAGTGTG ACTTTTGCTGAA A[G/gap]CAGCAG TTTTCTTCATGG AAGGAAT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22381 QUINONE OXIDOREDUCTASE HOMOLOG-1 - HOMO SAPIENS (HUMAN), 349 aa.	5.9E-191	21

4374	cg43920610	334	TCATTTGCACAA GAATTTTTCAAA C/A/TCTTTTCAA ATGTGTCAACTG AGCAT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22381 QUINONE OXIDOREDUCTASE HOMOLOG-1 - HOMO SAPIENS (HUMAN), 349 aa.	5.9E-191	21
4375	cg43119894	87	CACACTGCCTGG TATACACCGCCA G[gap/G]TAGGCA TTCAGAAAAGTT TCITTTT	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA75235 LACTOSYLCEAMIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.9) - MUS MUSCULUS (MOUSE), 387 aa.	2.3E-190	2
4376	cg43926852	1389	CATTTTCCAGAA GAGGCCCTGAG GC[C/gap]TGGAG AGGCAAGCAG CCTACTGAG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08567 PLECKSTRIN (PLATELET P47 PROTEIN) - Homo sapiens (Human), 350 aa.	2.9E-190	2
4377	cg43926852	259	CAAGAGAGGATT TGATAAAATGAG G/A/GAATAATGTT CTACTCTCCTTT CTTTC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08567 PLECKSTRIN (PLATELET P47 PROTEIN) - Homo sapiens (Human), 350 aa.	2.9E-190	2
4378	cg43926852	343	AAATATACITTTCA CACACATACTG C/TJTCAATGGG TGCTGTCITTTCT CAAT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08567 PLECKSTRIN (PLATELET P47 PROTEIN) - Homo sapiens (Human), 350 aa.	2.9E-190	2
4379	cg43931961	1793	GAAAAGGTAAGA CCTCGTTTGTAGT T/G/TJTAACGTGT TAAAAAATAACA CTTGG	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60256 41-KDA PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE-ASSOCIATED PROTEIN HOMO SAPIENS (HUMAN), 369 aa.	2.9E-190	17
4380	cg43931961	2087	AACITTTGTGTTTT GGCAATCGTTTT A/GJTAACATAAAT AAAATGAAAGCT AAA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60256 41-KDA PHOSPHORIBOSYL PYROPHOSPHATE SYNTHETASE-ASSOCIATED PROTEIN HOMO SAPIENS (HUMAN), 369 aa.	2.9E-190	17



4381	cg43919278	1897	AAATGTTTGTG TGGGAAAAAAA A[A/gap]CTCATT GGCAGATCCAAG AATGACA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4382	cg43919278	2004	AGCAAGGCAGCT CCCCAGCCTCAC TTC/TTCACCTCC TGATTGAGGGCC GGGTT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4383	cg43919278	2022	CCTCAGCTCTCA CTCCTGATTGAG G[G/C]CCGGGT TGTGTCCAGCA CCAATT	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4384	cg43919278	2092	AATAAACCAACA ACTTATAATTGT G[A/G]CACCAGA TGCTTAGGATCC TGGTGC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4385	cg43919278	2113	TGTGACACCAGA TGCTTAGGATCC T[G/C]GTGCTGG GTTAGCTAAGAG AATAGA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4386	cg43919278	2114	GTGACACCAGAT GCTTAGGATCCT G[G/C]TGCTGGG TTAGCTAAGAGA ATAGAC	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X
4387	cg43919278	2511	TTCAGGCTCCTT TTTTATAAACTG G[G/T]GATTTTC TTTTGTCTAAAAA ACAC	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43911 LISSENCEPHALIN-X - HOMO SAPIENS (HUMAN), 360 aa.	3.6E-190	X

4388	cg43996402	378	CTTTTATTAGAC AAGACAACAGTA CTATAATTTACC CCTTGCTAAAGG TAT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
4389	cg43922311	226	CTGGGGGCTGG GGCCAGGGCT CTG[Gap]CGAC CTAGAGGTGTGG ACGGCACAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43293 HYPOTHETICAL 60.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 570 aa (fragment).	3.3E-189	
4390	cg43933608	2187	GAATCAACATTT AGTCTTCATTAT C[Gap]/TTTTTTTT TTTTTTTGAGACA GAGTT	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.5E-189	8
4391	cg43933608	2201	TCCTCATTATCTT TTTTTTTTTTTTg ap/TGAGACAG GTTTCGATCTAT TTTAA	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.5E-189	8
4392	cg44002198	218	GGAGAGGAATC GGGTGGGGGC GCC[C/Gap]GCAG CAGGGGAGAGA CACTACACAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7
4393	cg44002198	323	CACACGGACACT GAAACACGAGC A[C/Gap]GGCACAG CCACAGGGAGG AATGGTG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7
4394	cg44002198	332	ACTGAAACCACG AGCACGGCACA GC[C/Gap]ACAGG GAGGAATGGTG GAGCTGGGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7

4395	cg44002198	420	CTGCCACGAGTT CCTTGGCGAGG AG[C/gap]CTTGT CCGTGTTACTAA AGAGCCAC	C	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7
4396	cg44030684	1304	ACTGGTGTGCAG GTGTGAGGCTCC T[G/A]CAGGCC ACTCTCTTCAGC AGCCAC	G	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14254 SURFACE ANTIGEN - HOMO SAPIENS (HUMAN), 379 aa.	7.9E-188	17
4397	cg44030684	1422	TATCTCGAAGG ACCAGAAGTGCT G[C/T]GTGTTTCAG GCCATCTCTGGC TGTC	C	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14254 SURFACE ANTIGEN - HOMO SAPIENS (HUMAN), 379 aa.	7.9E-188	17
4398	cg44030684	1755	TCTGGGTAGGA CGGTCACTGTCC TT[C/T]CTCCTGG ACTGGTCTTCCC AGCCC	T	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14254 SURFACE ANTIGEN - HOMO SAPIENS (HUMAN), 379 aa.	7.9E-188	17
4399	cg44030684	2397	CCAGTGGTCCCA GCTCCCCACCCT G[G/gap]CCCCTGC CCCAGCCTGTGT AGCTCTT	G	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14254 SURFACE ANTIGEN - HOMO SAPIENS (HUMAN), 379 aa.	7.9E-188	17
4400	cg43935246	767	ACACTTTTCATGT GGTCAATCAATT G[T/gap]TTATTGC TTTATACAGCAT GATTA	T	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43261 HYPOTHETICAL 92.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 811 aa (fragment).	1.6E-187	14
4401	cg43935246	769	CTTTCATGTGGT CAATCAATTGTTT [gap]/TTATTGCTTT ATACAGCATGAT TTAAT	gap	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43261 HYPOTHETICAL 92.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 811 aa (fragment).	1.6E-187	14

4402	cg43068807	623	GATCATTATTTA GTCCCTACAACCG ATT/CJGCATTGTT CCACTTCCCAT CATT	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15284 JOSEPHIN MJD1 - HOMO SAPIENS (HUMAN), 361 aa.	5.8E-187	14
4403	cg43309217	19	TTTTTTTTTTTT TTTTT[G/C]CATG GTGAGAAAGATT TTTATTGGA	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92610 MYELOBLAST KIAA0211 - HOMO SAPIENS (HUMAN), 1267 aa.	2.4E-186	18
4404	cg43993614	133	TTTACAAGTAG CAAAGTCCCTCC G[ap]/TTTTTTTT CCCCAGGTGAAT GTACAT	gap	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10
4405	cg43993614	171	GGTGAATGTACA TGAATATAAAA G[C/T]GGCTGAT GTCCACACTGCT CGGCC	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10
4406	cg43993614	261	AGTCCCCGGAG CGGTGGGGCGG GGC[C/gap]TCCT CTTCTCCAGTTC CAGCACGCT	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10
4407	cg43993614	275	TGGGGCGGGGC CTCCTCTTCTCC AGT[C/T]CCAGCA CGCTCATCAGTC GTCCTC	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10
4408	cg43993614	281	GGGGCTCCTCTC TCTCCAGTTCCA G[C/T]ACGCTCAT CAGTCGTCCTCC TGCIG	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10

4409	cg43983614	60	TTATTTCATAGA AAGCATTTTATT A/TTCAGAACAG TATGGTTTTCT ATGT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75794 HT-1080 PROTEIN - HOMO SAPIENS (HUMAN), 336 aa.	3.1E-186	10
4410	cg43927276	1173	CACCTCCTTGAG AATTTTTTTTTT T/gapAAGCTTAT AGTAAGGATACA TTCAA	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P50616 TOB PROTEIN (TRANSDUCER OF ERBB-2) - Homo sapiens (Human), 345 aa.	3.1E-186	17
4411	cg43957632	1459	GAGCGAGCGGG CGGGCGGGCAG GTG[gap]CACG GCCCTGCGAGC GGGAGCCGCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185	2 (2q33)
4412	cg43957632	286	TGCCGAGCTCG GTGCTGGTCTCT TTCA/CAAAATAT AAATACGTGTGT CAGAAC	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185	2 (2q33)
4413	cg43957632	300	CTGGTCTCTTC CAATATAAATA C[G/ATGTGTCAG AACTGGAAAAATC CTCCA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185	2 (2q33)
4414	cg43922383	192	CAACGGCATCTG AAAATGGTGTGT G[G/ACGTCGCG CGCGCCAGCTAT CGTCAG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
4415	cg43047610	185	TGGGGCCAGAA GGGTGCTGGG AGG[C/gap]CAGG TTCTGGGGATCC CCTCCATCC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB37839 TRANSDUCIN ALPHA- SUBUNIT - HOMO SAPIENS (HUMAN), 350 aa.	7.3E-185	3 (3p21)

4416	cg43950796	212	CCCGGCCCCAA GTTAGCAGCTGG GA/C/TGATGCAA TCCTGTGAGTCG CAAGCC	C	T		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
4417	cg43950796	295	GCAGGCTGGAG TCCCCTGCCGCT GG[C/gap]CCTAA AATAAGCGTGCG CCATAGCC	C	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
4418	cg42269542	1339	GGGGGACAACT CCTACCGTTCCT CC[G/C]ACACAT GCCCCACTAAAC CATCTGA	G	C		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14560 F25965_3 - HOMO SAPIENS (HUMAN), 903 aa.	4.4E-184	
4419	cg44001387	1331	CAGCACAAATGGT GTTGCTTTAATG G[A/gap]AAAAA AAACAGTAAAG TGAAATA	A	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O14832 PEROXISOMAL PHYTANOYL-COA ALPHA-HYDROXYLASE PRECURSOR (PHYTANIC ACID OXIDASE) - Homo sapiens (Human), 338 aa.	8.4E-184	10
4420	cg44001387	1340	GGTGTGCTTTA ATGGAAAAA A[A/gap]CAGTAA AAGTGAAATATT ACTGTTT	A	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O14832 PEROXISOMAL PHYTANOYL-COA ALPHA-HYDROXYLASE PRECURSOR (PHYTANIC ACID OXIDASE) - Homo sapiens (Human), 338 aa.	8.4E-184	10
4421	cg43304269	235	GATGACCTCATC TTCACACTGTCCA C[A/C]GGGCACA GGGCAGACCCGG GGTGCTC	A	C		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75532 HYPOTHETICAL 45.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 416 aa (fragment).	8.7E-184	19
4422	cg44007066	2084	AATGCTCTCTGC AGCAGGAAATTG C[A/gap]TGAAC GAGCCTCCTTCA CTGACCT	A	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB50224 HYPOTHETICAL 41.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 373 aa (fragment).	1.7E-183	

4423	cg44128927	1076	GTCTGAGCTGG GACCTGCTCCC AC[G/C]CCTGCTT CTTAAGGTCCT GCTCGG	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD38070 REVERSION-INDUCED LIM PROTEIN - HOMO SAPIENS (HUMAN), 330 aa.	2.8E-183	5
4424	cg43004357	1289	TCTGGCAACAAC TCCTCCAAGGG C[AC]GGGGTGG GGGGCGGGGG CGGGTAC	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF- RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4425	cg43004357	1297	CAACTCTTCCAA GGGCAGGGGT GG[G/T]GGGGCG GGGGCGGGTAC AGGTGGAG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF- RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4426	cg43004357	1302	CTTCCAAGGGGC AGGGTGGGGG GG[C/G]GGGGC GGGTACAGGTG GAGAGGTG	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF- RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4427	cg43004357	1434	CTGCTGGTCCG GGTCTCCACCCC G[C/gap]CATGGG CAGAGGCTCCG GGAGGCCCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF- RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4428	cg43004357	291	GCACGTGGAAGT CAAAGGGTTTCT C[T/gap]TTTTTTT TTTTTCCCCTTT TAGAA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF- RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4429	cg43004357	304	AAAGGGTTTCTC TTTTTTTTTTTTT T[gap]CCCCCTTT AGAAAGCTATACA TAAAA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF- RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14

4430	cg43004357	480	ATCCAACAGTTT TTTGCATTTTTT [gap]/TJAAATTAAT TTTTCATTTTTT AAAA	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF- RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4431	cg43004357	87	ATAGTCGTTACA AAAAGTTTTTTT [T]/gap]CTTTTAAA TAAATTCACACA AAGAA	T gap	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF- RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4432	cg43004357	850	ATGGCGTGAGTG CTCTAAGGATAG A[C]/gap]CTACGG TATTCTAGAGCA AAACCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF- RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4433	cg43004357	966	GCTCACCCCTTA CTTTTTTTTTTTT T/gap]AGCTTTTC TCTCATTTTTTT TTGT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q07352 TIS11B PROTEIN (BUTYRATE RESPONSE FACTOR 1) (EGF- RESPONSE FACTOR 1) (ERF-1) - Homo sapiens (Human), 338 aa.	4.6E-183	14
4434	cg43919094	365	CCTAATAATAGA GATCTGAGGTGG T[C]/TJACCAGGAG ACTACGTTCTTT GATT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76004 ATP(GTP)-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 358 aa (fragment).	9.9E-183	2
4435	cg43919094	454	AAAACITGAAGT TGAGGCTTGGG A[G]/JAGTATCAG CTCAGTATATCC TTCCT	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76004 ATP(GTP)-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 358 aa (fragment).	9.9E-183	2
4436	cg43959681	2439	ATACAGAGAAGG GTCTTTTTTTTTT T/gap]AAGTATTT CAGTGAAAACCT GGTGT	T gap	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43684 SPLEEN MITOTIC CHECKPOINT BUB3 - HOMO SAPIENS (HUMAN), 328 aa.	6.8E-182	10



4437	cg43959681	262	GGAAGCAAGGA GGCGGCGCGG CCG[C]gap]AGCG AGTGCGGAGTA GTGGAACGT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43684 SPLEEN MITOTIC CHECKPOINT BUB3 - HOMO SAPIENS (HUMAN), 328 aa.	6.8E-182	10
4438	cg43959681	2565	TATGGAAGCTT TGTTGCTTCCT A[C]gap]AAATAC ATGCTTATTCCTT AAGGGA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43684 SPLEEN MITOTIC CHECKPOINT BUB3 - HOMO SAPIENS (HUMAN), 328 aa.	6.8E-182	10
4439	cg43986852	182	ATCGTCGTTTTTCA AATATTACAAAA [A]gap]AGGAAGA AAAATACAAGGG AAGCAG	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26651 TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475) - Homo sapiens (Human), 326 aa.	2.9E-181	19 (19q13.1)
4440	cg43986852	183	TCGTCGTTTTTCA ATATTACAAAA [A]gap]GGAAGAA AAATACAAGGGA AGCAGA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26651 TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475) - Homo sapiens (Human), 326 aa.	2.9E-181	19 (19q13.1)
4441	cg43945307	241	CGGGGTGGGG AGGGTGTGTCAG TC[T]gap]GCAGA GAAGCTCCTGG GAGAATGGA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15194 HYA22 - HOMO SAPIENS (HUMAN), 340 aa.	3.7E-181	3
4442	cg43923337	1106	AGACAAAACATG ACTGAAAAGAGC A[C]TCTGTACTT TTCAAAGCCACTG GAGGG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa.	3.7E-181	14
4443	cg43923337	1133	TGTACTTTTCAA GCCACTGGAGG GA[G]A]AAATGGA AAACATGAAAC AGCAAT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa.	3.7E-181	14

4444	cg43923337	1196	CTGAATAATCAA AGACTAATTGT GAGJTTTACTT TTTAATAGATATG ACTT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa.	3.7E-181	14
4445	cg43923337	1253	CAACATGGAATG AAATAAAAAATAA [A/G]TAATAAAAG ATTGCCATGAAT CTTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa.	3.7E-181	14
4446	cg43989631	293	ACAGGGGAGAG AAGGGGCAGGG AAG[G/T]CCTGG GGGAGGGAATG GCAGACCC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75056 KIAA0468 PROTEIN - HOMO SAPIENS (HUMAN), 384 aa.	1.6E-180	
4447	cg42717910	327	CACGCCGCTCC CCATCCCCGCAG CG[C/gap]GTCTG CACCGGAGACTC TGCGGGGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60547 GDP-MANNULOSE 4,6 DEHYDRATASE - HOMO SAPIENS (HUMAN), 372 aa.	2.1E-180	
4448	cg43950166	2824	AATTTAAAGCAT CATATAAATTAA ACJGGTGTCTATT GGTAATAATCTC ATAT	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92623 MYELOBLAST KIAA0227 - HOMO SAPIENS (HUMAN), 336 aa (fragment).	1.9E-179	14
4449	cg43928466	1637	AAAAATATAATAA TCATAAAGTCTG ATJACAGGACA TCGCCCTTTGGGA ACTA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76091 NITRILASE HOMOLOG 1 - HOMO SAPIENS (HUMAN), 327 aa.	2.4E-179	1
4450	cg43928466	1639	AAATATAATAATC ATAAAGTCTGAA ATJCAGGACATC GCCTTTGGGAAC TAGA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76091 NITRILASE HOMOLOG 1 - HOMO SAPIENS (HUMAN), 327 aa.	2.4E-179	1

4451	cg43267504	1425	GCCATAAAATGT GCTTCTCTCTT CIA/GGGATGTT GTTTGGCTGTCTG ATCTTT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q01638 ST2 PROTEIN PRECURSOR - Homo sapiens (Human), 328 aa.	4.9E-179	11 (11p14.3)
4452	cg43944312	427	TCACCTTGAGG CGTCTGGCTG GGC/gap]CCCGT TTCCACACCAGC ACATGGTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97434 P116RIP - MUS MUSCULUS (MOUSE), 1024 aa.	4.4E-178	17
4453	cg30490224	1906	TAGATTCGGTTA CAATAAACACAGC A/A/GJATGCACCA GAGACACAAGG CTTGAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)
4454	cg30490224	1907	AGATTCGGTTAC AATAAACACAGCA A/A/GJTGACCA GAGACACAAGG CTTGAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)
4455	cg30490224	3110	CAGAGCCTCAAT TATTAAGGAAAA G/gap/CJTCCTCA GGAAAAATACTA AAATATT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)
4456	cg30490224	3137	CTCAGGAAAAA TACTAAAAATTT T/gap]CTCTTCCT CATAAGCTTCTA AATTA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)
4457	cg30490224	3327	ACACAGGCTCTAA ACTCAGCATGCT TTT/gap]GGTGAG TTTTTCTCCAAAA GGGGCA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)

4458	cg30490224	3346	ATGCTTTGGTGA GTTTTCTCCAA A[A]gap]GGGGCA TATTAGCAATTA GAGTTGT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30968 GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R) - Homo sapiens (Human), 328 aa.	1.2E-177	4 (4q21.2)
4459	cg43984598	296	ATCCACAGGTACT GCTTTTACTACT GT[G]GATTGTT GCCAGCATTTAT AACTT	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC33734 CELL DIVISION PROTEIN - HOMO SAPIENS (HUMAN), 327 aa.	1.5E-177	X
4460	cg43969747	1870	GCACGGGCCCT AGAGCTGAACG GCA[G]gap]GGGT CAAAGGTCAGAG CATCTGCAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4461	cg43969747	1873	CGGGCCCTAGA GCTGAACGGCA GGG[G]gap]TCAA AGGTCAGAGCAT CTGCAGAGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4462	cg43969747	313	CGGGCTGATTGA TCTCTGCATCTT C[A]TTTTTTTC CCGAGCAACATC TGCGT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4463	cg43969747	318	TGATTTATCTCT GCATCTTCATTTT T[C]TCCCGAGC AACATCTGCGTG TCGG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4464	cg43969747	333	TCTTCATTTTTT CCCGAGCAACAT [C/]TGGGTGTCG GTCTGCTTTTATT ACC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16

4465	cg43969747	382	CCTCCAGACTG AGCCCCGACCT G[G/gap]CCCAGC CTGGCCCCGTCC CCAATCCA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4466	cg43969747	415	TGGCCCGTCCC CAATCCAGTGGG CT[G/gap]GCCAG GCCACCTGCACC AGGGAGGA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4467	cg43969747	541	ACGCGGCGCAGG GAGGGGCAGAG AAC[G/A]CACTAG CTTGGGGGTGG GCACCAGC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4468	cg43969747	566	GCACTAGCTTGG GGGTGGGCACC AG[C/gap]CTCAG ACCCCTCAGCAG CTTTGGGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
4469	cg43972734	437	TTTTTTTCTCTG CTTTCTGCTTA A/GAACAAATAT GGCTTCTCTTT TGCC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15555 T-CELL ACTIVATION PROTEIN - HOMO SAPIENS (HUMAN), 327 aa.	8.3E-177	18
4470	cg44035397	446	ACTGGAATCTTT CTTCTCAACAGG G[G/gap]CTGCAG GGTCTACCCCTC CGACTCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45826 C2H2-150 - HOMO SAPIENS (HUMAN), 326 aa.	1.7E-176	7
4471	cg43933591	1024	GGCTAGGGACC CAGGGCAGAATC TA[C/T]ACGGTCC AAGGGAGGGA CGGTGTT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa.	1.7E-176	8

4472	cg43933591	1763	TCACGCCATAAG TGGAATTCCTCA TTC/TGAGTCGTT GACTTCTCGACG GAATG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa.	1.7E-176	8
4473	cg43933591	728	CCACACGGCATAAC ATCCACACACAC TIG/gap]CCTCGA GGGCTGGGAA GACTAAAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa.	1.7E-176	8
4474	cg43933592	400	GAGGCCCTAGTTA AGAAATCCTTGC C/C/T]TAGTGGTG AACAAAGGACTAA ACACA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA24081 EXTR2 PROTEIN - HOMO SAPIENS (HUMAN), 330 aa.	2.2E-176	1
4475	cg43985951	132	TAATATTAGTAAT TAAATAGCAACG C/T]TCATCCCC AACCGAATGTA CAAC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q99501 GAR22 PROTEIN - Homo sapiens (Human), 329 aa.	2.2E-176	22 (22q12)
4476	cg43985951	87	GGTCTTCAGAAC ACCGGGCTCGC CC[gap/G]CCTCC TCTAAGGCATT AATAATAT	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q99501 GAR22 PROTEIN - Homo sapiens (Human), 329 aa.	2.2E-176	22 (22q12)
4477	cg43985951	87	GGTCTTCAGAAC ACCGGGCTCGC CC[gap/G]CCTCC TCTAAGGCATT AATAATAT	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q99501 GAR22 PROTEIN - Homo sapiens (Human), 329 aa.	2.2E-176	22 (22q12)
4478	cg43313822	407	TTTCATGATGTT GCATAGGCTGG CA/T]CGGAATTC CAGGGCTCAAGT GATCCT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P16260 GRAVE'S DISEASE CARRIER PROTEIN (GDC) (MITOCHONDRIAL SOLUTE CARRIER PROTEIN HOMOLOG) - Homo sapiens (Human), 332 aa.	9.5E-176	10

4479	cg43989723	1552	ACTGTGCCTTGT TGCTCTGCTGGG G[G/gap]CCATAG CTGGCACTGCCC ACCGTAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
4480	cg43989723	1562	GTTGCTCTGCTGG GGGGCCATAGC TG[G/gap]CACTG CCCACCGTAAAG GCCCTGCG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
4481	cg43987060	151	TGGACAAGGG CATGAGGGGCG TGG[C/gap]CCCC CAGCAGGCAGC GGCGGTTCTT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04899 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN) - Homo sapiens (Human), 354 aa.	4.1E-175	3 (3p21)
4482	cg43967060	859	AGGCTTCAAACA GGGAGGCCTGT GG[C/gap]AACCC CTCCCCTACGTC TGGAGCTG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04899 GUANINE NUCLEOTIDE-BINDING PROTEIN G(I), ALPHA-2 SUBUNIT (ADENYLATE CYCLASE-INHIBITING G ALPHA PROTEIN) - Homo sapiens (Human), 354 aa.	4.1E-175	3 (3p21)
4483	cg43919107	101	AGATGAGGTCCC CTTCTCGGTGGA A[C/gap]CCCCAC ACCAGTGCTCTT CCCATGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q11206 CMP-N-ACETYLNEURAMINATE-BETA- GALACTOSAMIDE-ALPHA-2,3- SIALYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3- SIALYLTRANSFERASE) (ST3GALIII) (ALPHA 2,3-ST) (GAL-NAC6S) (STZ) (SIAT4-C) (SAT-3) (ST-4) - Homo sapiens (Human), 333 aa.	1.1E-174	11
4484	cg43967532	2654	CCTGGTCCCTTT GCTGTCACTATT A[C/G]ATAATGGA CTTGCACTTTTC CTCCC	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8

4485	cg43967532	3127	GATTACAATGTC CACTACTGACAG G[C/gap]GCAGTG CGTGTGTGTGAC CCACCGG	C	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
4486	cg43967532	3147	ACAGGCGCAGT GCGTGTGTGTGA CC[C/gap]ACCGG GTTCCCGGGCA CTGTCCCGC	C	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
4487	cg43967532	3150	GGCGCAGTGCG TGTGTGTGACCC AC[C/gap]GGTT CCCGGGCACTG TCCCCCCCCG	C	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
4488	cg43967532	688	CCCAGGACTCTA TCCAGAAATGATT A[T/C]TGTAAAGC TTTACAAATCCC ACCTT	T	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
4489	cg43967532	90	AAAAGCATGAAA ATAAAATGAACA C[G/AT]ACGGGA ATTACTATTAACA TAAGC	G	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
4490	cg43980846	294	AATCCGGCACAA GCTCTGTCTGTG C[G/C]ATCAAGG CTGACCCAGCAG CCTCAA	G	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P35212 GAP JUNCTION ALPHA-4 PROTEIN (CONNEXIN 37) (CX37) - Homo sapiens (Human), 332 aa.	2.8E-174 (1p35.1)	1
4491	cg43919276	1331	GAGGCAATAAAG A ATATTTGGCCTT C/ATTAATAAAAA AAAAAATAAAAA AAAAA	A	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD48057 RING FINGER PROTEIN A07 - MUS MUSCULUS (MOUSE), 456 aa.	3.7E-174	



4492	cg43083550	3035	CTGGGGTGGTG GCTCAGCCTGT AAIT/CICCCAA CTTTGGGAGGCC AAGGCA	T	C		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15430 LEUKOCYTE ANTIGEN CD84 - HOMO SAPIENS (HUMAN), 328 aa.	9.8E-174	
4493	cg43250735	298	AAGGGTGAACAC TGATTTTTTTTTT T/gap]CTTTTAG AAACAAAAACCA TCCAC	T	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q62609 NEURONAL OLFACTOMEDIN- RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL) (1B428B) - Rattus norvegicus (Rat), 485 aa.	1.2E-173	9
4494	cg43250735	384	ATCATCGCATAA ACTGAACATACG A/gap]GTTACC ACCTCAAGGGAA TAACAGA	A	gap		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q62609 NEURONAL OLFACTOMEDIN- RELATED ER LOCALIZED PROTEIN PRECURSOR (NOEL) (1B428B) - Rattus norvegicus (Rat), 485 aa.	1.2E-173	9
4495	cg43918085	242	GGGGCAGGAG CAACTTGTAATA ATT/GJAAAATGT AAACGTGAAAAA AAGGAT	T	G		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45699 HYPOTHETICAL 37.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 361 aa.	1.9E-173	
4496	cg43918085	263	AATTAAATGTAA ACGTGAAAAAA gap/AJGGATGGA ATAAAAGTCCCT ACTAT	gap	A		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45699 HYPOTHETICAL 37.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 361 aa.	1.9E-173	
4497	cg43281313	1153	TCAATTTCTTT CTGAGCCAGACT [A/G]GTTACGCT ATTCAAATCTTT CCC	A	G		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99496 DING GENE - HOMO SAPIENS (HUMAN), 336 aa.	2.5E-173	1
4498	cg43281313	1430	TAAATATTATGT ATTCTGACITTT gap/AJTTTTCCCC CGGAGTCTTGTA TATTT	gap	A		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99496 DING GENE - HOMO SAPIENS (HUMAN), 336 aa.	2.5E-173	1

4499	cg43281313	1632	ATTGTCATGCAA TGTCTTTTTTTTTT gap/TCCATTCTT TTCCCTGTAATT TTGG	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99496 DING GENE - HOMO SAPIENS (HUMAN), 336 aa.	2.5E-173	1
4500	cg43928859	1097	CCACAATAGGAA CATCAAAAGAAA ATT/GJTTCAGT TTGATTTTTTTT CTTT	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75598 HYPOTHETICAL SBI03 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	8.8E-173	12
4501	cg43928859	1145	TTTTTCTTTCT TAAAAAATAAA A/gap/GGAAAGTAA ATAAATTAAATTG CCAA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75598 HYPOTHETICAL SBI03 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	8.8E-173	12
4502	cg43928859	1226	TTCTTAAAAAAA GAGGGGGGGG G/gap/GCAGTAG GTGGAGTTGTG AAATATA	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75598 HYPOTHETICAL SBI03 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	8.8E-173	12
4503	cg43928859	1355	TGGCCTGTGCCA CAAGAGGCAGT GC/C/gap/AACCA TATTTTAGCAAAA GCTAGGA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75598 HYPOTHETICAL SBI03 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	8.8E-173	12
4504	cg43930118	101	CTCTGTAATACA ATGTGGTGAAAA C[G/A]TCTTAATT CAGGACATCTTC CACCT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD17940 SUCCINYL-COA SYNTHETASE ALPHA SUBUNIT (EC 6.2.1.5) - HOMO SAPIENS (HUMAN), 331 aa.	1.8E-172	2
4505	cg44000768	1448	CGGCCCTCAGCC CTGGACTGTTAG AG[G/A]TCTGC AGCTGCTCCTGC TCTCTGA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75500 PUTATIVE GLIALBLASTOMA CELL DIFFERENTIATION-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 334 aa.	9.1E-171	9

4506	cg44000768	1458	CCTGGACTGTTA GAGGTGCTGCA GCT/GGCTCCT GCTCTCTGATCT TATTGCT	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75500 PUTATIVE GLIALBLASTOMA CELL DIFFERENTIATION-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 334 aa.	9.1E-171	9
4507	cg43923012	101	CACTCCAACATA AAAAGTAGAATT CIA/GGCCACTTC CACTTAATATTCT ATAG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43210 HYPOTHETICAL 37.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 330 aa (fragment).	9.1E-171	X
4508	cg43923012	149	TAGAATGAAGTT GTACCACAAACC ATT/CIAGTAACCT ACACAGGGGGA AAAGTT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43210 HYPOTHETICAL 37.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 330 aa (fragment).	9.1E-171	X
4509	cg43923012	161	GTACCACAAACC ATAGTAACCTTAC AIC/gap/AGGGG AAAAGTTACTGA AATAAAA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43210 HYPOTHETICAL 37.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 330 aa (fragment).	9.1E-171	X
4510	cg43925222	4156	TAGGAAACCCCT TGTTGATCTTTTC TTA/GACTGGGAT GGGGCTGAGC ATGCT	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12765 HYPOTHETICAL PROTEIN KIAA0193 - Homo sapiens (Human), 346 aa.	4.3E-170	7
4511	cg43925222	4184	CCTTTGTGTATC TTTTCTGACTGG GIA/GTGGGGGC TGAGCATGCTTG TGCAGA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12765 HYPOTHETICAL PROTEIN KIAA0193 - Homo sapiens (Human), 346 aa.	4.3E-170	7
4512	cg43925222	4449	TTAGTGCTCAAT AATATAAGACCT GT/GTGTATTATA GAACGAGTCTTT CTTAT	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12765 HYPOTHETICAL PROTEIN KIAA0193 - Homo sapiens (Human), 346 aa.	4.3E-170	7

4513	cg43925222	4506	ACAGAGCAGGTA TATGCGCTGTTAG AT[C]CTTAGCTG TGGGGTTCCTT ACTAT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12765 HYPOTHETICAL PROTEIN KIAA0193 - Homo sapiens (Human), 346 aa.	4.3E-170	7
4514	cg43925222	4757	TCCTCAGTTGAG CTCTCAGCCCTTA GT[G]AAGGAAG CACGTGGAGGA GGGACGG	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12765 HYPOTHETICAL PROTEIN KIAA0193 - Homo sapiens (Human), 346 aa.	4.3E-170	7
4515	cg43941339	1563	CGAGTCTGGTCC CGACGATGCTGT G[C/gap]TCTGCC TCCTCCTGCTGC TGCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10451 OSTEOPONTIN PRECURSOR (BONE SIALOPROTEIN 1) (URINARY STONE PROTEIN) (SECRETED PHOSPHOPROTEIN 1) (SPP-1) (NEPHROPONTIN) (UROPONTIN) - Homo sapiens (Human), 314 aa.	8.2E-170 4 (4q21)	
4516	cg43251632	300	CTCCCACCCACGC CGGGCAGGCAC AG[C/gap]CATCT TTTTAAATCCG CGCTGATT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD38537 TRANSPORTIN-SR - HOMO SAPIENS (HUMAN), 975 aa.	2.5E-169	
4517	cg43251632	301	TCCCACCCACGCC GGGCAGGCACA GC[C/gap]ATCTT TTTAAATCCGC GCTGATT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD38537 TRANSPORTIN-SR - HOMO SAPIENS (HUMAN), 975 aa.	2.5E-169	
4518	cg44032718	152	ACGCACCCGGG AATCGCAGGAG GAC[A/G]AGGCT CAGCTCTTGCCA GGCCAAAT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa.	5.7E-169	X

4519	cg43926685	999	GGAAAGCTAAGA GGAAGATTCAAT Algap/AJTAACTA GCTTGAAGCCTG ACCTAG	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4520	cg43926685	999	GGAAAGCTAAGA GGAAGATTCAAT Algap/AJTAACTA GCTTGAAGCCTG ACCTAG	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4521	cg43926685	1032	GCTTGAAGCCTG ACCTAGCCAGAA GAlgap/AGTGCC TGTCGCTGCAG CCGCACC	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4522	cg43926685	1033	CTTGAAGCCTGA CCTAGCCAGAA Algap/AGTGCC GTCCGCTGCAG CCGCACC	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4523	cg43926685	1104	GTGTGTCTGGAA CACGCTGCTCCC CIC/gap/TGGGCC AGCTGTTGGGAT TCTGATT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4524	cg43926685	1109	TCTGGAACACGC TGCTCCCCCTGG GIG/gap/CAGCTG TTGGGATTCTGA TTAAAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)

4525	cg43926685	1133	GGCAGCTGTTG GGATTCTGATTA AA[A/gap]GAGGG GAAACGATCATC CTGGACAG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168	1 (1p36.33)
4526	cg43987324	279	TGGCCCCCCCCAA ACCTAACCTATC T[G/C]ACAAATCAA TAATCATCTTTTG ACTA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41895 ASB-3 PROTEIN - HOMO SAPIENS (HUMAN), 518 aa.	3.8E-168	2
4527	cg43959938	456	CCCTCTAGAGTT TTGCGGTTACTT CT[C/G]TAGGATG AATTCAGCACT GCAGG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13642 SKELETAL MUSCLE LIM-PROTEIN 1 (SLIM 1) (SLIM) (FOUR AND A HALF LIM DOMAINS PROTEIN 1) (FHL-1) - Homo sapiens (Human), 280 aa.	5.2E-168	X
4528	cg43280431	1032	TCGGAAATTTAG AAGCCATCTATG A[G/T]AGAAAGTT CAGTCACTTTAT TTATT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83025 KIAA1073 PROTEIN - HOMO SAPIENS (HUMAN), 643 aa.	2.9E-167	
4529	cg43942787	1269	ACTGGCATTITG AAGGCATGGCC CA[A/G]GAGAAG AGACACTAGCCA TAAATC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15327 NUCLEAR PROTEIN - HOMO SAPIENS (HUMAN), 319 aa.	3.6E-167	10
4530	cg43329903	1372	ACACCTCATTCT GGCCGAGAGTA GG[G/gap]CAGCT GCCTCCAGACTC TGGGGAGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16684 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.9E-167	12
4531	cg43949591	699	CTCTTTCACATC TGGGCACACGTC T[G/gap]CCTTCA GGCTGTAAGAAT TTCATTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.6E-166	18

4532	cg43949591	798	TCTCATCCCTTC CATAAGGAAAT G[C/gap]TCTGCC AATCAAGTTTC ATTCAGT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43008 HYPOTHETICAL 19.5 KDA PROTEIN - HOMO SAPIENS (HUMAN), 367 aa.	2.6E-166	18
4533	cg43996522	156	AGAACATAATTC TTTCCCAGAAGG G[G/gap]AAGGGG GAGCTATACTTA ATCGGAT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P56180 PUTATIVE PROTEIN-TYROSINE PHOSPHATASE TPTE (EC 3.1.3.48) - Homo sapiens (Human), 551 aa.	3.3E-166	
4534	cg43924431	1490	GCTCATGCCAT AGCAAACCCGC GG[G/AT]GCGCA GCGTGGGGCCC CG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.2E-166	5
4535	cg43924431	253	ATAAACTACAAC ACCCCTTCACA G[C/G]TCATAAA TTACCAATAATTA TCCA	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.2E-166	5
4536	cg43924431	353	ACCGTGTGGC CTCCACCCCCA CC[C/T]CAGTCTT TTACAGATGGTT TTTCAA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.2E-166	5
4537	cg43924431	596	GCTCTATGCCAG CATTTCTCCTTAA TTA/JTTAAGGAAT GTGAGCACCTTC CTTC	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q16637 SURVIVAL MOTOR NEURON PROTEIN 1 - Homo sapiens (Human), 294 aa.	4.2E-166	5
4538	cg43926509	8012	TCTACAGGACGA ATTGAGGCTTAA A/C/ATTTACTGT TAATGATACTGG TTTAT	C	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15165 CLONE 22 - HOMO SAPIENS (HUMAN), 306 aa.	4.2E-166	18

4539	cg43962058	308	AGTACAATCCAG TATATGCAGAA G/GC/TACTCAG CATCACACTCGT GATCAA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:075880 H-SCO1 - HOMO SAPIENS (HUMAN), 301 aa.	4.8E-165	17
4540	cg43962058	736	CGCAGGCAGGA ATGCACCTGGCTG TG[C/gap]CTCGC CCGCCCATGTCC TTCCACAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:075880 H-SCO1 - HOMO SAPIENS (HUMAN), 301 aa.	4.8E-165	17
4541	cg43951985	385	AAGAGACAAATG GAAACATTCCAT TT/AJCCCTTATTG AACAGAACTTTC TTTCAT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.5E-164	22
4542	cg43951985	588	TGCCCTTCCAAA GGTGGGCAATGT G[C/gap]CTCTTC CTGGAAAGGTTAT TTTACAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.5E-164	22
4543	cg43951985	601	GTGGGCAATGTG CCTCTTCCCTGGA A[G/gap]GTTATTT TACAAGCACGGG CCCCTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.5E-164	22
4544	cg43951985	709	GCAACTGTCCC GCCTTGAGTCTG AT/CJGTCAGAAG AGCATGTCAGTC CACTT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43357 HYPOTHETICAL 55.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 505 aa.	2.5E-164	22
4545	cg43936047	1255	CTGTGCACAAAC GTTTATACTAAA TT/AJAAATATCAA ACTACATTCTTCT GAA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD40550 P38IP - HOMO SAPIENS (HUMAN), 733 aa.	4.3E-164	13



4546	cg43936047	1574	GACTCAAAATTT TGGAGTGGTTGG C[G/A]TGCCTCTC TTCATTTTACTTT TTGA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD40550 P38IP - HOMO SAPIENS (HUMAN), 733 aa.	4.3E-164	13
4547	cg43936047	1578	CAAAATTTTGA GTGGTTGGCGT GC[C/gap]TCTCT TCATTTTACTTTT TGACTGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD40550 P38IP - HOMO SAPIENS (HUMAN), 733 aa.	4.3E-164	13
4548	cg43936047	669	GAGAAGAGGCC CAAGTGGCTAGC CA[A/G]TTCATTG CAGATGTCATTG AAAAAT	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD40550 P38IP - HOMO SAPIENS (HUMAN), 733 aa.	4.3E-164	13
4549	cg44003630	1615	GCTGCCGACAG CCAAGACGTACT GG[G/T]AGGAGA AAGCGCCGCCG TGAGCCCTG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
4550	cg44003630	1621	GACAGCCAAGAC GTACTGGGAGG AG[A/G]AAGCGC CGCCGTGAGCC TGGGTCTC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
4551	cg44003630	1622	ACAGCCAAGACG TACTGGGAGGA GA[A/G]AGCGCC GCCGTGAGCCT GGGTCTCC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
4552	cg44003630	163	GCAGGAAGATCC AACCCCTCAAAG C[A/T]GGTGGCAT GGGTGCCACTG GGAGGG	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	

4553	cg44003630	190	GATCCACCCCT CAAAGCAGGTG GC[AG]TGGGTG CCACTGGGAGG GGATCTGG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
4554	cg43945743	1071	TGAGTCCAGCA TTCACCTTCTCAC A[C/T]GGGCTTCT CCAAACGTGGCA GCGGCC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4555	cg43945743	1333	TCCAGTTTAAA AAAAA A[gap/A]GTCTTCT TAACCCCTGATGC TGCTCTC	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4556	cg43945743	1354	AAAAAGTCTTCT TAACCCCTGATGC T[G/gap]TCTCCC GACCATAGATTA GGGAAGC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4557	cg43945743	1519	TTAGACCTCCCC ACGAAACAAAGT G[G/gap]ACTCCT GTCCCTGCCAC TCAGCGG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4558	cg43945743	1531	ACGAAACAAAGT GGACTCCTGTCC C[C/gap]TGCCAC TCAGCGGCCAC CCCCCAA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4559	cg43945743	1615	TGTGAGCCCCAA GCCCAACCCGC AG[G/gap]ATCTT CCAGCCACATGA GGCCATTT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)

4560 cg43945743	18	CGTTTTTTTTTT TTTT[G/T]CCGA AATGACAAAGTAC CGTTTATT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4561 cg43945743	314	AAGTGCAGGAG CCCTGGGCTGG GGG[G/gap]CCTC TGGCCTCTGCAG CCGGGTGGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4562 cg43945743	73	TTACACAAATGA ACCCAGCCTCTG G[C/gap]TTGGGC ACCGTCCCACG GACCAGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4563 cg43945743	859	TCCAGCCCAGG GCCCAGGGTGG GGC[C/gap]ACAG GAGCTAACGGA GAACCTGGCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18827 SYNDECAN-1 PRECURSOR (SYND1) (CD138) - Homo sapiens (Human), 310 aa.	9E-164	2 (2p24.1)
4564 cg43920818	1929	AGAAGTAAAC TCAGAATGTAA A[A/T]CTTGTTT CTTTCAGTTTATT AAAT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15390 HYPOTHETICAL PROTEIN KIAA0009 - Homo sapiens (Human), 314 aa.	3.9E-163	8
4565 cg43963378	158	GAAAAATTAGGA CTGGAGGGGC AC[C/gap]AGTTC TTCCTAAGGGGA GCTTGAGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75064 KIAA0476 PROTEIN - HOMO SAPIENS (HUMAN), 1386 aa.	7.4E-163	1
4566 cg43922270	1062	TGAACAAGGGTG CCCATGTGGTTG C[C/T]CCTTCTGT CATCCAGAGAAA GTGCT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa.	1.3E-162	2

4567	cg43922270	777	AGTAGAGTCTTT TTTTTTTTTTTTT T/gapTTACATTG TCATTTAAGAAG GCTGC	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa.	1.3E-162	2
4568	cg43922270	778	GTAGAGTCTTTT TTTTTTTTTTTTT T/gapJACATTTGT CATTTAAGAAG CTGCC	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa.	1.3E-162	2
4569	cg43922270	802	TTACATTTGTCAT TTAAGAAAGGCTG C/gapJCCTGCGG TATTCATAATTCA TTGTT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14140 HYPOTHETICAL PROTEIN KIAA0127 - Homo sapiens (Human), 314 aa.	1.3E-162	2
4570	cg43949225	184	GATTGTTGCCT TGGATGCCCTG G/C/gapJAAATCT CGTGAGGCATTG AACTAGA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P05198 EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2- ALPHA) - Homo sapiens (Human), 314 aa.	1.3E-162	14
4571	cg43997225	1871	AACTGCAAGGG ATGCTGTATAGC A/A/GJACATCAG AAGTCGGAAGGA ACTGA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15777 FETAL BRAIN PROTEIN 239 (239FB) - Homo sapiens (Human), 294 aa.	2.1E-162	11
4572	cg43997225	2048	TAAATACCCAA GTTGTCCTCTTA CT/gapJTCCTCT CCCCCTCTCCCAT TTTGAC	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15777 FETAL BRAIN PROTEIN 239 (239FB) - Homo sapiens (Human), 294 aa.	2.1E-162	11
4573	cg43248117	1226	GAGTAAATGAGG GAGTCCAGTCCC C/A/GJGTGAATC TCCTTTTGCT TATCA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14894 MU-CRYSTALLIN HOMOLOG (NADP- REGULATED THYROID-HORMONE BINDING PROTEIN) - Homo sapiens (Human), 314 aa.	1.2E-161	16 (16p13.1 1)

4574	cg43965825	1557	AGGCATATTGA GCTCCACATTAA C[C/gap]TTGCGG CAGGCGTCTACT TGCTCTG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P17936 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3) (IGF-BINDING PROTEIN 3) - Homo sapiens (Human), 291 aa.	1.9E-161	7
4575	cg43965825	376	CTCAGTCATGGC CACAGTTGTATC A[TA]ATAGCATC TCTAACATTTCAT CTAG	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P17936 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 3 PRECURSOR (IGFBP-3) (IBP-3) (IGF-BINDING PROTEIN 3) - Homo sapiens (Human), 291 aa.	1.9E-161	7
4576	cg439657287	162	GGGCAGGGGT TTCAGGGGGCTC AG[C/gap]CTCTT CATGGGCGAGG CCTCAGCCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBL-NEW- ACC:CAB46375 HYPOTHETICAL 40.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 352 aa.	2.4E-161	3
4577	cg42712022	1386	TTAGAGGAAACA CATAGAGCTGGA A[C/gap]CTGTTA ATGGAAGCAGT CACAGCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75804 KI-1/57 INTRACELLULAR ANTIGEN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	2.4E-161	9
4578	cg42712022	1415	TTAATGGAAAGC AGTCACAGCTGA GT[gap]TTTTCG GAGAACCACAGGA AATTAAA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75804 KI-1/57 INTRACELLULAR ANTIGEN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	2.4E-161	9
4579	cg43993462	344	ATAGAGCTCAGC GATACAGAGGG CC[A/G]ACTGTCT ATGACGTTAAAC ATCTAC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5
4580	cg43993462	615	TGGAACCTGTAGT CTCACTTCTTAC C[gap/A]AAAAAA AAACAATGAAC GGATTCA	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5

4581	cg4393462	624	AGTCTCATTCT TACCAAAAAA A[gap/A]CAATGA ACTGGATTGAGC CCACTCA	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q63965 TRICARBOXYLATE CARRIER - RATTUS NORVEGICUS (RAT), 357 aa (fragment).	5.1E-161	5
4582	cg43926058	463	CCCACTGTGTGG CCGAGCTCTGG GG[G/gap]CCCTG CCTTGCCCTGCC CCTCCCTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76061 STANNIOCALCIN-2 - HOMO SAPIENS (HUMAN), 302 aa.	1.7E-160	
4583	cg43920504	134	ATGTATAAAG AAATTCACCCCT C[AG]GCTCTAT TCACTCTTTATC CTGAG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13291 SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE - HOMO SAPIENS (HUMAN), 335 aa.	2.2E-160	1
4584	cg43920504	626	TGTTCAATTTGG TTTTTCCATTTTC [AC]GCGAGAAA GGCCCTTTGTTG GTCCTC	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13291 SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE - HOMO SAPIENS (HUMAN), 335 aa.	2.2E-160	1
4585	cg43920504	636	GGTTTTCATTTG TCACGCGAGAAAG [G/T]CCCTTTGTT GGTCTCTGGTGT CAGC	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13291 SIGNALING LYMPHOCYTIC ACTIVATION MOLECULE - HOMO SAPIENS (HUMAN), 335 aa.	2.2E-160	1
4586	cg43134484	1242	CGAAGTGGCTCT CAGGGGCCAGT GA[G/gap]GGCTG GGCCACACAGAG ATGCATGCG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92788 RAD GTPASE - HOMO SAPIENS (HUMAN), 308 aa.	5.8E-160	
4587	cg43134484	1398	GGGAGGCTCTTC AGTGCGGTAGCT AT[C/T]TTGTTTAC ATGCAGATTTT GTAAT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92788 RAD GTPASE - HOMO SAPIENS (HUMAN), 308 aa.	5.8E-160	

4588	cg43929687	173	TTGTA CTAGGG C GTGGGCTGTTGC C[C/gap]TGGCAC GGCTGGATGAAC ACTTGCA	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB51351 DJ475B7.2 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 717 aa.	8.5E-160	
4589	cg43933630	574	GGTGGCAACGG C TTCGGGGCCCTCA GG[C/gap]ACAGT GTGGGGGCCCGC CTGCCTCCT	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC:A-1,3-D-MANNOSIDE B- 1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4 N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa.	1.4E-159	5
4590	cg43933630	677	GGCGGACCCCA C GGCCGGCCCAA GCC[C/gap]GACG CCAGGCAGAAC CCTTTGGGCG	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC:A-1,3-D-MANNOSIDE B- 1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4 N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa.	1.4E-159	5

4591	cg43933630	707	CCAGGCAGAAC CCTTTGGCGG GGC[C/gap]GTAT CTGGCCCTCCG GGGACGGCAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC:A-1,3-D -MANNOSIDE B- 1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4- N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa.	1.4E-159	5
4592	cg43933630	716	ACCCTTTGGCGG GGGCCGTATCTG G[C/gap]CCTCCG GGGACGGCAGT GACGACAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O77836 UDP-GLCNAC:A-1,3-D -MANNOSIDE B- 1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4- N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa.	1.4E-159	5
4593	cg43987224	406	CAACCATTC AAG GGTCAGGGCTCT G[C/gap]CTTCCC ACCAAAGGAGG GCCCCGAAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15785 HTOM34P - HOMO SAPIENS (HUMAN), 309 aa.	1.6E-159	20



4594	cg43987224	407	AACCAITCAAGG GTCAGGGCTCTG C[C/gap]TTCCCA CCAAAGGAGGG CCCGAACA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15785 HTOM34P - HOMO SAPIENS (HUMAN), 309 aa.	1.6E-159	20
4595	cg43987224	665	CTACAAGGGCAG CACTCAGTCTGC A[G/gap]CCCACT TGGGCAGGACA AAGCCAAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15785 HTOM34P - HOMO SAPIENS (HUMAN), 309 aa.	1.6E-159	20
4596	cg42718246	1431	GCTGCATGTTTT CAACTACAATAA GT[C/gap]CACTGTA ATAAAAAGTTTT GTTA	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13287 HOU - HOMO SAPIENS (HUMAN), 307 aa.	1.1E-158	2
4597	cg42831359	175	AGTGGGTTTTGG AACGGGAGGCA GA[G/gap]CATCT GGGACAGACC CTCCTGGAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75911 RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE RETSR1 - HOMO SAPIENS (HUMAN), 302 aa.	2.9E-158	1
4598	cg42831359	333	CCTGCCCTCCCTG TGGGGGTCAGTT AT[C/gap]ACCATCA GTCCTGTGCAAA GGTCC	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75911 RETINAL SHORT-CHAIN DEHYDROGENASE/REDUCTASE RETSR1 - HOMO SAPIENS (HUMAN), 302 aa.	2.9E-158	1
4599	cg43923892	2095	AAATTACTCCTA AAAAGTTAATATA T[C/gap]TCTGTAA AAGCAATGCTTT TCAA	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AA45558 CYCLIN ANIA-8A - RATTUS NORVEGICUS (RAT), 527 aa.	2.9E-158	3
4600	cg42910888	1140	TCACCCAGATGT CCCTTTGATGGC C[G/gap]TTGTGAA GGCCATTGGGA CCAATA	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa.	7.7E-158	8

4601	cg42910688	1389	GTGTTCTCTCTATG TTTGGATAGTAG GAJGAAGTAAAG CTTACAAGAAGT GCCT	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa.	7.7E-158	8
4602	cg42910688	1926	ATGTATAATCAG AAGTCTGAATTT TTT/CJATAAACA TATAGCATAAAA ACTTC	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa.	7.7E-158	8
4603	cg42910688	1949	TTTATAAAACATA TAGCATAAAAC[ T/CJTCAGTACT TTGGTTGACCCT TGTA	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55040 GTP-BINDING PROTEIN GEM (GTP- BINDING MITOGEN-INDUCED T-CELL PROTEIN) (RAS-LIKE PROTEIN KIR) - Homo sapiens (Human), 296 aa.	7.7E-158	8
4604	cg43272443	1395	AAGCTTTTTTTTT TTTTTTTTTTTTTT gapJGAGACGGAG TCTTGCTCTGTT GCCC	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa.	7.7E-158	1 (1p22)
4605	cg43272443	1461	TGCAGTAGCACG ATCTCGGCTCAC TTT/gapJGCACCC TCCGCTCTCTCAG GTTCAAG	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa.	7.7E-158	1 (1p22)
4606	cg43272443	1478	GGCTCACTTGCA CCCTCCGCTCT C/A/GJGGTTCAA GCAATTCTCCTG CCTCAG	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa.	7.7E-158	1 (1p22)

4607	cg43272443	1622	GCTGGTCTTGAA TTCTTGACCTCA G/G/TTGATCCAC CCACCTTGGCCT CCCAA	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P13726 TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III) (THROMBOPLASTIN) (CD142 ANTIGEN) - Homo sapiens (Human), 295 aa.	7.7E-158	1 (1p22)
4608	cg43921539	1602	CCTGCTCAAGCG GTCCGGGGAAT GG/G/TTTTTGT TTTTCTTCATTG TTGAG	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14661 SYNTAXIN-16A - HOMO SAPIENS (HUMAN), 303 aa.	2E-157	20
4609	cg43921539	3347	TGTTCAAGCTTT TTAAAGTGCTGA G/T/CJCTTACAAA CCCTGAAGGAA GGTGA	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14661 SYNTAXIN-16A - HOMO SAPIENS (HUMAN), 303 aa.	2E-157	20
4610	cg43921539	3476	CCCATTTGGGTA AAATAACGGATC T/A/GJATTAGAAA CTGTTTAAAGGA GGGGC	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14661 SYNTAXIN-16A - HOMO SAPIENS (HUMAN), 303 aa.	2E-157	20
4611	cg43984495	796	TGTTTAACCTCAA TGTAATGTGTAG A/TJCTAATACCTT TAGTGGGGGTACA AGT	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20774 OSTEOINDUCTIVE FACTOR PRECURSOR (OIF) (OSTEOGLYCIN) - Homo sapiens (Human), 298 aa.	4.2E-157	9
4612	cg43048935	315	TACAAAACATGT AGAAAGATGCCTC TT/CJGAGATGGC TTTAAATGCCC AGTAT	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78397 MYD88 - HOMO SAPIENS (HUMAN), 296 aa.	8.8E-157	3
4613	cg43048935	664	GCTCTCTTCCTC TCTCTGTGCTTC AT/CJTAGAGGTA TAAATACTGGTA CATTG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78397 MYD88 - HOMO SAPIENS (HUMAN), 296 aa.	8.8E-157	3

4614	cg43953563	400	GCAGACTTGTGC TGGTCAGTGAAC A/C/AJCTTTTTT TTTTTCACCAGT CTGT	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa.	1.1E-156	1
4615	cg43953563	414	TCAGTGAACACC TTTTTTTTTTTTT gap/TJCACACAGTC TGTGACATGGTG AATTA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa.	1.1E-156	1
4616	cg43953563	414	TCAGTGAACACC TTTTTTTTTTTTT gap/TJCACACAGTC TGTGACATGGTG AATTA	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa.	1.1E-156	1
4617	cg43953563	597	ACAGTGTGAAC CCATACCTGTCA T/G/CJGGCAATA GGAATGCATATT GATAAG	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa.	1.1E-156	1
4618	cg43953563	75	CATGAAGCCACC CATACAATCACA A/T/AJTTTATCTA ACACATTTAATT TGGA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P40855 PEROXISOMAL FARNESYLATED PROTEIN (33 KD HOUSEKEEPING PROTEIN) - Homo sapiens (Human), 299 aa.	1.1E-156	1
4619	cg43254730	1016	TTGAGATGAGGA ATTTAGAAGAT A/T/AJATGAAGC CTAAAAGATCAC TATCT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa.	1.8E-156	22
4620	cg43254730	279	TGAGGTATGGG GGTCACTGAGGA G/A/C/gap]CCCCCA GAGTCACTGACC CCTCCCGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa.	1.8E-156	22

4621	cg43254730	283	GTATGGGGGTCA CTGAGGAGACC CC[C/gap]AGAGT CACTGACCCCTC CCGCCACC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43800 NIPSNAP1 PROTEIN - HOMO SAPIENS (HUMAN), 284 aa.	1.8E-156	22
4622	cg43329580	241	CTGTCCCCCAGC CTGTGGGCAGT GC[C/gap]ACACG GCAGGCTAGGG GAGGGGTGA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA06742 SQV-8-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 327 aa (fragment).	3.4E-156	11 (11q13)
4623	cg43130238	188	AAAATTACAAAC AGCACTGATATT C[A/G]GCCAGTAT ACAAGTCTGGTC ACAGC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21222 UBIQUITIN SPECIFIC PROTEASE UBPA43 - MUS MUSCULUS (MOUSE), 368 aa.	7.1E-155	
4624	cg43950590	885	TCTGGAGGGTG GGGAGAAAGTGG CT[A/C]JAGTGTTA TAAGGTATACTG GACAAC	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75323 GBAS - HOMO SAPIENS (HUMAN), 286 aa.	1.9E-154	7
4625	cg43981925	2094	ACAAGGAACCGC TCGCCGCCGCC GC[C/gap]TCCGG TCACTGGCACGG ACTTCTGA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa.	6.4E-154	8
4626	cg43981925	710	CACACACACAGA ATTAAAAA [A/gap]TCAAAGG CAATCATTCTAA ATGTAC	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa.	6.4E-154	8
4627	cg43981925	710	ACACACACAGAA TTAAAAA [gap/AT]CAAAGG CAATCATTCTAA ATGTAC	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa.	6.4E-154	8

4628	cg43981925	737	CAAAGGCAATCA TTCTAAATGTACT [A/T]TGATAGCAT GTAAAGATGCA AGTA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa.	6.4E-154	8
4629	cg43934638	966	GAGAAAGGAGAA GCTTACAAAAA AA[A/gap]AAATC CTCTTCTATATTG CAGTGT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4630	cg43934638	967	AGAAGGAGAAG CTTACAAAAA AA[A/gap]AAATC CTCTTCTATATTG CAGTGT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4631	cg43934638	968	GAAGGAGAAGCT TACAAAAA A[A/gap]AATCCT CTTCTATATTGC AGTGTCT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4632	cg43934638	970	GGAGAAGCTTAC AAAAA A[gap]/ATCCTCTT CTATATTGCAGT GTCTCT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4633	cg43934638	1122	GGCTGAGTTTGT ATTATTACTGATA [T/G]GAAGAATAG AGTACCAATGTC ATTA	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4634	cg43934638	1222	TCTCAGATTG TAATCTCTCTTT [gap]/CJGGGAGCT GAGCTAGTGCTT TTAGGA	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5

4635	cg43934638	957	GTAGAACTGAGA AGGAGAAAGCTTA C(gap)/AAAAAAAA AAAAAATCCTC TTCTATA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4636	cg43934638	958	GTAGAACTGAGA AGGAGAAAGCTTA C(gap)/AAAAAAAA AAAAAATCCTCT TCTATAT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49069 CALCIUM-SIGNAL MODULATING CYCLOPHILIN LIGAND (CAML) - Homo sapiens (Human), 296 aa.	1E-153	5
4637	cg44001553	996	CCCAAGACCTTT AGCCCCCAAAGA G(gap)CACGGC CTCACCCCAACT GCCTGAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92559 MYELOBLAST KIAA0270 - HOMO SAPIENS (HUMAN), 345 aa (fragment).	3.5E-153	19
4638	cg44001553	167	ACTCAGGCAGAC TCCAGGGAGGA GG(gap)GGGG GTTCCACGGCTG ACGCCCAAG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92559 MYELOBLAST KIAA0270 - HOMO SAPIENS (HUMAN), 345 aa (fragment).	3.5E-153	19
4639	cg44001553	264	GAGGCAGGGAC CCAGGCTCCCAT CC(gap)AGGTGG CCCCTGTACCTG CCCTGCC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92559 MYELOBLAST KIAA0270 - HOMO SAPIENS (HUMAN), 345 aa (fragment).	3.5E-153	19
4640	cg43247677	2273	TGATCCCAATAA GTTGTAAACAG GIC/AAAAAAAAA AAAAAAAAAAAAA CAAGA	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14617 DELTA-ADAPTIN - HOMO SAPIENS (HUMAN), 1153 aa.	1.7E-152	19
4641	cg43928724	1932	CCTGGGCCAGG GTCTGTGTGAAT GT(gap)GGCAC TGGCCCAAGGTTT ATACCTTA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60539 PUTATIVE TUMOR SUPPRESSOR PROTEIN - HOMO SAPIENS (HUMAN), 289 aa (fragment).	4.1E-152	3

4642	cg43951092	104	TTTTTTTTTTTT TTATCTCCACAT T/ATGACATTTAT TAATAACATTTCT GG	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC: AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.5E-152	14
4643	cg43951092	291	TCTTTAACTAAA ACTCCAAGCAGG [G]TATCAGATAC AAACCCCAACTG CAGG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC: AAD45179 RIBONUCLEOPROTEIN - HOMO SAPIENS (HUMAN), 346 aa.	4.5E-152	14
4644	cg43930854	210	GCTCTATCCACC CCTACAGCTTCC C[C]TGGCCAAC CAGGTTCAAAGC CCATCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC: Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa.	2.1E-151	12
4645	cg43930854	325	CCACAGAGAGA GGATGGGAACT AG[G/A]GTAGAA GCTACAAGGGCT AAGAACT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC: Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa.	2.1E-151	12
4646	cg43930854	52	TTTTTTTTTTTT TTTCTACTGCAAA TTGTTTATTAAAA CA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC: Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa.	2.1E-151	12
4647	cg43930854	5410	AGAGGGTTGGAA TGAAGACTCCGA A[G/gap]CCACCA GGATGGGAAACA TGAGGCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC: Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa.	2.1E-151	12
4648	cg43930854	5410	GAGGGTTGGAAT GAAGACTCCGAA G[gap/G]CCACCA GGATGGGAAACA TGAGGCT	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC: Q14165 HYPOTHETICAL PROTEIN KIAA0152 - Homo sapiens (Human), 292 aa.	2.1E-151	12



4649	cg43988751	180	CGGCTCCAAGAA GGCCCCCAAGG GG[G/gap]ACTTA CCTTCAGGGGG CTGAGCCAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	
4650	cg43988751	180	GGCTCCAAGAAG GGCCCCCAAGG GG[gap/G]ACTTA CCTTCAGGGGG CTGAGCCAA	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	
4651	cg43988751	221	GCTGAGCCAAG GGGAAAGGGG TGG[C/gap]CCCA GAACAGGGGAA GGGCAGGCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	
4652	cg43988751	230	AGGGGAAAGG GGTGGCCCCAG AAC[A/G]GGGA AGGGCAGGCA TGGGGGAA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	
4653	cg43988751	43	TTTTTTTTTTT TTTTTTTTTTTG TTTGAAAACCA AACCTCAAAAAG CCA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	
4654	cg43988751	45	TTTTTTTTTTT TTTTTTTTTTGT GTTAAAAACCA ACCTCAAAAAGC CACT	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	7.6E-151	

4655	cg43135797	400	GGCATGGAGCG TGGGCCACGAG GGC[C/gap]ACCT CCCCAGGAGCC CACAGCAGCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O14732 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE 2 (EC 3.1.3.25) (IMP 2) (INOSITOL MONOPHOSPHATASE 2) (MYO- INOSITOL MONOPHOSPHATASE A2) - Homo sapiens (Human), 288 aa.	1.6E-150	18
4656	cg43135797	44	TTTTTTTTTTTT TTTTTTTTTTTG[C /gap]CCATTATTT TGATTATTGCAT TCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O14732 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE 2 (EC 3.1.3.25) (IMP 2) (INOSITOL MONOPHOSPHATASE 2) (MYO- INOSITOL MONOPHOSPHATASE A2) - Homo sapiens (Human), 288 aa.	1.6E-150	18
4657	cg43258297	60	TTTTTTTTTTTT TTTTATGGGGC[ A/G]CGGGGGT CTTATTCTGCA GATT	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB50866 DEOXYRIBONUCLEASE III (DNASE III) - HOMO SAPIENS (HUMAN), 304 aa.	3.8E-150	3
4658	cg43919239	1089	ATGCTTTCTGT CCCTGCAGGCG GA[gap/C]GCTGA ACCTCCGTTGCT GCTGGGAG	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
4659	cg43919239	1167	CTCTCTAAGTAG GCAATAGATCCA G[G/gap]CCCCCTA GGCTGTCCCCAC AGCCTCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	

4660	cg43919239	1167	TCTCTAAGTAGG CAATAGATCCAG G[ap]/GICCCCTA GGCTGTCCCCAC AGCCTCT	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
4661	cg43919239	1174	AGTAGGCAATAG ATCCAGGCCCT A[G]gap/GCTGTC CCACAGCCTCT GTCCTCG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
4662	cg43919239	1175	GTAGGCAATAGA TCCAGGCCCTA G[G]gap/CTGTCC CCACAGCCTCTG TCTTCGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
4663	cg43943351	1714	GGTGGGCGAG ATTCTGGACTGA GGATGGGCAG GGGAGGGAGAA AGGTGCTC	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa.	4.5E-150	17
4664	cg43943351	1880	ACTGGGGCTGA GCCGGGCCCTC CAG[G]gap/CTCA TGCCCGGCTGC AGGTGAACAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa.	4.5E-150	17

4665	cg43946935	162	ACGCGAAAGGTG TTTGCGGATCCG C[C]gap[GAGAAG TTGTTGGCCCCA GGAGCAT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60671 CELL CYCLE CHECKPOINT PROTEIN HRAD1 - HOMO SAPIENS (HUMAN), 282 aa.	1.8E-149	
4666	cg39524115	1245	TTCTCCTGCCTC AGCCTCCCAAGT A[A]GJCTGGGATT ACAGGCACGTAG CACCA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA13473 CD89_U11 - HOMO SAPIENS (HUMAN), 275 aa.	4.8E-149	
4667	cg39524115	1385	CCGGCCTTGGC CTCCCAAAGTGC TG[A]GATTACA GGCATGAGCCA CCACGCC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA13473 CD89_U11 - HOMO SAPIENS (HUMAN), 275 aa.	4.8E-149	
4668	cg39524115	1391	TTGGCCTCCAA AGTGCTGGGATT A[C]TAGGCATGA GCCACGACGCCT GGCCT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA13473 CD89_U11 - HOMO SAPIENS (HUMAN), 275 aa.	4.8E-149	
4669	cg43930377	718	CAATGTTGTTTAT ATAAGTATACCA C[gap]ATTATAAG TCTACTGGAGAT CCAAA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment).	7.8E-149	4
4670	cg43917492	1706	CGCCCAAAGTGAC TTGCTGAATACC A[T]CJACAAAAT CTGAACCCCAAAG ATGAG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa.	1E-148	4
4671	cg43917492	2086	ACTTTCATAC TG GTTATTTTTTTTT T[gap]TAATTCTG TCAGTGAGCAGC ATTTC	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa.	1E-148	4

4672	cg43917492	2087	CTTCATACTGG TTATTTTTTTTTTT T/gapJAATTCTGT CAGTGAGCAGCA TTTCC	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa.	1E-148	4
4673	cg43917492	2087	TTTCATACTGGT TATTTTTTTTTTTT gap/TJAATTCTGT CAGTGAGCAGCA TTTCC	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa.	1E-148	4
4674	cg43917492	3146	CGAAGCACCGTT GCTCGGAGCAG CC/C/gapJGGCGG GGAGCAGGAGC TCAGGGACA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60746 TETRASPAN NET-4 - HOMO SAPIENS (HUMAN), 268 aa.	1E-148	4
4675	cg43917036	1328	AGCATCCAGAG AAGCTCTGTCTG C/GA/CTGCAAA GCCATGGCTGCA GACATC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13239 PUTATIVE SRC-LIKE ADAPTER PROTEIN (SLAP) - HOMO SAPIENS (HUMAN), 276 aa.	1.3E-148	8
4676	cg43041577	2015	TGAAACCAGAA CTTTTTTTTTTTTT gap/TJAATCTGTA AATAGGTGTACT TTTTG	gap	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45767 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	2.7E-148	10
4677	cg43943919	68	GAGTCAGAACAT TAGACTTATAGT G/GA/JAGGAGCA GAAC/GAACCCCT GGCCTG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46921 DA159A1.1 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 399 aa.	2.7E-148	X
4678	cg44921374	1526	GAAAAATCTCT CTCAAAACAAAA CJA/gapJAAAAAA ACCTACACACAA CTGAGTG	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148 (12q23)	12

4679	cg4492:1374	1652	ACAAATGTACTA GTTCTTTTGT [A/gap]AAAAAGG GGTAGGATTAG GTTTCA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4680	cg4492:1374	1662	TAGTTCTTTTGT TTAAAAAGGGG [G/gap]TAGGATT AGGTTTCATATA TTAAAG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4681	cg4492:1374	2203	TGCATTTTCAGC AATATTATCGCC A[C/gap]AGACTC TGATTGCTCAGT CCACACA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4682	cg4492:1374	400	AGTTCAACTGTT CTCAATCTATGC TT[gap]AAAAAAA AAAATGACAAA TAATAA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)

4683	cg44921374	412	CTCAATCTATGC TAAAAA A[A]gapTTGACAA ATAATAAATTCTA CATTTC	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4684	cg44921374	412	TCAATCTATGCT AAAAA A[gap]ATGACAA ATAATAAATTCTA CATTTC	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4685	cg44921374	539	AGCTGTAACCTCA GTGTGTTTTC A[G]A[CTGCCTAC GTTAGTACCAGG TATTC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4686	cg44921374	583	GGTATTCATATA AACTCTGTAGAG G[C]TCATTTACA TTTCGTAAATTCT GTAA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCON-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)

4687	cg44921374	786	AATCAACTACTG ATCATAACAGCC C[A/C]ATTAAAAA CTCAAAACACTTT ATATT	A	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4688	cg44921374	855	ATCCAGCAATGC CAATATAGGTAA TTT/CJTATAGCC CCTATTGCAAA GTGAT	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
4689	cg43927534	317	TGATGTGTCATT CTCCCCAGCAG GG[G/gap]AGGG GGTGGAAATGGCT TGGGTTGTA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P23249 PROTEIN MOV-10 - Mus musculus (Mouse), 1004 aa.	9E-148	1
4690	cg43965796	131	CAAAAATTCACA GCGCCTGTGAG GA[G/gap]CCTTT GGCTGGAACTG GTGACACCT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
4691	cg43965796	383	AGCACCTCTCCC AGCTCCAGCCCA TTC/TJGGCTGGA GAGGAAAAGGG CAGAAAA	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
4692	cg43965796	462	CACACCTACTAC ACAGATGATAAA A[A/gap]TCCCAC AATCGTATCTGT TCATGTT	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1



4693	cg43985796	902	TGCTGTAGGCCT CCTCGAACATGG C[C]gap]TTGCAG GGGAAGCGGGC CTTCAGCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
4694	cg43942977	1171	TTCTCTCCAGC AGCCTGGGGG CA[G]gap]GGCAG AGCCTCCAGTCG GACCCCTT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.6E-148	
4695	cg43942977	1173	CTCTCCAGCAG CCTGGGGGCA GG[G]gap]CAGAG CCTCCAGTCGGA CCCCCTCC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q12846 SYNTAXIN 4 - Homo sapiens (Human), 297 aa.	9.6E-148	
4696	cg43281322	1073	ATGTCAACATTTT TGATTCTAGCTA C/TCTGTATTAT TCACCTAGCTTG TCC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P78380 LECTIN-LIKE OXIDIZED LDL RECEPTOR - HOMO SAPIENS (HUMAN), 273 aa.	5E-147	12
4697	cg43281322	2207	CCAGAAAACCCAC CAATCGGCTTTC AT/A]TTTGCAAT TTGTAGTTTATG TGAA	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P78380 LECTIN-LIKE OXIDIZED LDL RECEPTOR - HOMO SAPIENS (HUMAN), 273 aa.	5E-147	12
4698	cg43985545	134	AGAGCAGAAAG GGACACCTCCAT AGA/TGTGCTA TGGACCCATTTT TGCTTT	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q15013 HYPOTHETICAL PROTEIN KIAA0110 (HA06866) - Homo sapiens (Human), 274 aa.	6.3E-147	6
4699	cg43985545	292	CATCAGCCTATC AGGAATCTGAG G[G/A]GAGGCAG ACAACCAAGAGG AGAGTT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q15013 HYPOTHETICAL PROTEIN KIAA0110 (HA06866) - Homo sapiens (Human), 274 aa.	6.3E-147	6

4700	cg43985545	313	GAGGGGAGGCA GACAACCAAG GA[G/A]AGTTGCT TCCTCTCTCACC AGGAAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q15013 HYPOTHETICAL PROTEIN KIAA0110 (HA0666) - Homo sapiens (Human), 274 aa.	6.3E-147	6
4701	cg42718779	1443	GGGCTGAGAAT GAACCTGACTAG AG[C/G]TTCCTGGA GATACCCAGAGG TCCCCC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O75712 GAP JUNCTION BETA-3 PROTEIN (CONNEXIN 31) (CX31) - Homo sapiens (Human), 270 aa.	1.4E-146	1
4702	cg43937734	1520	GGTTCCTTGCCT CCTTCTGGTGCT C[C/gap]TACTCC AAGTCTATTTCAT TTTTCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE III) - Homo sapiens (Human), 259 aa.	3.5E-146	8
4703	cg43937734	2139	TCCTAGTATTTT CTTACCTGAAG[ G/T]AGGGCCATT TATTTTAAATTC ACT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE III) - Homo sapiens (Human), 259 aa.	3.5E-146	8
4704	cg43937734	561	CTCGCTGACCTA ATAAGGCCATGC A[gap/A]GTGTGC GGGGAGCTAC ATAAAAGC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE III) - Homo sapiens (Human), 259 aa.	3.5E-146	8
4705	cg42924529	168	AGTCTGGGACTC CTGGCCCTCCAG G[C/gap]CCCTCC TCTCCCAGAGAC CCTGATG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O15120 1-ACYL-SN- GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE BETA (EC 2.3.1.51) (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE- BETA) (LPAAT- BETA) - Homo sapiens (Human), 278 aa.	3.1E-145	

4706	cg42924529	186	CTCCAGGCCCT CCTCTCCCAGAG A/C/GCCTGATG CAGCTTGTTGGC TGGACC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O15120 1-ACYL-SN- GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE BETA (EC 2.3.1.51) (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE- BETA) (LPAAT- BETA) - Homo sapiens (Human), 278 aa.	3.1E-145	
4707	cg43961927	165	TTATTTTAACCCA GGCCAGGGAG G/C/gap/GAAGCT TCAATCCTGCTG CTTGGTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60828 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)) - HOMO SAPIENS (HUMAN), 265 aa.	4E-145	
4708	cg43961927	165	TATTTTAACCCA GGCCAGGGAG G/C/gap/C/GAAGC TTCAATCCTGCT GCTTGGTT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60828 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)) - HOMO SAPIENS (HUMAN), 265 aa.	4E-145	
4709	cg43985220	2180	TAAATTAACCTCAT TGCCGCTGGATT [C/A]TGTTTCAGCC TTTAAAAATATTT CTT	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa.	5.1E-145	8

4710	cg43985220	2369	GTGTTGTAATAAT TAAAAATGCTTC T[G/A]TAAAGTTT TCAAGGTAGGGA GTGAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa.	5.1E-145	8
4711	cg43985220	2420	TTTATTATTGTGT ATATCTAATATA T/gap]TAAAGTATG TGTGATACTAAG GTTTG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa.	5.1E-145	8
4712	cg43985220	2421	TTATTATTGTGTA TATCTAATATAT T/gap]AAGTATGT GTGATACTAAGG TTTGA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P29218 MYO- INOSITOL-1(OR 4)- MONOPHOSPHATASE (EC 3.1.3.25) (IMP) (INOSITOL MONOPHOSPHATASE) (LITHIUM- SENSITIVE MYO-INOSITOL MONOPHOSPHATASE A1) - Homo sapiens (Human), 277 aa.	5.1E-145	8
4713	cg43269627	319	TTTTGATAATAAG CAACCTTGATGAT A/GTCTATTCAA GAAAGCCAGAG CCCA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q15404 RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1) - Homo sapiens (Human), 277 aa.	1.1E-144	10
4714	cg43256169	289	CTGGGTGCCGC ACAGTCTGCTCC CT[G/C]GGGACA GAAACCCACAGG GTCGAGC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa.	5.9E-144	

4715	cg43256169	401	GGGAGGGCACA CAGGCTGGTG GCA[C/gap]CCAG TGCCAGGCCC CTTAGCTGGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa.	5.9E-144	
4716	cg43256169	414	GGCTGGGTGGC ACCCAGTGGCCA GG[C/gap]CCCTT AGCTGGGCCGC AGGCAGCAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa.	5.9E-144	
4717	cg43256169	428	CAGTGGCCAGG CCCCCTAGCTGG GC[C/gap]GCAGG CAGCACTGAGCC GCCTGGAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13098 G PROTEIN PATHWAY SUPPRESSOR 1 (GPS1 PROTEIN) (MFH PROTEIN) - Homo sapiens (Human), 471 aa.	5.9E-144	
4718	cg43983449	945	CCCTGAAAAGAA ATACACAGCCTA G[T/G]CATAGTAT ATCATATAAAGG TTATT	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4719	cg43983449	952	AAGAAATACACA GCCTAGTCATAG T[A/G]TATCATAT AAAGTTATTTT CTTAT	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4720	cg43983449	1041	TCCATAGTTCCC TTACTAGGCAGT G[C/gap]CACATA AAGTTATTAGTT AACATT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4721	cg43983449	343	CATAAGACAATG GAGCTTTAAAAA A[gap/A]GGTTAG GTTTACATCTTT AAAACT	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	

4722	cg43983449	650	GTCAGCAAAATG CCTTTGACTGAC G[C/gap]CCTGGA TTATTTTACCACT TAACCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4723	cg43983449	899	ATGGTAATAGTA ACTAAACTACAT C[C/T]AACCCCTGA AGGTAGAAAAAT CCCTG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4724	cg43983449	931	GAAGGTAGAAAA ATCCCTGAAAAG A[A/T]ATACACAG CCTAGTCATAGT ATATC	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
4725	cg43925411	61	AAACAAAGGTAC CAGTCGCCGCC GC[G/gap]GGAGG AGGAGGAGCCG GAGCCTCTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	9.5E-144	10
4726	cg43971525	103	ACCTCTGAAGTA AGGCACAACACA A[T/C]TCCATTGT CACTGTGGCAGA AGTCC	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment).	1.2E-143	11
4727	cg43971525	181	AAGACTGTGGTC CACGGGCCTAA GG[C/gap]ACTTG AGCTTTTCCCTC AACTGAAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment).	1.2E-143	11
4728	cg43971525	322	ATGAACATCAAG AATTACTAGACA T[G/T]TAAAAGTG TCITTAAGTGTC TTTCC	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75337 LIPRIN- BETA2 - HOMO SAPIENS (HUMAN), 783 aa (fragment).	1.2E-143	11

4729	cg44027658	1145	TGAGAGAAATT GAGATGTGTAAA A/A/gap]TCTAGTT ACTGCCTGTAAA TG GTGT	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
4730	cg44027658	191	GGCCTCGGGCA CCGCGTCCTGTG GG[G/gap]CGGCC GCCTGCCTGCC CGCCCGCCC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
4731	cg44027658	227	CCTGCCCGCCC GCCCGCAGCCC CTT[G/C]GCTGC CGGCCCTGGG CGGCCGCTG	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
4732	cg44027658	228	CTGCCCGCCCG CCCGCAGCCCC TTG[G/C]CTGCC GGCCCCCTGGG GGCCGCTGC	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)

4733	cg44027658	249	CTTGGCTGCCG GCCCCTGGCGG GCC[G/C]CTGCC ATGGGCACCGA CAGCCGCGC	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
4734	cg44027658	250	TGGCTGCCGG CCCCTGGCGG CCG[C/G]TGCCA TGGGCACCGAC AGCCGCGCG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
4735	cg4399829	1084	GAAGCAGGGCC CTGACTGCCCC CC[C/gap]GGCCC CCCTCTCGGGCT CTCTCACC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa.	2.1E-143	22 (22q11.2)
4736	cg4399829	1198	TAAATGCAAAGC ACACCTCGGCC GA[G/gap]GCCTG CGCCCTGACATG CTAACCTC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa.	2.1E-143	22 (22q11.2)



4737	cg4399829	1199	AAATGCAAAGCA CACCTCGGCGG AG[ <i>gap</i> ]CCTGC GCCCTGACATGC TAACCTCT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (human), 271 aa.	2.1E-143	22 (22q11.2 )
4738	cg43917524	372	CTTCCCAGTCTT TTTTTTTTTTTTT T[ <i>gap</i> ]GAGACAG GGTCTAGCTGTC ACCCAG	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43025 PTD017 - HOMO SAPIENS (HUMAN), 258 aa.	3.2E-143	
4739	cg44000122	153	CAAAGGTGGCAA ACATATTATTGC [C/A]TCACTGTAA ATAGAGAAAATC TTGT	C	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14657 TORSINB - HOMO SAPIENS (HUMAN), 266 aa (fragment).	6.7E-143	9
4740	cg44000122	399	GCAGCTGTGCTG TGATTATGAGAC A[G/A]ATACAATG ATTCACACTGGC TGGAA	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14657 TORSINB - HOMO SAPIENS (HUMAN), 266 aa (fragment).	6.7E-143	9
4741	cg44000122	988	AGACGGTGAAG GATTCACAGCC AG[G/C]GCTGTAT TAGCAGCTAGAG CGATGG	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14657 TORSINB - HOMO SAPIENS (HUMAN), 266 aa (fragment).	6.7E-143	9
4742	cg44020482	132	GGCAGGCGGAC CCCAGCCCCGG GGG[G/ <i>gap</i> ]ACAT GAGGGCCAGGG GAGGGCAGTG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q92561 HYPOTHETICAL PROTEIN KIAA0273 - Homo sapiens (human), 330 aa.	2.9E-142	8

4743	cg43334997	1155	CTGCGCTCTGAG ATGAGCTGCCCT C[G]GCTCCCT CCGGGTGGCG CGCCCGG	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75973 C1Q- RELATED FACTOR - HOMO SAPIENS (HUMAN), 258 aa.	2.9E-142	
4744	cg43958563	172	ATGACTGTATT ATTTGTACAAA T[C]GCAGTAACA CTTCTCTTTCC TCT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)
4745	cg43958563	341	AGTGGGAATGA AACAGGCAGAG G[C]gap]CAGCAG GTTCTCGGCTA GGGCTCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)
4746	cg43958563	354	AACAGGCAGAG GCCAGCAGGTTT CT[C]gap]GGCTA GGGCTCTGCCTA TAACGCCCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)
4747	cg43958563	368	AGCAGGTTTCTC GGCTAGGGCTCT G[C]gap]CTATAA CGCCCTGGTCCT GCTCATC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)
4748	cg43958563	369	GCAGGTTTCTCG GCTAGGGCTCTG C[C]gap]TATAAC GCCCTGGTCCTG CTCATCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)

4749	cg44984063	1836	AAATACAGTTAA ATGTGTTATTG CTT/gapJTTTAAAA TTATAAAAAAGCA AAGAGA	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13145 PUTATIVE TRANSMEMBRANE PROTEIN NMA PRECURSOR - Homo sapiens (Human), 260 aa.	6E-142	10
4750	cg44984063	1839	TACAGTTAAATG TGTTATTGCTTT TT/gapJAAAAATTAT AAAAAGCAAAGA GAAGA	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13145 PUTATIVE TRANSMEMBRANE PROTEIN NMA PRECURSOR - Homo sapiens (Human), 260 aa.	6E-142	10
4751	cg43951474	1863	ATGGCTCTGCCT GTCCTCCCCAG TTC/gapJCAACCAG GGTGGGGGGA CAGGGGCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76038 SECRETAGOGIN - HOMO SAPIENS (HUMAN), 276 aa.	6E-142	
4752	cg43951474	1864	TGGCTCTGCCTG TCCTCCCCAGT CIC/gapJACCAGG GTGGGGGGGAC AGGGGAC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76038 SECRETAGOGIN - HOMO SAPIENS (HUMAN), 276 aa.	6E-142	
4753	cg43951474	1918	AGTGCATTCAAT TTGTGCTTTCTT GATGGGCTTTC TGCTTAGTCTGA AAGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76038 SECRETAGOGIN - HOMO SAPIENS (HUMAN), 276 aa.	6E-142	
4754	cg43973724	2810	GCTTTATTCAA CTAAGGTACTTA CIC/JAAAAACCTT AGGTTTATACA GGTGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75070 KIAA0483 PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	1.3E-141	1
4755	cg43119818	1895	AGCCCTGCTTCT GACATAATCCAG TT/gap/JAAAAATAA TAATTTTAAAGAA ATAAA	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P00915 CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I) - Homo sapiens (Human), 260 aa.	6.9E-141	8 (8q22)

4756	cg43119818	2057	TAGTAATCTGTA AGCATAAGCTTA T[G]gap]CTTAAAT TCAAGTTTAGTTT GAGGA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P00915 CARBONIC ANHYDRASE I (EC 4.2.1.1) (CARBONATE DEHYDRATASE I) - Homo sapiens (Human), 260 aa.	6.9E-141	8 (8q22)
4757	cg43919223	208	ATCTTTTCTTAC AGGATTCCTTAC GTT]CAGGAATAG ATGGACATGGCC TGGC	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P41439 FOLATE RECEPTOR GAMMA PRECURSOR (FR- GAMMA) (FOLATE RECEPTOR 3) - Homo sapiens (Human), 243 aa.	1.4E-140	11
4758	cg43326633	3746	CCTCAAAGCCAG GTGCTGGCCAAA T]A/G]CCTTGATC ACAGCCTCCATG GCCAG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O15049 HYPOTHETICAL PROTEIN KIAA0341 - Homo sapiens (Human), 546 aa (fragment).	1.5E-140	
4759	cg43922710	125	CTCTACCCAGCT AAATACACATTAT [G]gap]GCATTTA GCAAACCTAACTT ACAAGT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74897 KIAA0874 PROTEIN - HOMO SAPIENS (HUMAN), 601 aa (fragment).	4.9E-140	
4760	cg43935709	449	ACAACAACCTATA TTTTGGACAAAA C]A/C]ATTTTTTTT TAATCTGTCCTG TAAA	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20
4761	cg43935709	505	TACTTCCTTTTGA GTCTCTGATGGC [C/T]ACAACATTT CATTGAGATGT TTGG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20
4762	cg43935709	695	TGCCCATGGTGG AAATGCTGGAAA A]A/T]TTAAAGGT AAGAAATAAAAC ATAGC	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20

4763	cg43935709	92	GATGGATAGATT TTTTTTTTTTAA[ A/G]GAAATTAGC CTCCCTGGGTAC TTAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20
4764	cg43935709	941	TCCTGCTGGCT TTCAATTCACAG G[G/gap]CCTGCA GCCITGTCCTG GAAGGTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20
4765	cg43950100	927	AGGATGGAAAG GTGGAAGGGTAA ATTG/AJGCACAG GGAGAAAAACAA AGTGTTG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14881 PIG8 - HOMO SAPIENS (HUMAN), 318 aa.	1.7E-139	11
4766	cg44030891	368	CCCCAGCCCTG GCTGCCCTCTGC GG[C/T]CCCCAC CCCAGCCCTGC CCCTAGGT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99750 MYOGENIC REPRESSOR IMF - HOMO SAPIENS (HUMAN), 246 aa.	2.1E-139	6
4767	cg43936172	355	ACCTCATGTCTC TGGGCCGGGAA GC[C/gap]ACGAT CCCTCATCCATC AGGCCTGC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60429 F17127_1 - HOMO SAPIENS (HUMAN), 528 aa.	2.7E-139	19
4768	cg43917807	1667	ACTCCCTTAGGC ATGCAGGTAAC G[gap/C]CCCCCA CGCCCCCCCCGC CACCTGCC	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa.	1.2E-138	17
4769	cg43917807	466	GAGAAGATTAAAC AAAGTCCCTTCT TTC/TCAATATCA GGATAGTCATGA GTTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa.	1.2E-138	17

4770	cg43917807	467	AGAAGATTAAAC AAGTCCTTTCTT C/C/TAAATATCAG GATAGTCATGAG TTGCA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa.	1.2E-138	17
4771	cg43917807	564	GAACATATGAGAT TCCTGCTCCCTC C/G/gapJGGGGAG CCAAGGAGCTTG CAACTGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa.	1.2E-138	17
4772	cg43917807	723	AGAGAAATGGACA GTGTGATCCTTG TT/CJTGTGCTAG CCATTGGGTGAT GCACC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q63742 P34 PROTEIN - RATTUS NORVEGICUS (RAT), 307 aa.	1.2E-138	17
4773	cg43285114	427	GCGGGCACCC GTGGGGTCTTTG GC/GA/GCTCAC AGGACAAATGGCA GTGGAGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD23440 LR8 - HOMO SAPIENS (HUMAN), 270 aa.	1.9E-138	7
4774	cg43303845	271	TGGTGTAGCCCC CTGGCCGCCGA AG/G/gapJAGGAG CCGGACACTTGT CTCCCGTC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa.	1.9E-138	
4775	cg43992302	1911	CATTCTCATTG TTTCATGTTTGA C/C/TTTTAAGGT GAAAAAAGAAAA TGGCC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O45934 Y43F4B.5 - CAENORHABDITIS ELEGANS, 595 aa.	4.5E-137	4
4776	cg43992302	2082	TTTGCATAAATC ATAAATGTATGT C/C/TJCTCTCTGA ATTGTTTAAATGT GTGC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O45934 Y43F4B.5 - CAENORHABDITIS ELEGANS, 595 aa.	4.5E-137	4

4777	cg43935076	229	CCAAACCCAAAG CAATTTGGGGTT CIA/GGCCAAGC CAGACAAAGGA CCCACAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4778	cg43935076	409	AAGTGAAAGGTT TGGGTGGCGTG GGC/gapJCTCAT GCCACACTGATT GGTCAGTA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4779	cg43935076	410	AGTGAAAGGTTT GGGTGGCGTGG GC/gapJTCATG CCACACTGATTG GTCAGTAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4780	cg43935076	443	ACACTGATTGGT CAGTAGACAGG GGG/gapJACAT GCCAAACACCAC AGGGCATC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4781	cg43935076	450	TTGGTCAGTAGA CAGGGGGCACAC TG/gapJCAAAAC ACCACAGGGCAT CAGATGCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4782	cg43935076	451	TGGTCAGTAGAC AGGGGGCACAT GC/gapJAAACA CCACAGGGGCATC AGATGCTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4783	cg43935076	629	ACACTGTTTAA GCAGTATGTTTA AT/gJGGATGAT TTCCACAAACTA TCCAC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1

4784	cg43935076	643	AGTATGTTTAATT GGATGATTCCA C/TJAAACTATCC ACGAAGTTTCTA ACCA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
4785	cg43952219	675	CAGTGGTTAGTA GTTTTTTTTTTT T/gapJCCTTTTT TAAAGCATAAGC AATAG	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa.	2.5E-136	X
4786	cg43922796	692	CAGGGCACCCAG ACAGCAGCGGC CCCT/CJTTCCCA GGAGGTACAGG AGACAGGA	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q00004 SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68) - Canis familiaris (Dog), 622 aa.	3.2E-136	1 (1q42)
4787	cg43947491	537	AAACTTTTAATTGAT ATGAGAAATTACA T/CJCTGTCAAAG ACCTGGGCAGTA CACT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P30040 ENDOPLASMIC RETICULUM PROTEIN ERP29 PRECURSOR (ERP31) (ERP28) - Homo sapiens (Human), 261 aa.	1.8E-135	12
4788	cg43994220	136	TGCCCTTTGAAGT CAGTTCTGGGT T/C/gapJCCCAGC TCTGGCTGACCA TTTTGTT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
4789	cg43994220	186	TCCCTGAGTGTC TGAGTCCCCGG CA[G/gapJGCGGC CTTCACTCAGGG TCAGCGGG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
4790	cg43994220	187	CCCTGAGTGTCT GAGTCCCCGGC AG[G/gapJCGGCC TTCACCTCAGGT CAGCGGC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19



4781	cg43948495	1584	CGCGGAGCGTG CGGTCTGGACCA CC[C/gap]AAGGG AAAACCCCTCAT TTTAGCAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4782	cg43948495	1623	TCATTTAGCAC AGCGGCCTGG GC[T/A]GCGTCC AAGCTCTCGTAC TGAATAT	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4783	cg43948495	1649	GCGTCCAAGCTC TCGTAAGTAATA T[A/G]GGCAAAG CTATCTCCTTTG ACGIGA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4784	cg43948495	1707	TCCGAATGCTCC CAAAGCGGTCAA A[C/T]TCTCGGGC CAGAGCCGCCA GIGACG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4785	cg43948495	1708	CCGAATGCTCCC AAAGCGGTCAA C[T/C]CTCGGGC CAGAGCCGCCA GTGACGT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4786	cg43948495	2526	GAGGCTGATCTC GCCGAAGCGCTT G[gap/G]AACTGG TGGAAGAGCCG GTCCTCGA	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4787	cg43948495	2567	CGGTCCTCGAG GTGCTCGGCGG GCA[G/T]CGCGA GGGCCAAGGCG CCGGGGAAG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3

4798	cg43948495	2573	TCGAGGTGCTCG GCGGGCAGCGC GA[G/C]GGCCAA GGCGCCGGGGA CGCGAATC	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4799	cg43948495	2579	TGCTCGGGGG CAGCGCAGGG CCA[A/C]GGCGC CGGGACGCGA ATCACCGCG	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4800	cg43948495	28	TTTTTTTCAGGTT TAAAAATCCATC[ C/gap]TCTGTCAA AGTTTTTACTGA CAACT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4801	cg43948495	31	TTTCAGGTTTAA AAATCCATCCTC T[gap/C]GTCAAA GGTTTTACTGAC AACTTTC	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4802	cg43948495	409	CTAGCTTGCCCA ATGTCCTTAGTG CT[A/G]ACTGGA GGTACTGCTGG GAAAAGT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4803	cg43948495	463	GGGTGGGAAGG CGTAGAGCATGC CT[gap/T]GTGCC GTCTCTGCCCTT GGACCCCC	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
4804	cg43948495	510	CCCCCACTGG CAAGCTGATCAC CC[C/gap]TGCGG CCTGCTTCTGTT TCAAGTAG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3

4805	cg43916993	1938	ATCCGCTTGATT CCACTTGGTTT GT/AJAAAGTTT CCAAATCTTTGG AGAGT	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
4806	cg43916993	833	CCACAAAGGG GGACGATCACG GCC[C/gap]AGCA AAAGCGATGCTG AGAGGGGAA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
4807	cg43916993	855	GCCAGCAAAAG CGATGCTGAGAG GIG/AJGAAACAG TCCAGAGTCCAA CAGCAG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
4808	cg43916993	945	TATGTATAGGG CCGGGGCTTC TGIC/gap]CCAGG GCTCCCTGGAC CAGGACGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
4809	cg43916993	947	TGTATAGGGGCC GGGGCTTCTG CC[C/gap]AGGGC TCCCCTGGACCA GGACGCCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
4810	cg34758981	1158	TTTTTATTAAATAC AAGTCACTTT A/CJAAAAATTTG GATTTTATAT ATA	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPR0T-ACC:P48307 TISSUE FACTOR PATHWAY INHIBITOR 2 PRECURSOR (TFPI-2) (PLACENTAL PROTEIN 5) (PP5) - Homo sapiens (Human), 235 aa.	1.6E-132	7
4811	cg42910848	281	GACAGGTGTGG GAGGTAGCTCGA AA[C/T]ATACAGA GTGTTCCGAACA CTAGAG	C	T			SILENT- NONCODI NG 888	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa. (fragment).	3.1E-132	

4812	cg42910848	295	G TAGCTCGAAAC ATACAGAGTGT C[G/A]CAACACTA GAGACGTCTTCT GGCTG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14988 GTPASE- ACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 308 aa (fragment).	3.1E-132	
4813	cg43317146	162	CAGCTTTGCTGA AACTGTACTTTG G[G/A]CTCCAGA CTTCACTGTCTC TAGGCA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30567 H5AR - MUS MUSCULUS (MOUSE), 330 aa.	5.3E-132	4
4814	cg43317146	81	AGATTCATTTTCT TGAGTGGCACTG [C/gap]CATGCTC ATTCAGTGAAAA CTTGIG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30567 H5AR - MUS MUSCULUS (MOUSE), 330 aa.	5.3E-132	4
4815	cg43317146	82	GATTCATTTTCTT GAGTGGCACTG C[C/gap]ATGCTC ATTCAGTGAAAA CTTGIG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30567 H5AR - MUS MUSCULUS (MOUSE), 330 aa.	5.3E-132	4
4816	cg43957878	85	TCCCACTACAAA AATACAGAGGAG ATT/CJAGGGTGT TCCTGTATCCGC CTCAT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99753 CISPLATIN RESISTANCE ASSOCIATED BETA PROTEIN - HOMO SAPIENS (HUMAN), 252 aa.	7.1E-132	1
4817	cg43087636	1059	TAAATTTATTTT TAGGAAGTCAAA T/AJAAATATAATA AAGGGTTGAGCC CTC	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30793 GTP CYCLOHYDROLASE I (EC 3.5.4.16) (GTP-CH-I) - Homo sapiens (Human), 250 aa.	1.5E-131 (14q22.1 )	14
4818	cg43087636	1145	AAGTGAAGTCTC AATAGTGTAAGT A[C/T]GTGCACAA AACCAGTCCAG ATAAC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30793 GTP CYCLOHYDROLASE I (EC 3.5.4.16) (GTP-CH-I) - Homo sapiens (Human), 250 aa.	1.5E-131 (14q22.1 )	14

4819	cg43087636	1314	TTTCTTCTCTCCA ATAAAAGTGGTG TIA/GIGTGCCGA AAGTGCTAAAT ATTAG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30793 GTP CYCLOHYDROLASE I (EC 3.5.4.16) (GTP-CH-) - Homo sapiens (Human), 250 aa.	1.5E-131	14 (14q22.1)
4820	cg43918679	1275	TGCCTGTCTACA CCAGTCCTGTCC C/C/gap/JAGGACT CCCCTTCTGTGG TCTGGAG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3E-131	21
4821	cg43931621	1023	GCATTAGAATGC TGGATGAGACTT A/A/gap/JAAGCTT CAGTTCACCTGTA AAACTA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment).	4.7E-131	5
4822	cg43931621	1025	ATTAGAATGCTG GATGAGACTTAA A/A/gap/JGCTTCA GTTCACTGTAA AACTAA	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment).	4.7E-131	5
4823	cg43931621	760	AACCGTGTCTAT AATTTTTTAAAG [G/A]AAAAAACCT GCTTCCAAAC TTAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment).	4.7E-131	5
4824	cg42859936	185	TACTTGGAAATAC ATGCCATTATCT C/T/C/GCATTTTA CAAATAAGAAAT CAICA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99644 DELTA SARCOGLYCAN - HOMO SAPIENS (HUMAN), 256 aa.	8.1E-131	5 (5q33)
4825	cg42382358	1842	CTCCCCACCCAC CACCCTCCCG CG[G/gap]CAAGC CAGCCCCGTGCA CGGAAGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P08294 EXTRACELLULAR SUPEROXIDE DISMUTASE [CU-ZN] PRECURSOR (EC 1.15.1.1) (EC-SOD) - Homo sapiens (Human), 240 aa.	5.7E-130	4 (4pter)

4826	cg43948922	1714	GGTCCGAGGAC AGAAGCGGCCG GTG[G/gap]CGGG ACGCAGGGGAG GCAGGGTGAC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75190 MSJ-1 - HOMO SAPIENS (HUMAN), 241 aa.	1.2E-129	11
4827	cg43948922	735	AGAGATTACAA CAATTTTAAAGA C[A/gap]AAAAAA AAATGGTCCTA TTATGTG	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75190 MSJ-1 - HOMO SAPIENS (HUMAN), 241 aa.	1.2E-129	11
4828	cg43948922	745	AACAATTTTAA GACAAAAA A[A/gap]TGGTCC TATTATGTGGTC CCAACAA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75190 MSJ-1 - HOMO SAPIENS (HUMAN), 241 aa.	1.2E-129	11
4829	cg43928955	225	GGCGAAGAGCT GGGTCCTGCAG CTC[C/T]GGTGG GAGCCTCCTCAG TTCTTTTC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4830	cg43928955	254	GGGAGCCTCCT CAGTTCTTTTCG GAT[C]GCACTCC ACCCCGCGAAT CCGGTG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4831	cg43928955	315	TGCGGAGAGCG GGCTTAGTGCC TC[G/C]CCGGCT TCGTGGCCTCCC AGGCTTC	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4832	cg43928955	337	CTCGCCGGCTTC GTGGCCCTCCCA GG[C/T]TTCGCTC TGACCCGTGCTG GGCTGG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	

4833	cg43928955	364	TCGCTCTGACCC TGTCTGGGCTGG ATTCJGGAGGCC GGACCGCCCTTC CTGGCG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4834	cg43928955	460	AGGATAGACGG GCGGGTGACCC GTGA/GJCCCG TACCCACGAGTT TGGGTCCC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4835	cg43928955	486	CCCCGTACCCAC GAGTTTGGGTCC CTTCJTGAGGCAT CTCTCCAGGCCT CTGCC	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4836	cg43928955	667	TTGAGAACCCCTC TCGAGGAGTCTG GIC/GJCTCATGA GGATGCCAGAAC AAJGG	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-129	
4837	cg43950545	203	ATCCCCACAAC AGATAGAAATGAA TTTCJTTTTTAGG AGCAATGACAT GCCTT	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	3.5E-129	13
4838	cg44938448	103	AAGAATCATAGA CAGCTACTACCA C[G/A]GCTGCTTC GTTTGGACAAA ATAAC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4839	cg44938448	963	CATGTAAAAAGC TGCTTTGTTGGC C[C/T]GTTATTCC CACTGACCCGTC TGAGT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1

4840	cg44938448	1149	CCATGGTAATTT TTCACAAATTAAA JAGJACACATTT GGGTTGTGCAAC AGTG	A	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4841	cg44938448	129	GCTGCTTCGTTT GGACAAAATAA CIC/GIAGGAGGC ATCCACGGGATT AGTTAC	C	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4842	cg44938448	1284	TTTTCTTTTTAA CCTTTTATGCC T/AJTTCAGTAGG GGAAGTTTCCTT GAAA	T	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4843	cg44938448	1311	GAAAGTTAGAGA GCTGCAATCTC TTT/gapJAAGTATC AATGTAAGAAG CAGATG	T	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4844	cg44938448	1321	GAGCTGCAATC TCTTAAGTATCA AT/CJGTAAAGAA GCAGATGACCCA ATTGG	T	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4845	cg44938448	1332	CTCTTAAGTATC AATGTAAGAAG CA/CJGATGACC CAATTCGGAAGG TGGTTC	A	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4846	cg44938448	166	ACGGGATTAGTT ACACGGTATCAA CT/CTTACCACCA CAGCAGAATCAA CAGTG	T	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1



4847	cg44938448	6409	CGCGGCTGCCC GTTGGTTCGCGC CGA/GGCCGTT CTACTCCAGGCA GACGGGA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4848	cg44938448	6463	GAACACGGCG CCTCAGCGTCCC CTG/CJCCCCGTT GGTCTGCTCGG GCCCTT	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75035 KIAA0447 PROTEIN - HOMO SAPIENS (HUMAN), 254 aa.	4.8E-129	1
4849	cg43972431	1024	GAAGAAGTTTAA CACTGGAGAATT C/GA/CTATGGTG AGCCTAAGCAAT ATATA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD16888 CDC42 EFFECTOR PROTEIN 3 - HOMO SAPIENS (HUMAN), 254 aa.	7.1E-129	2
4850	cg43931286	1069	GGATGAGTTC TTTGTAAGGGTG G/G/gap/CAGGCC TCGTAAGAAAGA TGTAGCA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27775 30S RIBOSOMAL PROTEIN S7 HOMOLOG - HOMO SAPIENS (HUMAN), 242 aa.	1.4E-128	17
4851	cg43298916	116	GCTATGGCATCT TTAATTATAAAA [gap/A]TAAGCAA ATAAAATAACTT GCATCT	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa.	1.7E-128	8
4852	cg43298916	193	TTTATATGCACAT GGAGCTTAAAAA gap/AJTGTAAATT AACAAATAATAAT GACA	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa.	1.7E-128	8
4853	cg43298916	2603	GTGGTCTCAGG GGAGCAGGGGA AA[gap/G]ACAT GGCAGAGGAAG TTGGTAAAG	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa.	1.7E-128	8

4854	cg43298916	425	ACGAAGCTTTGG AAGTTTAAGGG G[ap]/G/AATTGG AGGAGTAGGG TGGGGGAA	gap	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P52823 STANNIOCALCIN PRECURSOR - Homo sapiens (Human), 247 aa.	1.7E-128	8
4855	cg44128041	940	ATATATTTATGG CCGGGCAGGGT GT[G/ap]GGGCC ATGCCTCCTCAG GAGCCGAA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	
4856	cg44128041	943	TATTATGGCCG GGCAGGGTGTG GG[G/ap]CCATG CCTCCTCAGGAG CCGAAGCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	
4857	cg44128041	1082	TGCAGGACCTCG TGCCACCCCGA GG[G/ap]CTGAG CCTGGTCCACG AGGGTGCC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	
4858	cg44128041	1115	TGGTCCCACGAG GGTGCCGTGTC CC[C/ap]TGACA GGGCCAGTGCA GTTTGGTGT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	
4859	cg44128041	1153	TGCAGTTGGTG TGTCCTCCGCCT TTT/A]CCAGGAGA AGAACCTGAAGA ACTAT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	

4860	cg42891437	989	GGGACAGGGC CTGGAGTCAGAG CT[G]GGGGC GTGAGGGGCGA AAGGGGAC	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75425 ORF3,SPLICEVARIANT_B - HOMO SAPIENS (HUMAN), 235 aa.	2.4E-127	7 (7q21)
4861	cg42891437	991	GGACAGGGCCT GGAGTCAGAGCT GG[G]GGGCGT GAGGGGCGAAA GGGGACAA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75425 ORF3,SPLICEVARIANT_B - HOMO SAPIENS (HUMAN), 235 aa.	2.4E-127	7 (7q21)
4862	cg43995142	110	GTTTCTCATTTTG TTAAAGCTGCAA G/gap]CAAGTTTC TTTCACAAATTACA CTTC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60660 ASH2L1 - HOMO SAPIENS (HUMAN), 628 aa.	8E-127	
4863	cg43949897	913	GGAGCCACCAA GCACTTTGAGC TG[G]gap]CCTCG CCCCCTAGGAG GAGAGGGTC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60499 SYNTAXIN 10 - HOMO SAPIENS (HUMAN), 249 aa.	1.8E-126	19
4864	cg42549778	1633	TGTGTGTGTGCA CTGCTGTGTGTG T]gap/G]TGACG CACAGGAAGCCT TTCCACA	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD29690 PUTATIVE ZINC FINGER TRANSCRIPTION FACTOR OVO1 - MUS MUSCULUS (MOUSE), 267 aa.	3.7E-126	
4865	cg44002192	1646	GGACTACATCTC CCAGCCCTTCAC G[C/]GTTAAATA TGAGTGGTTTA AAAGG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75204 HYPOTHETICAL 25.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 238 aa.	1.5E-125	16
4866	cg44002192	2337	AAGACCTTCAGT GTAGATCCAGAT G[G/]C]CCAACT GTCCTTGTTAAG TTACTT	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75204 HYPOTHETICAL 25.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 238 aa.	1.5E-125	16

4867	cg44002192	2876	ACTGGTCATCTC CTGAGGACCTGT A/C/AJATGACCT GTGGACTGTTCC GCACG	C	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75204 HYPOTHETICAL 25.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 238 aa.	1.5E-125	16
4868	cg43949061	863	GCCCGGGAGTG TTCCGAACGGAG CTG/CJGCTCCG CCACGCCCACTC CTACCCC	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19
4869	cg43307940	36	TTTTTTTGATTTT TTTTTTTTTTTTTG TGTAGCATAGT GAGTGGAGTTTA TTT	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09861 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.1E-125	15
4870	cg43307940	37	TTTTTTTGATTTT TTTTTTTTTTTTTG G/TJAGCATAGT GAGTGGAGTTTA TTTT	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09861 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.1E-125	15
4871	cg43307940	46	TTTTTTTTTTTTT TTGGTAGCATAGT T/AJGAGTGGAGT TTATTTTTATAAT TTG	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09861 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.1E-125	15
4872	cg43307940	887	TGTCAGAAAAAT CAATAGCATCAA A/AgapJCTGGTC TAACGTAGCACC TAGATT	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09861 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.1E-125	15
4873	cg44002548	1707	ACCGGAATTTTA TATTAAGGGG C/C/AJTCCTTTT AAATATATGCCG TGTA	C	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45746 HYPOTHETICAL 49.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 454 aa.	1.1E-124	17

4874	cg43988302	179	AGCAGGAACCTC CTCACCCACCC TTG/gapGGGCC TGCCTGAGTCAT TCTCCGT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:O75352 SL15 PROTEIN - HOMO SAPIENS (HUMAN), 247 aa.	3.8E-124	17
4875	cg43988302	382	AAACATTGGC CAGGATAGTGT AIA/CJACAGCTG GAAATTGCTGCT AGAGGA	A	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTRMBL-ACC:O75352 SL15 PROTEIN - HOMO SAPIENS (HUMAN), 247 aa.	3.8E-124	17
4876	cg43303925	1244	TTGGTTACAAGA TCCAGACTTGGG CIC/TJGAGCGGT CCCCAGCCCTCT TCAITGT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40851 SIRTUIN TYPE 3 - HOMO SAPIENS (HUMAN), 399 aa.	4.4E-124	11
4877	cg43920467	661	AGAGAAGCCATG AGTTTCCACAG CIA/GICAGAGT GAGTCCTGAGCA CAACAC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q06136 FOLLICULAR VARIANT TRANSLOCATION PROTEIN 1 PRECURSOR (FVT-1) - Homo sapiens (Human), 332 aa.	4.9E-124	
4878	cg43920467	779	AAAGAAAGAGAG AGAGAGAGAGA GAC/GJAGAGAG ACAGAGAGACAG AGAGACA	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q06136 FOLLICULAR VARIANT TRANSLOCATION PROTEIN 1 PRECURSOR (FVT-1) - Homo sapiens (Human), 332 aa.	4.9E-124	
4879	cg43927337	992	GCAAGATGAATG GGAAAGAAAATA TTT/gapJAGCTTAA GATCTGTTTGCA AATGGA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa.	1.1E-123	14
4880	cg43927337	1300	TGCACTGAGTCA GCTCAAGTGTGC CIA/gapJAAAAAA AAAAA CAACAC	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa.	1.1E-123	14

4881	cg43927337	1318	GTGTGCCAAAAA AAAAAAAAAAAA A[A/gap]CAAACA CCAAACAACAAC AAACAAA	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa.	1.1E-123	14
4882	cg43927337	830	TGGGAAGCAAGT GGCTGAGGGC TC[A/G]GCTGGG ACTGGGAGGGA AAGGGCTA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q92537 HYPOTHETICAL PROTEIN KIAA0247 - Homo sapiens (Human), 303 aa.	1.1E-123	14
4883	cg43948130	519	TTGTGGTTTTTG TTTTTTAAAAAA [A/gap]GGCCCCC AGGGCAAGTTAT TTACAG	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13243 SPlicing FACTOR, ARGinine/SERINE-RICH 5 (PRE-MRNA SPlicing FACTOR SRP40) (DELAYED-EARLY PROTEIN HRS) - Homo sapiens (Human), 272 aa.	2.4E-123	14
4884	cg43948130	519	TGTGGTTTTGT TTTTTTAAAAAA [gap/A]GGCCCCC AGGGCAAGTTAT TTACAG	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13243 SPlicing FACTOR, ARGinine/SERINE-RICH 5 (PRE-MRNA SPlicing FACTOR SRP40) (DELAYED-EARLY PROTEIN HRS) - Homo sapiens (Human), 272 aa.	2.4E-123	14
4885	cg44026811	296	GAGAACAGTTTC ACAATAAATAAT C[G/A]CTTCTCTA AACTGTACAAA TCCTA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q03229 ENDOTHELIN 3 PRECURSOR, PLACENTAL SUBTYPE (ET-3) - HOMO SAPIENS (HUMAN), 224 aa.	2.7E-123 (20q13.2)	20
4886	cg44003626	138	GGCCTCCAGCTA TGGGGTCCAGG GT[C/T]TGAACCT CAGGGCCTGGC AGCTTCA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15025 MRNA (HA1652) FOR ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 296 aa (fragment).	2.7E-123	
4887	cg44003626	690	CATCTCAGCCTC TCATCCAGCTGA G[G/gap]CTCTGG CCACACCGTGCA AGTGGCT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15025 MRNA (HA1652) FOR ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 296 aa (fragment).	2.7E-123	

4888	cg43271722	241	CAGCTGGGGAG GCCCGGCTTGT TC[C/A]GACCAAG ATTCGCCGAAGC ACCAGC	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60795 DNA SEQUENCE FROM COSMID 398G5 FROM A REGION OF THE TIP OF THE SHORT ARM OF CHROMOSOME 16, SPANNING 2MB OF 16P13.3. CONTAINS RAR (RAS LIKE GTPASE) LIKE - HOMO SAPIENS (HUMAN), 236 aa (fragment).	3.1E-123	
4889	cg43973009	961	ACAAATGAATCT GTGGATGCATCA A[C/G]CTATCGTC AGTCAAAACCCCT TTAAA	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P19075 TUMOR- ASSOCIATED ANTIGEN CO-029 - Homo sapiens (Human), 237 aa.	3.4E-123	12
4890	cg44028574	2334	TCGGAACCATCA GCAGAGCCCCA GG[C/G]AGAGTC CTCACCTAAGGG GCTGGIG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI-15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa.	4E-122	20
4891	cg44028574	939	CAAAAGTCATGA GTCCCTGGCTTG G[C/gap]CCCACC ACCTGGTGACTC CGTCCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27724 CGI-15 PROTEIN - HOMO SAPIENS (HUMAN), 329 aa.	4E-122	20
4892	cg43986720	1022	TCTCGCCGGGA CATCTGCCAGTG G[C/T]CTCCTGG GCAACTCAGAAG CAGGTG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121 6 (6p12)	
4893	cg43986720	1723	GTGCTGGGTCAC CCGCCCGGGAA TG[C/gap]TTCCG CCGGAGTCTCG CCCTCCGGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121 6 (6p12)	

4894	cg43986720	1740	CGGGAATGCTTC CGCCGGAGTCT CGC/gapJCCTCC GGACCCAAAGTG CTCTGCGC	C	gap		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4895	cg43986720	45	AATTAAATCTTT AATACAAAATGC[ T/gap]TTTTTTTTT TTTAAGATATATC TGT	T	gap		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4896	cg43986720	540	TCAGGGAGAGA GAGATTGGAAC ATTAGJAATTTA TATACAAAACC GGTACA	A	G		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4897	cg43986720	57	TAATACAAAATG CTTTTTTTTTTTT T/gapJAAGATATA TCTGTATTTCTTT GTCG	T	gap		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4898	cg43986720	657	ATACTGAAAAA AACCTACTCTT TTATJATTAATA ACTGTTTAAATT CTA	A	T		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)



4899	cg43986720	658	TACTGAAAAAA ACCCTACTCTTT AATJTAAATTA ACTGTTTTAAATTT CTAA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
4900	cg43114691	2497	GATCTGTGTGTC TTTTTCAGAAAC [G/A]TCTGTGACA GGCCCATCAATT TTGA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13109 MELANOMA UBIQUITOUS MUTATED PROTEIN - HOMO SAPIENS (HUMAN), 438 aa (fragment)	8E-121	19
4901	cg43932788	602	AACAGCTAGATC AATTTTAGAGAT G[G/gap]CCTAAT AGGCTGGGAA ACAAGTTA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75940 30KDA SPLICING FACTOR - HOMO SAPIENS (HUMAN), 238 aa.	8.4E-121	10
4902	cg43958448	375	ATGGAGAGCTCC TCAGCAGGCGG CC[G/A]GGGAGA AGTCAGCCCCAC AGCGGGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43069 HYPOTHETICAL 73.5 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 650 aa.	3.1E-120	
4903	cg43923128	2111	TTCAAAAATCAG ATATTTTTTTTTT T/gap]GTTCCCT TCTACATAAAAA CCICA	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa.	3.2E-120	1
4904	cg43923128	2825	ACATCTTTCTTC TGGGCAATAGTA [G/gap]GCCTGGT CTGAAGTCTTAG GTCAT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa.	3.2E-120	1
4905	cg43923128	2826	CATCTTTCTTCT GGGCAATAGTAG [G/gap]CCTGGTC TGAAGTCTTAGG TCAATT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa.	3.2E-120	1

4906	cg43933691	1085	CTGGGGCATCTCT TCTGAGTCTTCT TTCCTGCGATTCA TTTTGGATGTTA ACTTG	C	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14976 PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 248 aa.	4.1E-120	2
4907	cg43004093	527	GCTGGGCCAGC TAACCCCTCTGTG TCGTCCTTGG GCAACAGCCTT CCGGCCG	G	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa.	6.6E-120	
4908	cg43004093	564	CAGCCTCCGGC CGCCGGTTCAAT AGTCGTGAAGA TGTTGGAGCGCC GCTTG	G	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA83051 KIAA1099 PROTEIN - HOMO SAPIENS (HUMAN), 804 aa.	6.6E-120	
4909	cg43963595	1291	TAGAAAGTGCCC GTGGAGCCGGC AGG[Gap]AGGCC CCCGCCGCGCT AGAGAACCA	G	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.5E-120	17
4910	cg43963595	1441	GGGCGGACTCC GCAACGCGTTCC TATTCGTACACC ACCTCCCCCTCG GCCCTG	T	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.5E-120	17
4911	cg43937103	1465	TTAATGTGACAG TTTAAAGGATTT IACIAGTAGGGA ATCAGAGTCCTT TGCAG	A	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q14696 HYPOTHETICAL PROTEIN KIAA0081 (HA1009) - Homo sapiens (Human), 233 aa (fragment).	1.1E-119	15
4912	cg43937103	1527	CGACTCAATAAC CTCATTTGTTTCT IAGIACATTTTT CTTTGATAAAGT GCCT	A	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q14696 HYPOTHETICAL PROTEIN KIAA0081 (HA1009) - Homo sapiens (Human), 233 aa (fragment).	1.1E-119	15

4913	cg43936370	957	CTGTTGTGGAGA AGGTGGCGTTTC C/C/CCTTTTCC ATAATAAAATAG AAATG	A	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43672 TRANSCRIPTIONAL COACTIVATOR ALY - HOMO SAPIENS (HUMAN), 233 aa (fragment).	1.1E-119	
4914	cg43936370	806	TGTGCGGCCAAT GATGGATTGTT T/C/TTTTATGTT TTAAAATAGGAT TTAA	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43672 TRANSCRIPTIONAL COACTIVATOR ALY - HOMO SAPIENS (HUMAN), 233 aa (fragment).	1.1E-119	
4915	cg43950398	898	AACAAAATGAAA CAGATCTCTCCT T/G/TTACATAAA ACAGCTAAAAAT TTGGC	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75545 HYPOTHETICAL 26.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 230 aa (fragment).	1.4E-119	1
4916	cg43950398	966	TCATGTATTGG CTTGAAAAAAA A[gap/A]CAACAA CAAAACAACACAG TTACAAG	gap	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75545 HYPOTHETICAL 26.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 230 aa (fragment).	1.4E-119	1
4917	cg43972658	163	GGCAGACTCCAT GTGTGTCAAACG C/T/CJGTGCATGA ATCAGGTTTTTA GAAGG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74894 KIAA0871 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa.	1.8E-119	
4918	cg43972658	450	AAGAAATTTGAT TCTTCCCTTTGAT T/A/JCTCTTGGGA AAGAACACATTT CCCA	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA74894 KIAA0871 PROTEIN - HOMO SAPIENS (HUMAN), 469 aa.	1.8E-119	
4919	cg44002087	1031	AAGAGACCACCA GCAGTGACACCT G/G/CJCAATGAC AGATGCAAGCCC AACACC	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60712 HYPOTHETICAL 26.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 236 aa.	2.9E-119	

4920	cg43256868	728	TACTGAATACAT TGGTTCCTTAGA C(A)G GCATCAAC AAGCATAATTTTA AGAA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60648 HYPOTHETICAL 23.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 217 aa (fragment).	3.7E-119	13
4921	cg29350504	200	ATAGTTTCATGAG TCAAATTTCAAAT [T/gap]AAATGAAT GACATAATATAT AAAAAT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05814 BETA CASEIN PRECURSOR - Homo sapiens (Human), 226 aa.	4.7E-119	4 (4q21.1)
4922	cg29350504	251	AAATAAAGGGAC AAAGTTTCATTTT [T/gap]CCATATAA ACTCATTCAAAC ATACT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05814 BETA CASEIN PRECURSOR - Homo sapiens (Human), 226 aa.	4.7E-119	4 (4q21.1)
4923	cg43040359	557	CAATAATTTATAT AAATTATTTCTT T/C CCAAACTAG ATATTTAATAATC CAC	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45737 HYPOTHETICAL 83.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 745 aa (fragment).	6.6E-119	
4924	cg43271520	219	TGCAGACATGCT GTCACTGCTCCA C(A)G CATCAACG CTGGCAGTCCTT GGGC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to REMBLNEW-ACC:G339409 T-CELL RECEPTOR GAMMA CHAIN VJCI-3(CII)- CIII REGION - HOMO SAPIENS (HUMAN), 318 aa (fragment).	7.6E-119	7 (7p15)
4925	cg43302689	490	GGGAAGCAGGG GATGGGGGAGG TAG G gap CCAG GCCCCGCTGC TCAGGAGCTC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34087 CGI-92 PROTEIN - HOMO SAPIENS (HUMAN), 265 aa.	8.5E-119	9
4926	cg44008583	1906	AGAGTAGTTGAA ATCTTTAGGAAT G A T ACTTCTGA GGCCCAAAAAAT GTGAC	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q15041 HYPOTHETICAL PROTEIN KIAA0069 (HA1508) - Homo sapiens (Human), 226 aa (fragment).	9.7E-119	

4927	cg43067745	135	AATGGATTCTAT TCTGACCAATAC A/C/G/JACAGAAA GAGATCACAGAC TCCCTA	C	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
4928	cg43067745	145	ATTCTGACCAAT ACACACAGAAAG A/G/AJATCACAGA CTCCCTACCTTA GAAGA	G	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
4929	cg43067745	150	GACCAATACACA CAGAAAAGAGATC A/C/TJAGACTCCC TACCTTAGAAGA AGGA	C	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
4930	cg43067745	78	TATTGCATTGAA AGGTCATTGCAG T/GC/JAAAAGGTTG GGGATTGCTTGC TGCTA	G	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
4931	cg43108465	1231	TATTTCCACATC ACATCACAGTTC C/C/TJAAAACGAG TTTAAAGTCTCA AAATT	C	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60666 HYPOTHETICAL 26.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 228 aa.	4.8E-117	1
4932	cg43108465	756	TGTGATTGAATT AGTGCATGGTAA T/G/gap/CATGGC ATATACATTGCTT AAGGTG	G	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60666 HYPOTHETICAL 26.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 228 aa.	4.8E-117	1
4933	cg43919033	1057	CATATGTGGACA CCCTCCTGTCCC C/T/gap/GGCCCC TTTCCCTTTCACC CAGATT	T	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)

4934	cg43919033	124	CGCCATCTCTGC AGAAGAACTCCT G[ <i>gap</i> ]GCCACA CACAGAAGGAAA GTGATC	A	<i>gap</i>			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ787M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)
4935	cg43919033	894	TGCTATGAAACA TGTGAAAAGTGA TTTATTCATGGT TTAATTGTGGAT TTTAT	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)
4936	cg43919033	895	GCTATGAAACAT GTGAAAAGTGAT TTTATTCATGGT TAATTGTGGAT TTAT	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)
4937	cg43919033	896	CTATGAAACATG TGAAAAGTGATT TTTATTCATGGT AATTGTGGATT TATTA	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46693 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)
4938	cg42893815	1119	TAAATAAAGAA GTGGTGTGTTTT TTATCCCGTGGC CAGATTTTAAAG AAACTT	A	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD45360 APOBEC 2 PROTEIN - HOMO SAPIENS (HUMAN), 224 aa.	8.6E-117	14
4939	cg43934644	131	CAGGTGACGCTC GCTCCGCTCGTC C[ <i>gap</i> ]GCTCGT CATGGCCTACCC GGGATAC	C	<i>gap</i>			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P28676 GRANULIN - Homo sapiens (Human), 217 aa.	1E-116	2
4940	cg43935587	2560	CGGTAAGGCTAT CATTCAAGACTC TTTATGGCTGTA ATAATATTCAGG TTTAT	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q14141 SEPTIN 2 HOMOLOG - Homo sapiens (Human), 424 aa (fragment).	1.3E-116	X

4941	cg43926002	1227	AGATGCCATCCT CTTCTCTTTCT [A/C]GTTTGCTCA TACTACATTGAG TAGA	A	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4942	cg43926002	1321	TCCTAAAAGCAA AATAAAACTATT [C/T]GAATGAAA GACAAAGAAATC AGGT	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4943	cg43926002	1448	TCCTTTATTATTA TTTTTTTTTTTT[ gap]GAAAAAAGC TCATTTTCATGCT CTGC	T	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4944	cg43926002	2097	GACACACTATCA TAGTTAACATAG TTT[gap]AAGTTCA GCACTTGCTCTCA TTTTAA	T	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4945	cg43926002	2302	TGTCCTTTCAAA CTCCAAGGTTCC C[C/T]TGTTGGCC CTCTCCCTTACC CTGGGA	C	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4946	cg43926002	2402	ATAATTTAACTAC CCTTAATTACTT gap/AJAAAAAAA AAAAAAAGCTTT ATGAT	gap	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4947	cg43926002	2417	CTTAATTACTTAA AAAAAAA[A A/gap]GCTTTATG ATTTTCATAACTT ATTG	A	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10

4948	cg43926002	2417	TTAATTACTTAA AAAAA gap/AJGCTTTATG ATTTTCATACTT ATTG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MX11 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
4949	cg42545645	214	TTTCAACAAAAG AATTTCTAAGC A/C/TTTGCTGCTG TTACCAGACACT TGAGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76081 REGULATOR OF G PROTEIN SIGNALING - HOMO SAPIENS (HUMAN), 217 aa.	1.6E-116	
4950	cg42545645	394	ATCTTTTATGAAC TGTTGAATTTGGG gap/GJTCCTGCAA TGGCACCTGGTAA GTGAC	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O76081 REGULATOR OF G PROTEIN SIGNALING - HOMO SAPIENS (HUMAN), 217 aa.	1.6E-116	
4951	cg43993887	770	AAGGCATCTGAA CTTTTAATGAAC T/T/GJGAAGGACA ACAGCATCTTCC CAAA	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75934 PUTATIVE SPLICEOSOME ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 225 aa.	3.4E-116	1
4952	cg43932292	3000	TAAAAATTTTTTG GTCTTTTGTAA A/GJAGAGTGTGC TGCTGTAAGAA TCTC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15631 TRANSLIN - Homo sapiens (Human), 228 aa.	4.3E-116	2
4953	cg43921057	221	AGCCAATATAGT TTCTCTCTCCATA T/TAJTAACATAAA CAGCTACAAGAA CCCT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB38041 UNR- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-116	12
4954	cg43921057	84	AACTAAAAACAA TTAGATGTTTCAG A/GJAGCAGTGTA CAATGAACGAGA AATCA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB38041 UNR- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-116	12



4955	cg43258389	707	GAGGGTAACTCT GCTGGACATTCC A/A/CITTCACCTCA TCTGCGTGTCCC CCACA	A	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q22412 T11G6.8 - CAENORHABDITIS ELEGANS, 658 aa.	1.6E-115	5
4956	cg42832298	51	ATAACCTTTATTT AAATAGATTTA A/CITTTAGGAAA GCTCATTTTATAT GAG	A	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75446 MSIN3A ASSOCIATED POLYPEPTIDE P30 - HOMO SAPIENS (HUMAN), 220 aa.	2.4E-115	4
4957	cg43307713	101	CTGGCCCCGTCA CGGCCGCTGAA GGC[ <i>gap</i> ]AGCAC TGCTGGGCAAG GAGAAACAA	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43381 HYPOTHETICAL 42.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	3.1E-115	
4958	cg43307713	141	AGGAGAAACAAG GCCACACCTGCA A/C[ <i>gap</i> ]CTGGCT GCAGGGTGAGG TGGCTCC	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43381 HYPOTHETICAL 42.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	3.1E-115	
4959	cg43307713	33	TTTTTTTTTTTT TTTTTTACCAAA T/A/TGCCCTTTAT TTACATACGAGA AAA	T	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43381 HYPOTHETICAL 42.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	3.1E-115	
4960	cg43951899	221	CCCCTCCAGTTT GGGGGTCTAAAC C/G/A/AACAGGA GAGGTGCAGGG GACCAGG	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9
4981	cg43951899	307	GCAAGGGGTCC CAGGGCCTGGA GCC[C/ <i>gap</i> ]GAGG CCCAGCCAAAAG CACACAGCA	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9

4962	cg43951899	369	TTTATAGTGGAA GCTCCAGGCCCT G[C/gap]CCCTCC CCGGGGGCCCTC GAGGTCGG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9
4963	cg43951899	372	TAGTGGGAAGCT CCAGGCCCTGC CC[C/gap]TCCCC GGGGGCCCTCGA GGTCGGGGA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9
4964	cg43998647	1269	TCTTTTCTCAG GCCTGAGGGGG AA[C/gap]CATTTT TGGTGTGATAAA TACCCJA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBL-NEW-ACC:AAD34072 CGI-78 PROTEIN - HOMO SAPIENS (HUMAN), 251 aa.	3.8E-114	1
4965	cg43982971	1329	CTTCTGATTGAG CGGTGGCCATGG C[C/T]GGTCTCC GTGGGGCAGGG TTGGGCC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q12381 PRE-MRNA SPLICING FACTOR - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 906 aa.	5.7E-114	
4966	cg43982971	1328	AGCCAGGTGTCT TCCCGGGCCCT GC[C/gap]AGACC CTGCTCACATTC CCTCTGCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
4967	cg43982971	1529	GGCTTGGGTGG CGTCGGGGCAG GGC[C/gap]GCCG AGGCTGGGAGG AAGCCCTTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
4968	cg43982971	1680	GGTGGCTGCTG GGTGGGGCCGG GAA[C/A]AAGGG CCCCTGACCCCTG TGTGCTGG	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	

4969	cg43982971	1773	AGCTTTGTGCCC CTGGATGCGCTA A/C/A/JATTCACTC TTGTTTGTCCCT GGACT	C	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:P97765 WW-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
4970	cg43948724	2006	TGTGAACCTACC TGCCCTGGAGAG G(G/gap)CCCAGG TCCCAAAATCTCT TCAAAATT	G	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
4971	cg43948724	2109	TCAGTTTTATGC CCCATTTGGATTA C(gap/T)TTTTTTT TTTTTTTTTTTTT ACTCT	gap	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
4972	cg43948724	2159	TTGAAAGCTTTG TTTTGTGGTAGT C(gap/G)CTTTTG GGAAGAAATCCAG TATTATC	gap	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
4973	cg43948724	2347	GAAATGCTGTGA GTAAATTTCTGT G(gap/C)ATTTTTT TTTTTAATTTGT TTTGC	gap	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
4974	cg43948724	603	GCATCAGACCTG CATTGAACAGTC C(G/T)GTGGAAA GGCCAAGCAGT GACCAGG	G	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)

4975	cg43946376	139	AGCGATATAATT TAAAGTTTTTTT [gap]/TTCATTAGAA ATAAATGTATAAA AATA	gap	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS	1.9E-113	21
4976	cg43946376	341	ATTCACCAGGAT C ACGACTGTTGGA C/C/AJAGCTGCT GGAGATGGACCT GCTACC	C	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS	1.9E-113	21
4977	cg43946376	391	CCCTCAGCAGCC A TCCCACACACAA G/A/G/CAAGTGAT CTCAATGTCCTCC AAACC	A	G				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS	1.9E-113	21
4978	cg43946376	832	AATGTATAAACA T TTCTCTGAAACC A/T/C/JAGCAGCCA TAAACAGTGCTG GTCAA	T	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:P97857 A DISINTEGRIN AND METALLOPROTEASE WITH THROMBOSPONDIN MOTIFS (SECRETORY PROTEIN CONTAINING THROMBOSPONDIN MOTIFS) - MUS	1.9E-113	21
4979	cg43083566	265	TAACAGACAAAT T TGGCTTTTATCC C/T/C/JTTTGATAC CAATATATGTGT ATACA	T	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O60487 EPITHELIAL V-LIKE ANTIGEN PRECURSOR - HOMO SAPIENS (HUMAN), 215 aa.	3.2E-113	11

4980	cg43971133	1167	TTGTTATATAGT GCTGACTTTTTT [G]TTTGAAT AAACAGATTGGT AACC	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa.	6.6E-113	4
4981	cg43971133	125	CCCCACGGGA AGGCAACTGCCT GA[G/A]AGGCGC GGCGTCGCACC GCCCCAGAG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa.	6.6E-113	4
4982	cg43971133	40	GCCGGCTGCC GCCCAGTTGTTA CTC/TAGGTGC GCTAGCCTGCG GAGCCCGT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa.	6.6E-113	4
4983	cg43971133	87	CCGTCGGTGCTG TTCTGCGGCAAG G[C/gap]CTTTCC CAGTGTCCTCCAC GCGGAAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa.	6.6E-113	4
4984	cg43257585	161	CCGCCCCACCCCT GCGCGCTCCTC CGC[gap]GICGGG GAAGAACCTGCG CGGCAGGAC	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60682 ACTIVATED B CELL FACTOR-1 - HOMO SAPIENS (HUMAN), 218 aa.	1.8E-112	
4985	cg43934153	159	ATGTCAGGAAGT AAAAAAGATTAC A[T/G]GCTGCTC GCAGTAAGTACG AGCTTT	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD42945 RING1 INTERACTOR RYBP - MUS MUSCULUS (MOUSE), 226 aa.	2.8E-112	3

4986	cg43916671	898	TGAAGGCGAGAAGG CCCACCATGCAG A[G/gap]CTGTGA ATCTAGAGGCTC TGAGCCA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99470 SDF2 - HOMO SAPIENS (HUMAN), 211 aa.	5.9E-112	
4987	cg42890336	1181	ATAATAAATGCA ATTATAAACTATA JA/TJAAAAGAGGG TGCAGAGGAGG GAATG	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97443 ZINC-FINGER PROTEIN BOP - MUS MUSCULUS (MOUSE), 490 aa.	1.2E-111	
4988	cg43980619	386	TTCATTCCGTCT GTTAAGGGCAG GG[C/gap]CGGGC TAGTGGCAGGA GAAGGTCAG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00501 TRANSMEMBRANE PROTEIN DELETED IN VCFS - HOMO SAPIENS (HUMAN), 218 aa.	2.1E-111	22
4989	cg43942219	944	GCGAGCGCGAC GCACGGCTGGC CAG[C/T]GACCCCT GCTTCAGCCCCGA CCTCAAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4990	cg43942219	178	GAATCCACTGGC GAAAGATGCCTT T[C/T]TAGGAAGC AGAGCTCCCTGA CTGGG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4991	cg43942219	184	ACTGGCGAAAGA TGCCCTTCTAGG A[A/G]GCAGAGC TCCCTGACTGGG CTAAGA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4992	cg43942219	190	GAAAGATGCCTT TCTAGGAAGCAG A[G/gap]CTCCCT GACTGGGCTAAG ATAGTTC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2

4993	cg43942219	208	AAGCAGAGCTCC CTGACTGGGCTA A/GA/JATAGTTCA GATTGATCTTAG GTCAA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4994	cg43942219	217	TCCCTGACTGGG CTAAGATAGTTC A/GA/JATTGATCT TAGGTCATGGT AAGAC	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4995	cg43942219	48	TTTTTTTTTTTT TTTTTTTTTAAAAA /G/GAAAAAGTGT TTATTATAGGCA ACA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4996	cg43942219	49	TTTTTTTTTTTT TTTTTTTTTAAAAA G/AJAAAAAGTGT TTATTATAGGCA ACAA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4997	cg43942219	54	TTTTTTTTTTTT TAAAAAGAAAAA gap/AJGTGTTTAT TATAGGCAACAA CACCA	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
4998	cg43957889	1187	GATATGGGAAGC TTCTGTGAGTGC A/G/TAGGATGG GGGCTGGAGTC ATIGTGA	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:000577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa.	2.7E-111	12
4999	cg43957889	1551	ATTACAGGTGTG CACCACCACGCC TTG/AJACTAATTT TGTATTTTAGTA GAGA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:000577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa.	2.7E-111	12

5000	cg43957889	203	AGGCGCAGAGT ATTGGGTTTGGC TG[G/gap]CCTCG ATTTAAAGAGAC AGAAGCTG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa.	2.7E-111	12
5001	cg43957781	60	CTGTTTACTTCA CTAAACCTGGA G[C/T]GAGGCAG GGAAAAGGTACA TCAATG	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75790 SEVEN TRANSMEMBRANE DOMAIN PROTEIN HOMO SAPIENS (HUMAN), 224 aa.	3.2E-111	19
5002	cg43960639	359	TGCATCATGAAA CAGAGGCAGGG CC[C/gap]TAAGC TGCCCAAGAGG CCTGGGCAC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB40416 P24B PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 217 aa.	9E-111	
5003	cg43036790	37	GACCAAGCTGTC TTGTTTTGCGTA C[A/G]TCAACACT ATGCTGCTTCCA ATATT	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.5E-110	
5004	cg43036790	68	ACTATGCTGCTT CCAATATTCTTA G[C/T]CATTCCAC AGGTAATGATTT TTCAA	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.5E-110	
5005	cg43986282	846	ACCTCCCCAGAC AGGCATTCCGAG T[G/C]GGAGGCG GGAGCACGTAC CGCAGGC	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.9E-110	12
5006	cg43986282	880	GAGCACGTACC GCAGGCGGAGC TAG[G/C]GAGGT CTAGATGGAGG GAGGGTCCA	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.9E-110	12



5007	cg43950821	807	AGAGCGCGCTC ATAAAGGCAGCT GA[G/gap]GGGGC ACCTGCCACCCC ACTGATGC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD41647 MAD2- LIKE PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	3.7E-110	
5008	cg43950821	811	CGCGCTCATAAA GGCAGCTGAGG GG[G/gap]CACCT GCCACCCCACTG ATGCCCAA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD41647 MAD2- LIKE PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	3.7E-110	
5009	cg43325007	537	AATCAGTGT ACTTCAGCAAC G/A/GAACCCCTGG GATAACACCCAGT TGG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43195 PEROXISOMAL MEMBRANE PROTEIN PMP 24 - HOMO SAPIENS (HUMAN), 212 aa.	4.8E-110	20
5010	cg43116651	791	TGGCAAGAAAT GGACCCACCTTT C/C/TGCACAGG ACCGGAGGCAA AGTCGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD28300 DNA- BINDING PROTEIN PREB - RATTUS NORVEGICUS (RAT), 417 aa.	1.6E-109	2
5011	cg43958410	189	TCCTTTCAGTTG CTGGGAGCGGT GA[G/gap]GCCCCA GCCCTTCCCCCT TCCGCCCA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEINE RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa.	7E-109	1
5012	cg43956410	256	GGGGCCTGGCA GGGGTGGAGTG ATG/T/gap/GATC TAAGGGTCCCTG GAGAAGGGT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEINE RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa.	7E-109	1
5013	cg43956410	348	GAGGTCTCAGG GCAAAGGGAAA GGT/G/TTTTGG TGAAGACTGAGG CAGTGCC	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEINE RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa.	7E-109	1

5014	cg43956410	366	GAAAGGTGTTTG GATGAAGACTGA G[G/gap]CAGTGC CTACCTCCCTCC ACATCTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97315 CYSTEINE RICH PROTEIN (CYSTEINE RICH PROTEIN-1) - MUS MUSCULUS (MOUSE), 193 aa.	7E-109	1
5015	cg43928772	164	TCCAGAAACTAT CTTAGATGAAAT AT/ATTGAAGAA TTCAGTTAAATAT TTAT	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa.	8.9E-109	2
5016	cg43928772	329	TCCAAAGGGCAG AACTTGAGCCAA G[C/G]GATAAATA TAAGCAACCAAT GGCT	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa.	8.9E-109	2
5017	cg43928772	500	GTCTTAAATAAG TTGCATTTTCAT G[G/gap]CAAGCC CTCCACTGCCAG CAATGGA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa.	8.9E-109	2
5018	cg43327495	160	TCAAGAAAGGGA AGAAAAGGCTCT G[C/gap]CTTATA CCATAAAAATCA AGTACTC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa.	5E-108	17
5019	cg43327495	161	CAAGAAAGGGA GAAAAGGCTCTG C[C/gap]TTATAC CATAAAAATCAA GTACTCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa.	5E-108	17
5020	cg43327495	229	GCAGGATATTG TTTCTCCAGTTT TTCTGGCTCTAA GAAATTACACTT TCAG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa.	5E-108	17

5021	cg43942004	1769	CCGTGGTCAGAG GTGCCACTGCG GGA[G/gap]CTCT GTATGGTCAGGA TGTAGGGGT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107	5 (5q23)
5022	cg43942004	1932	AGTGCTCCTCCCG TGTCCTCTCCCT G[C/T]CAAGTCTC AGAAGAGGTTGG GCTTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107	5 (5q23)
5023	cg43942004	2003	TCCCTCACCCCG ATGCCCCAGG CC[C/gap]ACAGC GTGGGAACCTCAC TTTCCCTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107	5 (5q23)
5024	cg43942004	2260	CACCCACCTCAC CAAAACGATGAA G[G/T]TATGCTGT CATGGTCCTTTC TGGAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107	5 (5q23)
5025	cg43976960	966	GCTCTCCTTTGC TTGTCCTCTTTG C[C/gap]TTCGGT AATATGTATAAA CTTACAT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
5026	cg43976960	1076	GTTTTAGTTTGA TAATAAATCTT T/gap]GGAACCTT AAAAAGATCTAG TCTGT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)

5027	cg43976960	1087	GATAATAAATCTA TTGGAACITTTAA A/TAAAGATCTAG TCTGTTACACCA TTTA	T		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
5028	cg43976960	1221	ACATTATTATTT TTCATTGTGAGA C/TJACTAAAACT GTTAATCAGACT ACA	T		SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
5029	cg43976960	2103	AAATTTAAACT GGCCTGGTTTGC C[gap/T]TTTTTA TCAAGAGAGCTT AACAGA	T	gap	SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
5030	cg43976960	2109	AAAAGTGGCCTG GTTTGGCTTTTT [gap/T]ATCAAGA GAGCTTAACAGA TAAAAA	T	gap	SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
5031	cg43979124	187	CAAGTTGCTGTT ACAACTACTGAGA A/C/AJTTCATGA AAACGGTATTTA ACAA	A	C	SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43023 TRANSMEMBRANE 4 SUPERFAMILY PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	2.1E-107	
5032	cg43979124	838	AATACAGTAAAT TCCAGGTGCCAC C/A/GJAGCTTCAG AGACCACAAGTT TCAAA	G	A	SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD43023 TRANSMEMBRANE 4 SUPERFAMILY PROTEIN - HOMO SAPIENS (HUMAN), 204 aa.	2.1E-107	
5033	cg43997460	2887	AGGCCGAAAGAA TCTCTTGCTGCT G/C[gap]AAAGAA CAGATTTTATATT TCTTCC	gap	C	SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O18147 T27E9.4 - CAENORHABDITIS ELEGANS, 625 aa.	3.5E-107	3

5034	cg43997460	4010	GACATTGTACTC AGTGGGCCCTTG GG[G]gap]CCTAG CCCAGCTCTGAG CAGAGGAC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O18147 T2FE9.4 - CAENORHABDITIS ELEGANS, 625 aa.	3.5E-107	3
5035	cg43933543	205	TAAGGGTTGGGT CTCCTGATGAAC TTCATTAAGTACC CAGTAAGCTCTT CTCTT	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34113 CGI-118 PROTEIN - HOMO SAPIENS (HUMAN), 212 aa.	3.5E-107	6
5036	cg43933543	45	TTTTTTTTTTTT TTTTTTTTTACA C/TATCTGCAGC AGATTTTATTAG ATG	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34113 CGI-118 PROTEIN - HOMO SAPIENS (HUMAN), 212 aa.	3.5E-107	8
5037	cg43948067	1147	TCTCTGTTTAA GTTAGATCACTT CA/TJTTCTCAG GTAATGACTTTA TTTT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5038	cg43948067	1148	CTTCTGTTTAA TTAGATCACTC AT/ATJTTCTCAG TAATGACTTTAT TTTT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5039	cg43948067	1149	TCTGTTTAAAGT AGATCACTTCAT T/ATCTCAGGTA ATGACTTTATTT TTT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5040	cg43948067	1150	TCTGTTTAAAGT GATCACTTCATT T/ATCTCAGGTA TGACTTTATTTT TTC	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20

5041	cg43948067	1413	GGTTTATAGCAT AGTAAGGTATTT TTA/GJ/CACAAAAT ATATTTTAAAACT ACAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5042	cg43948067	1614	CCTTAAGGAGAC TGAATATCAATA C[C]gapJAGTTTC CAAGGAGTTCTT GTTGAAT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5043	cg43948067	1789	TTATCAAAAAAAA AAAAA A/gapJCTACCCAA AATATAGTTGTAT TTTT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5044	cg43948067	65	TTTATTAACAAA GTTTTCTTAAT T/CJ/CACATTTCAA CTTTATTAATAG TC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34102 CGI-107 PROTEIN - HOMO SAPIENS (HUMAN), 211 aa.	4.5E-107	20
5045	cg43260407	446	TGCTGCTGTTTA CACAAAGTCCAGA C[G/A]CTGCCAG GGCCTGTTGGG ATCAGCT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P28650 ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (EC 6.3.4.4) (IMP- ASPARTATE LIGASE) - Mus musculus (Mouse), 457 aa.	5.6E-107	14
5046	cg43260407	479	GGCCTGTTGGG ATCAGCTCAGTC TG[C/T]GACTAAA ACAGCTGGATCA TCGACT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P28650 ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (EC 6.3.4.4) (IMP- ASPARTATE LIGASE) - Mus musculus (Mouse), 457 aa.	5.6E-107	14
5047	cg43967668	789	GGTAGGCCCCC CAGAGCTCCATG CT[C/G]GTGCGC GGCGGGGGCT GCTGCTGC	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa.	5.6E-107 3 (3p22)	

5048	cg43967668	790	G GTAGGCCCCC AGAGCTCCATGC TC[G/C]TGC GCG GGCGGGGGCTG CTGCTGCC	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa.	5.6E-107	3 (3p22)
5049	cg43967668	845	G GCGGGTCTGGG TCCGAACGCAGT GA[G/gap]CAGCC ACGGCCAGGC TGCACGTCT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa.	5.6E-107	3 (3p22)
5050	cg43297716	3201	G GGCTGGCTGCAT TCCCCAGGATG G[G/gap]CTTCGA GAAAGACAACT TGCTCG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15018 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION- STIMULATING FACTOR) (D FACTOR) (MELANOMA-DERIVED LPL INHIBITOR) (MLPLI) - Homo sapiens (Human), 202 aa.	1.2E-108 (22q12.1)	22
5051	cg43297716	3952	T AGCACATGGCCT TGGGTGACAAAT TT[C]CTCTTTGA TGAATGTACCCT GTGGG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15018 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION- STIMULATING FACTOR) (D FACTOR) (MELANOMA-DERIVED LPL INHIBITOR) (MLPLI) - Homo sapiens (Human), 202 aa.	1.2E-108 (22q12.1)	22
5052	cg43297716	992	G GGGGGCTGTC CAAGGGTGGCT GG[G/gap]CCCA GGGCATGCTAA ACCCAAATG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15018 LEUKEMIA INHIBITORY FACTOR PRECURSOR (LIF) (DIFFERENTIATION- STIMULATING FACTOR) (D FACTOR) (MELANOMA-DERIVED LPL INHIBITOR) (MLPLI) - Homo sapiens (Human), 202 aa.	1.2E-108 (22q12.1)	22

5053	cg43269003	1190	CAAAAGGATAAA AATGTGAACGAA GT[ <i>gap</i> ]TTAACAT TCTGACTTGATA AAGCTT	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC: AAD34784 HYPOTHETICAL 127.9 KD PROTEIN - DROSOPHILA MELANOGASTER (FRUIT FLY), 1181 aa.	1.2E-106	
5054	cg43924804	89	GCGCAGGAGGA GGAGGAGGCCG TGG[G/ <i>gap</i> ]CGAC GGCGATGGCGA CGGGGACGCG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC: O48696 F316.23 PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 525 aa.	5E-106	6
5055	cg43982339	1043	ACAGTGGCAAAA ATGAAAAA A[ <i>gap</i> ]/AJTAAAAAT TATAAAAGAGGC AAAAAA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC: P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa.	1.7E-105	12 (12q22)
5056	cg43982339	1043	ACAGTGGCAAAA ATGAAAAA A[ <i>gap</i> ]/AJTAAAAAT TATAAAAGAGGC AAAAAA	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC: P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa.	1.7E-105	12 (12q22)
5057	cg43982339	1087	AAAAAAGACAC ACTATTCTCTGC C[ <i>gap</i> ]/CJTCTAAA ACACAATTAAAT AAAAGAA	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC: P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa.	1.7E-105	12 (12q22)
5058	cg43982339	153	AACATCTCCCAT CTCTCTGGATT CJT/CJTITTTGCTT CATTATTCCTGC TAACC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC: P05019 INSULIN- LIKE GROWTH FACTOR IB PRECURSOR (IGF-IB) (SOMATOMEDIN C) - Homo sapiens (Human), 195 aa.	1.7E-105	12 (12q22)



5059	cg43995374	110	AAGATACGAGAT CCCGCTGCCTTG G[C]gap/AATTCT GTTATCAGAAAG ATAGTGA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5060	cg43995374	22	AGGAATAGAAA TTTTTTGTA[A/G] TATGGAAGTTGT AAAGCTGTGTTT T	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5061	cg43995374	384	CCCAGCCATGCC CTCTCCCCACCA C[gap]/A/AGCACC CCGCTGACCCCT AGTGTCC	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5062	cg43995374	385	CCCAGCCATGCC TCTCCCCACCCAC A[gap]/A/GCACCC CGCCTGACCCCTA GTGTCCA	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5063	cg43995374	385	CCCAGCCATGCC TCTCCCCACCCAC A[gap]/A/GCACCC CGCCTGACCCCTA GTGTCCA	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11

5064	cg43995374	385	CCCAGCCATGCC TCTCCCCACAC Algap/AJGCACCC CGCCTGACCCCTA GTGTCCA	gap	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5065	cg43995374	741	AGGAAGAAATGG AAATATCTGTGC Algap/GJGGCCCA AGCCCGGCCTG GTGCGGGA	gap	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q13158 FADD PROTEIN (FAS-ASSOCIATING DEATH DOMAIN-CONTAINING PROTEIN) (MEDIATOR OF RECEPTOR INDUCED TOXICITY) - Homo sapiens (Human), 208 aa.	2.8E-105	11
5066	cg44005345	2155	CAGCTGAAATTT GTTTCATAGCTG TTTCJGGTCACCC AGTTCTAGCCAA CCAGG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14493 CPE- RECEPTOR - HOMO SAPIENS (HUMAN), 209 aa.	5.8E-105	
5067	cg44005345	2837	GGTCACACTCAT CTGGTAGTGCAT GJGgapJCGACGC GCTCCCGGTGCT GAAAGTC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14493 CPE- RECEPTOR - HOMO SAPIENS (HUMAN), 209 aa.	5.8E-105	
5068	cg44005345	417	CAGCCTTCCAGG TCCTCAACTCCC GJC/TJGGACGCT GAACAATGGCCT CCATGG	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14493 CPE- RECEPTOR - HOMO SAPIENS (HUMAN), 209 aa.	5.8E-105	
5069	cg43988395	981	TGCAGCAAGTGC CCAGCAGAGCT GCTCJGCGCTAT CTGGCATTCTG CGAGGG	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60443 ICERE-1 - HOMO SAPIENS (HUMAN), 234 aa.	1.5E-104	7

5070	cg44912062	810	GGACCGCTGTG GACCTCGGGAC CTG[G/gap]ACGC CGTCCTGGCTGC GCAGGAGGG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15834 HEPATITIS DELTA ANTIGEN INTERACTING PROTEIN A - HOMO SAPIENS (HUMAN), 202 aa.	1.5E-104	11
5071	cg44912062	836	ACGCCGTCCTG GCTGCGCAGGA GGG[G/gap]CCGC TGGCATGGACTA AGAAATCCT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15834 HEPATITIS DELTA ANTIGEN INTERACTING PROTEIN A - HOMO SAPIENS (HUMAN), 202 aa.	1.5E-104	11
5072	cg43963123	1068	GCCAGGTGCCT GCATCTCACTGG TG[C/T]GGCCGT GGCACCTGAGG GAGCCAC	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17
5073	cg43963123	343	TCCTTTTTTTTT TTTTTTTTTTTT GTTTAAAGACA AAAGCTTACTC GT	T	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17
5074	cg43963123	346	TTTTTTTTTTTT TTTTTTTTTTTT GTAAGAACAAAA GCTTACTCGTG CT	T	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17
5075	cg43963123	449	CCCTCCATGGAA GGCACCAGGCG GG[G/C]AGGTGG GTCTGCTGGGAT GGGCAGG	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17
5076	cg43963123	739	CGGGGTCCCC ACAAAGCCTGOC AG[G/gap]CTGAG CCCTTGAATGG CCGTGGCT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17

5077	cg43983123	941	CTGGGTCGGGG GGAGGGGCACT GCG[G/gap]CCCT GGCCATCAGCCT GGCTGCTT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O0588 RADICAL FRINGE - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.7E-104	17
5078	cg43988007	1549	AGGTAGTTTTA GTGGTTGGGT T[C/G]TGTGTG TGCAATGCCTGTG CTTT	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q92605 MYELOBLAST KIAA0206 - HOMO SAPIENS (HUMAN), 193 aa (fragment).	3.6E-103	5
5079	cg43988007	315	AAATTGAGTCCA TCAGCTGTAAAT A[C/gap]AATTTA TATTGGCTCAA GTGGCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q92605 MYELOBLAST KIAA0206 - HOMO SAPIENS (HUMAN), 193 aa (fragment).	3.6E-103	5
5080	cg43934831	1109	CTCAGTAGCCTG GGGTTGGTGCA GA[G/gap]CGTCC AGAGAGGCAAG GGCATAAAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60610 DIAPHANOUS 1 - HOMO SAPIENS (HUMAN), 1248 aa.	1.9E-102	5
5081	cg43934831	969	GCAAAACAATT CTCAGCCAGGA GG[C/gap]TCCAC CTCCCATTTCCT TGTAACA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60610 DIAPHANOUS 1 - HOMO SAPIENS (HUMAN), 1248 aa.	1.9E-102	5
5082	cg43972159	894	TGCTGCCCTTA CCCCAGCAACG CG[G/gap]CGCGG CCAGAACCAGAA TGCAATAA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13845 BCL7B PROTEIN - HOMO SAPIENS (HUMAN), 202 aa.	2.6E-102 (12q24.1 )	7
5083	cg41045063	848	GGGTGGGAGTG TGGTGGGGGT AGT[G/T]TGTGGC AGGACAAGAGAA GGCATTG	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P32970 CD27 LIGAND (CD27-L) (CD70 ANTIGEN) - Homo sapiens (Human), 193 aa.	3.3E-102 (19p13)	19

5084	cg43943283	390	AATTGAGAGCGT TTTCGCACTCCA G/GCJGGCTGCT CCTGGCGGCTCT GCGGCC	G	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SPTREMBL-ACC:O76994 INTRONIC PROTEIN 259 - DROSOPHILA MELANOGASTER (FRUIT FLY), 259 aa.	1.1E-101	5
5085	cg43966995	149	TTTTTTTTTTTT TTTTTTTTTTTTTA /TCCATTTCACT GATTTTTATTAG GG	A	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to TREMBLNEW-ACC:AA42057 NADH:UBIQUINONE OXIDOREDUCTASE B22 SUBUNIT - HOMO SAPIENS (HUMAN), 179 aa.	2.3E-101	7
5086	cg43989564	34	AAGCTGAAATC ACAGGCTGATAG C/CgapJTCCATTT TAATTAATATTCT ACTAT	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL-TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.2) (5,10- METHENYL-TETRAHYDROFOLATE SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa.	2.8E-101	15
5087	cg43989564	65	TTTAATTAATATT CTACTATTCACTT T/CJTTTTTTTGGT TTTAAAGATGG TTT	T	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL-TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.2) (5,10- METHENYL-TETRAHYDROFOLATE SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa.	2.8E-101	15
5088	cg43989564	70	TTAATATTCTACT ATTCACATTTTTT T/ATTGGTTTTTA AAGATGGTTTTA TAT	T	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL-TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.2) (5,10- METHENYL-TETRAHYDROFOLATE SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa.	2.8E-101	15

5089	cg43926487	32	CTCTTTT TTTT T TTTTTTTTTTTTT C/CACGGAAACA GCCGTTTTTATT CCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27715 CGI-06 PROTEIN - HOMO SAPIENS (HUMAN), 574 aa.	3.8E-101	20
5090	cg43958634	1217	TAGATACAGGCA CCGAGCGTCGA GG[G/gap]CACAG CAGCAGGCCGG CCCTGTTCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa.	3.8E-101	1 (1q32)
5091	cg43958634	1288	GAAGAAGGGTG GTTGAGCTCCTG GC[C/gap]TCCGG ATCTGCAGCCAC TGAIGGCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa.	3.8E-101	1 (1q32)
5092	cg43958634	227	ATATAAACATA GAATAAACCGCA G[G/gap]AAGAAA TATTGGTCTGGA ATTCCCT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa.	3.8E-101	1 (1q32)
5093	cg43958634	315	TATCTCCCCCA CACTGGGGCAG GC[G/A]GCGGAA TAAGCTCCAGCG TTCATGC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa.	3.8E-101	1 (1q32)
5094	cg43958634	341	GCGGAATAAGCT CCAGCGTTTCATG C[G/A]CCACTCAC AGGACTGCTTAC CCCCA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD40382 TRANSCRIPTION FACTOR IIB - HOMO SAPIENS (HUMAN), 193 aa.	3.8E-101	1 (1q32)
5095	cg43983699	1819	TTTACTGTTACAA TGTCAGCCCGC C[gap/C]AGATGG TATCCTCCTATG GAAAAAA	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD20446 AP-3 ADAPTOR COMPLEX MU3A SUBUNIT - HOMO SAPIENS (HUMAN), 418 aa.	6.2E-101	10

5096	cg43983699	189	TTGCTAGAGGGA AGGAGCTCCTG GC/AGGTACATTC TACTTGGATAGA AGAGAA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD20446 AP-3 ADAPTOR COMPLEX MU3A SUBUNIT - HOMO SAPIENS (HUMAN), 418 aa.	6.2E-101	10
5097	cg43983699	36	TTTTTTTTTTTT TTTTTTTTTTTTTT GJTTCCTTCATC TTTTTATTGATAG C	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD20446 AP-3 ADAPTOR COMPLEX MU3A SUBUNIT - HOMO SAPIENS (HUMAN), 418 aa.	6.2E-101	10
5098	cg43980312	1090	ACACCTAGAAAT CAAAACCCACGTC ATT/ATCCTTGAGA GCAGACGGCCG TTAGCA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101 8 (8q22)	
5099	cg43980312	1094	TTAGAAATCAAA CCCACGTCATCC TTT/gap]GAGAGC AGACGGCCGTTA GCAAAGG	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101 8 (8q22)	
5100	cg43980312	2161	TTTATCATTAAG TGCCAGAATGGC TT/GCTTTAATGA AAACAAAAACA AAGA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101 8 (8q22)	
5101	cg43980312	3050	CGCTCGCTTCCT CCTCCTGCGCCT G/C/gap]TCCCCG CGCCCGCAGCT GCGCCCCG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101 8 (8q22)	

5102	cg43980312	521	GACTTGGACGG CTCACAGTTTAA AA[C/G]AAAATTA GTGGTAAATAG AAAAAG	C	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101	8 (8q22)
5103	cg43939240	347	CCTTCCCCTCCC GGGAGTGGCAG AG[C/gap]CGGGC ACACCACAGGCA GGCCCTCA	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43399 HD54+INS2 ISOFORM - HOMO SAPIENS (HUMAN), 206 aa.	1E-100	
5104	cg43939240	732	TCTCTTGGCCCC TCCCATTTCCCAG A[G/gap]GCTCAA GAGCCCTTAGG GCAGGGC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43399 HD54+INS2 ISOFORM - HOMO SAPIENS (HUMAN), 206 aa.	1E-100	
5105	cg43939240	733	CTCTTGGCCCCCT CCCATTTCCCAGA G[G/gap]CTCAAG AGCCCTTTAGGG CAGGGCA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43399 HD54+INS2 ISOFORM - HOMO SAPIENS (HUMAN), 206 aa.	1E-100	
5106	cg43941552	1041	ACAGGGTCAAGTG GAAGCCCCAAC GG[G/gap]AAAGG AAAGGCCCCCGG GCAAAGGGT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	1.6E-100	



5107	cg43941552	1175	GAGGATGGGAG TGGGCAGAGGT GGC[G/A]CCCAG GGGCCCGGGAA CTCCTGCCA	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	1.6E-100	
5108	cg42917153	969	CCCCCTTCTATC CTAAACACATCC AT/AJAAAAATG TGCTTATCACTG TGCTC	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P45973 HETEROCHROMATIN PROTEIN 1 HOMOLOG ALPHA (HP1 ALPHA) (ANTIGEN P25) - Homo sapiens (Human), 191 aa.	2.1E-100	12
5109	cg43252708	386	GGGTGGCTTCT GTCCACTTGCTG A[G/T]CAACTTGT TTCCCTTTTCACA GTGG	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75679 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa.	2.1E-100	
5110	cg43252708	393	CTTCTGTCCACT TGCTGAGCAACT T[G/T]TTTTCCCT TTCACAGTGGAT ATGAC	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75679 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa.	2.1E-100	
5111	cg43143591	62	TATTTTATTTA CAACAGAAATGG T[G/G]GGCTTTAT CCTCCATCTTA GGGA	T	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99966 MELANOCYTE-SPECIFIC PROTEIN 1 - Homo sapiens (Human), 183 aa.	3.4E-100	
5112	cg43925214	372	CCTCTGCACCTCG GGCGGATCGTTA A[C/A]TTCCCCAA GTTACAACTGAG TTGCT	C	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD44480 BUP - HOMO SAPIENS (HUMAN), 195 aa.	4.3E-100	10
5113	cg43925214	77	TTTTTTTTTTT TTTTTTTTTTTTT TTTGGAAACAA CACCTTATTATT CA	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD44480 BUP - HOMO SAPIENS (HUMAN), 195 aa.	4.3E-100	10

5114	cg43925519	283	TTGCGAGTTTCT GAATAGTAGAAA Cgap/AJAAAACA CATTTTAAATCT TTCTAT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:P78317 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 190 aa.	4.4E-100	4
5115	cg43925519	287	CAGTTTCTGAAT AGTAGAAACAAA Agap/AJACATTT TTAAATCTTTCTA TCAAT	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:P78317 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 190 aa.	4.4E-100	4
5116	cg43925519	461	TGCTCCAAGTCT GGGCATCGTGA CAT/CJTGCCGTG ATGCCCAGAAGA AAGTTA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:P78317 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 190 aa.	4.4E-100	4
5117	cg43941550	365	TCCCCAAGCTCC CATTTCTCCAGG GT/CJTGTCCCT GCGGTGTGGGC AGAAGC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
5118	cg43941550	370	AAGCTCCCATTT CTCCAGGGTTTG TTCgap]CCTGCG GTGTGGGCAGA AGCAGCTT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11886 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)

5119	cg43941550	372	GCTCCCATTTCT CCAGGGTTTGTC C/G/gapJTGCGGT GTGGGCAGAAG CAGCTTCT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
5120	cg43941550	472	TCCCGTTGGG CTTCCACTGACC CTTG/TCTCACCG GAGGCGTCCTA GATGTAG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
5121	cg43941550	482	GCTTCCACTGAC CCTGCTCACCGG A/G/gapJGCGTCC TAGATGTAGTAG AGCGGCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
5122	cg43941550	483	CTTCCACTGACC CTGCTCACCGGA G/G/gapJCGTCCT AGATGTAGTAGA GCGGCAC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
5123	cg43950149	285	ATATCTTGGCTG TATTATTTCCTAC IC/TGTGAGAAA GAGACTTAGTAT ATGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa.	7.1E-100	12

5124	cg44925165	2067	TGCCAACACCAA GCTCTGAGTTAA C[ <i>gap</i> ]/TGTGCTT TCTTCTCCTGGC CCTGACA	gap	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75672 HMGBCG PROTEIN - HOMO SAPIENS (HUMAN), 196 aa (fragment).	7.1E-100	
5125	cg42903839	860	GTAAGTGAATG TCTAGTATCTTCT [A/G]TTGAGAGTA CTACTATTAAATTA AGC	A	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32099 SOUL PROTEIN - HOMO SAPIENS (HUMAN), 205 aa.	8.6E-100	6
5126	cg43917034	1156	GAACACTGGCAGG TAGAGTGGAGG GG[G/ <i>gap</i> ]CGAAG CCACATCATCAA GGTGAGGG	G	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62302 TESTIS EXPRESSED PROTEIN 261 (TEG-261) - MUS MUSCULUS (MOUSE), 196 aa.	1.5E-99	2
5127	cg43917034	65	TTGAGTGCTTC TAGGTGCCAGG CA[C/ <i>gap</i> ]AAAGC CAGGCACTGTTA ATACAAA	C	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62302 TESTIS EXPRESSED PROTEIN 261 (TEG-261) - MUS MUSCULUS (MOUSE), 196 aa.	1.5E-99	2
5128	cg42646578	127	TAATCACATGTA ATAAAAACAAAT GT[A]TTAAAATA CAAAAATGTAAT GTATT	T	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD31085 KU70-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 288 aa (fragment).	2.4E-89	
5129	cg43968421	663	TCCCCCGCGGA GCTGACTTCAGC AG[C/ <i>gap</i> ]CCACA GCTGTGGGGCTT CAGCAGCC	C	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43240 HYPOTHETICAL 85.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 754 aa (fragment).	6.4E-99	1
5130	cg43327570	638	TACTCCTTCAGA GCACTGCTGAAA AT[C]GGATCAAA CGTGGAGATCCC CCAGA	T	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75223 WUGSC:H_DJ0777023.1 PROTEIN - HOMO SAPIENS (HUMAN), 188 aa.	3.5E-98	7

5131	cg43920704	16	TTTTTTTTTTTT TTTC/TCAAATTA TAGCATTTTTATT TTCCA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:G1488414 N8 GENE PRODUCT LONG ISOFORM, N8L PROTEIN=D52 HOMOLOG/LEUCINE ZIPPER PROTEIN {ALTERNATIVELY SPLICED, CLONE HK4A1} - HOMO SAPIENS, 248 aa.	1.2E-97	8
5132	cg43925352	1925	GGCCAAGTAGCTA TTTATTCTGGCT G/A/G/CAGACTG TAC/TTTTGTACT TTAAC	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.7E-97	6
5133	cg43925352	2077	TGGTTAACTTCT CCAAATAGTGT CT/A/GGAAGGA GTTTCTTTTCTT CTGTT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.7E-97	6
5134	cg43925352	2196	CGCACTCGCG CTCCTCTTCTCT CG/C/gap/TCGCG CTGGCGCTGG CGAAAGTCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.7E-97	6
5135	cg43925352	2225	CCTGGGCGCTG GCGAAGTCAGC TC/gap/C/TCGCG GGCCTCATCGTC AAACTCAT	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60738 KB07 PROTEIN - HOMO SAPIENS (HUMAN), 243 aa (fragment).	3.7E-97	6
5136	cg43981803	29	TTTTTTTTTTTT ACAACAAGCCAA [C/A]ACATATGCT TTATGGTTCTGT TTCA	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16635 TFAZZIN - Homo sapiens (Human), 292 aa.	7.1E-97	X
5137	cg43981803	31	TTTTTTTTTTTAC AACAAGCCCAACA [C/A]ATATGCTTT ATGGTTCTGTT CAAA	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16635 TFAZZIN - Homo sapiens (Human), 292 aa.	7.1E-97	X

5138	cg43956754	1327	TTCTATTCTGAAAT AACAAATTTTTT T/gap/GAAGGTCA AGTTTTTCAATG GCACA	T	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40377 PTD014 - HOMO SAPIENS (HUMAN), 187 aa.	1.4E-96	15
5139	cg43974514	1202	TTCTACCAGGGT CCAGGACTAAGG C/GA/TTTTCTC CATAGCCTCAAC ATTT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:G545780 DARPP-32=DOPAMINE AND CAMP-REGULATED PHOSPHOPROTEIN - HOMO SAPIENS, 204 aa.	2.8E-96	17
5140	cg43988005	226	TGGGGTCACCTG GCTTCCTGGG GA[C/gap]CCGCA AGGAGGGGAG GGAGCAGCA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13938 CALCYPHOSINE - Homo sapiens (Human), 189 aa.	3.6E-96	
5141	cg43935925	1130	GCGTCCATGGC GGCGCGAGCTG CAG[G/gap]CCAG AGCTCACGGTCT CCTCGGGCC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.6E-96	16
5142	cg43935925	148	AGAGTCTAAAT CAGCCCAAGAAA T[C/G]AGGATCAA GAAGGGGTAAAA AGCCG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.6E-96	18
5143	cg43935925	239	TCACTGAACACC TGCCCAAGTGTG A[T/C]GGCTTCCA TGCAGGAGACC CAAGTG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.6E-96	16
5144	cg43925764	443	AATATCAAGACC AATCTAGACTTTT [T/G]GTCTCTTA CATGTGAAATGG ATGT	T	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAC72976 MDC-3.13 ISOFORM 1 - HOMO SAPIENS (HUMAN), 190 aa.	7.5E-96	5

5145	cg43925788	911	AAAATTCTGGT AAAGCTTCCTA AIC/TGGGTAA GACCATGGGAG AGATAT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC: AAC2976 MDC-3.13 ISOFORM 1 - HOMO SAPIENS (HUMAN), 190 aa.	7.5E-96	5
5146	cg42750816	143	GCCACCAATGGC TTTGGGCATAAT GIC/gap/CCCTCC TCCATAAGGTCC CTACCTG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC: Q98764 HYPOTHETICAL 48.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 437 aa (fragment).	1.4E-95	
5147	cg43971745	1252	CAGACAGGAAGA GACCACCCCCC CC[gap/C]AAAAA AAGAGCCCTGAA GACCTCTG	gap	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1
5148	cg43971745	1252	CAGACAGGAAGA GACCACCCCCC CC[gap/C]AAAAA AAGAGCCCTGAA GACCTCTG	gap	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1
5149	cg43971745	308	CAGGCAGGAGG CAGTGGGCTGG CAGC/gap/CACCC CTGGGCACAGAA GAGCAGACG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1
5150	cg43971745	307	AGGCAGGAGGC AGTGGGCTGGC AGC[C/gap]ACCC TGGGCACAGAA GAGCAGACGC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1
5151	cg43971745	789	TGGTCTTGGGG GGTTGTCCCCCT CC[T/C]TCTGGCC TTGGGAAGACTCT TCCCTT	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC: P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1

5152	cg44924968	43	TTTTTTTTTTTT TTTTTTTTTTTTG /TGAACAAACAAA TAAATTTATTCGT CC	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.8E-95	7
5153	cg44924968	44	TTTTTTTTTTTT TTTTTTTTTTTTG G/TAAACAAACAAA TAAATTTATTCGT CCT	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD43192 WUGSC:H_DJ0726N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 191 aa (fragment).	6.8E-95	7
5154	cg43280516	666	CTTCTGGGACCT GCCGGCCTCCC GG[G/gap]CCAGC TGCCCCACCCCT GCCCATGC	G	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43107 PRENYLATED RAB ACCEPTOR 1 (PRA1) - HOMO SAPIENS (HUMAN), 185 aa.	6.8E-95	19
5155	cg43280516	718	TGTCTGCACGG CTCTGCTGCTCG G[G/gap]CCCACA GGCCGCTCCCAT CACAAAGC	G	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43107 PRENYLATED RAB ACCEPTOR 1 (PRA1) - HOMO SAPIENS (HUMAN), 185 aa.	6.8E-95	19
5156	cg43129980	18	TTTTTTTTTTTT TTTTTATTCCTTT CTGAAGAAACAAA CTTTTAT	A	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA76840 KIAA0996 PROTEIN - HOMO SAPIENS (HUMAN), 848 aa.	6.8E-95	
5157	cg43950632	1046	TTATGTTATATG TTACAAGCCTG C/AJACCCCGCGC CTCTTCTGCGG ACGC	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa.	2.3E-94	1
5158	cg43950632	1047	TTATGTTATATG TTACAAGCCTG A/CJCCCGCGCGC TCTTCTGCGGA CGCG	A	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa.	2.3E-94	1



5159	cg43950632	1048	TATGTTATATGTT TACAAGCCTGCA [C/A]CCCCGCC TCTTCTCGCGA CGCGG	C	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa.	2.3E-94	1
5160	cg43984244	163	AGTGGGGATGA GTGGCATTGCT GG[G/gap]ATATG GGTGTAAAGTTG ATAAGGTC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa.	2.9E-94	2 (2p23)
5161	cg43984244	278	GCTCTAAAGCAG TCAGTGACATT TT[gap]AGAGTG AAGAGGGCATT GCAGGGT	T	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa.	2.9E-94	2 (2p23)
5162	cg43984244	292	AGTGATACATTT AGAGTGAAGAG GG[G/gap]CATTG CAGGGTGCTAGT CCTCTTAA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa.	2.9E-94	2 (2p23)
5163	cg43984244	302	TTAGAGTGAAGA GGGGCATTGCA GG[G/gap]TGCTA GTCCTCTTAAGC TCTGACCG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa.	2.9E-94	2 (2p23)
5164	cg43984244	69	ACTGAGGCACCA TATAAAGGGTTC C[G/C]GGAGTCT CTAAAGAGCTGG AGCTAC	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39210 MPV17 PROTEIN - Homo sapiens (Human), 176 aa.	2.9E-94	2 (2p23)
5165	cg43993152	262	AACTCCTAACCT CAAGTGATCCGT C[C/T]GCCTTGG CCTCCCAAAGTG CTGGGA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27746 CGI-37 PROTEIN - HOMO SAPIENS (HUMAN), 180 aa.	3.7E-94	

5166	cg43993152	270	ACCTCAAGTGAT CCGTCCGCCCTTG G[C/gap]CTCCCA AAGTGCTGGGAT TACAGGC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27746 CGI-37 PROTEIN - HOMO SAPIENS (HUMAN), 180 aa.	3.7E-94	
5167	cg43018426	83	TGTAAACCAAC TCACCTGCACAC A[C/gap]AAATTAT GTGAAATTAGTT TATATA	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P01344 INSULIN-LIKE GROWTH FACTOR II PRECURSOR (IGF-II) (SOMATOMEDIN A) - Homo sapiens (Human), 180 aa.	4.3E-94	11 (11p15.5)
5168	cg43951338	304	ATCTCATTTCTA ATCATGTGCTTT G/gap]JAGACATTT AATACTATTTCAA TTAT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.4E-93	10
5169	cg43951338	323	TGCTTTGAGACA TTTAATACTATTT IC/TJAAATTATGCA GAGGAAATAATA TAAT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.4E-93	10
5170	cg43951338	455	GTTCCCTCTCTT CAACACAGCTGGA G[C/gap]TGACAA CAGATGGAAAAA CATTGG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.4E-93	10
5171	cg43951338	468	AAACAGCTGGAG CTGTACACAGAT G[G/gap]AAAAAC ATTGGTCAGAA AGCAGCA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36405 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 3 - Homo sapiens (Human), 182 aa.	3.4E-93	10
5172	cg43954317	182	TTTCCTTCTGAT GATTTAAACTC T/gap]TAAAGAAC AGGAAAGCATCT GGTAA	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55957 BH3 INTERACTING DOMAIN DEATH AGONIST (BID) - Homo sapiens (Human), 195 aa.	3.4E-93	

5173	cg42669492	91	TGAAAACATTT CAAACCCCTCTA A/C/TJAAGTATTT AATGAAAATAAA TTTAT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34106 CGI-111 PROTEIN - HOMO SAPIENS (HUMAN), 199 aa.	1.3E-92	5
5174	cg43968495	1534	CTGGCTCAGCCC CCGCAGACCTG CC/C/TJACCCCTT TCTGCGCACCCC TGACGG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5175	cg43968495	1597	CTCCCCCAGGC CTGCTGGGCACA CC/T/CJTATGCCA TCTCCCTCTCCA ACTICA	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5176	cg43968495	1636	CTCCCAACTTCA TCGGCCTCAAGC C/T/CJTGCCCTT CCTGGCTCTACC ACCTG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5177	cg43968495	1848	CATCGGCCTCAA GCCTGTGCCCTT C/C/TJTGCTCTA CCACCTGCTTCC CCAGG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5178	cg43968495	1652	CCTCAAGCCTGT GCCCTTCTGGC T/C/TJACCACCT GCTTCCCCCAGG GCCACC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5179	cg43968495	1675	CTCTACCACCTG CTTCCCCAGGGC C/A/GJCCGCCGG GCTTGGCGGCC TACACTG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3

5180	cg43968495	1732	TGGCAGCGGCC AATGGGAGCAAG AAJA/GJGCTGAAC GGCAGAAATTCT CCCCCT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5181	cg43968495	1767	CAGAAATCTCC CCCTACTGAGGC C[G/A]GCTGAGG TACAGGCAGGG GCAGGCA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5182	cg43968495	2254	TGTCAGGGGGC ACCCCAAAGAGG GG[G/gap]CACTG CCAGGTAGCTG GGGGAGTGG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5183	cg43968495	2286	CAGGTAGCTGG GGGAGTGGCAT GGG[G/gap]CAGG GGCCACAGTTCTC AGCAGCAGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB50743 HNRNP-E2 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 353 aa.	3.4E-92	3
5184	cg43973490	1222	TCCAATAGGAGT ATACTCTTTAATA [G/C]AACTGTATT TGAATAAGAATT CCAT	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P40616 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 1 - Homo sapiens (Human), 181 aa.	4.9E-92	
5185	cg43973490	2100	ATCTTCAGTGAT TCCTTGGCCTTC G[G/gap]CTGCAG CTCCGAGGCGG TTTCCTCG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P40616 ADP-RIBOSYLATION FACTOR-LIKE PROTEIN 1 - Homo sapiens (Human), 181 aa.	4.9E-92	
5186	cg43979776	770	CCCGGTGCTGC CTGCTCTCATCC AGT[C/T]CTTGG AAGAAATTTTATT CTGTT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O09003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	

5187	cg43979776	791	CCAGTTCTTGG AAGAAATTTATT [C/T]TGTTCTCG TTTTCGGCACCA TGGA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5188	cg43979776	797	TCTTGAAGAAA TTTTATTCTGTTT [C/A]TCGTTTTCG GCACCATGGAAG AAAT	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5189	cg43979776	802	GAAGAAATTTTA TTCTGTTTCTCG TTT[C/T]TCGGCAC CATGGAAGAAAT GCAGA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5190	cg43979776	835	CCATGGAAGAAA TGCAGAACAAAG C[C/T]GTGGTTT CTTGTGTTTAC TCAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5191	cg43979776	856	AAGCCGTGGTTT TCTTGTGTTTAA [C/T]TCATGGAGC GCAATTGAAAT TTCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5192	cg43979776	858	GCCGTGGTTTTC TTTGTGTTTACT [C/T]ATGGAGCG CAATTGAAATTT CAGG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5193	cg43979776	865	TTTCTTTGTGTTT TTACTCATGGAGI C/TGCAATTGAA ATTTTCAGGTAC CCTT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:009003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	

5194	cg43979776	887	GAGCGCAATTGAC AATTTTCAGGTA C/C/TCTTTCTAC ATGCTGACGTGC ATTGA	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O09003 B-IND1 PROTEIN - MUS MUSCULUS (MOUSE), 189 aa.	6.3E-92	
5195	cg43980242	1255	TTTTCTTTTTTT TTTTTTTTTTTTTT gap]GTTGGCTTT GCGTTAGGATGC TCTG	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P28438 ADP-RIBOSYLATION FACTOR 6 - Homo sapiens (Human), Mus musculus (Mouse), and, 174 aa.	1.7E-91	14
5196	cg43980242	411	GCAACTCCACG C CAGGCCGCAAA GG[C/gap]GCTCT CGCGGCCGAGA GGCTTCGTT	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P28438 ADP-RIBOSYLATION FACTOR 6 - Homo sapiens (Human), Mus musculus (Mouse), and, 174 aa.	1.7E-91	14
5197	cg43955549	222	TGAAACATACAA C ATACAGAAAAT A/C/A]CCCATTTA ACAAATACTAGT GTAA	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA82983 KIAA1031 PROTEIN - HOMO SAPIENS (HUMAN), 940 aa (fragment).	1.7E-91	16
5198	cg43987971	40	TTTTTTTTTTTT TTTTTTGGATGT G/A]TTATTTTT AATAGAAACCAC ATC	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92535 PHOSPHATIDYLINOSITOL-GLYCAN- CLASS C (PIG-C) - HOMO SAPIENS (HUMAN), 297 aa.	7.2E-91	1
5199	cg25236776	735	GCATACGGGGA C CCACCTGTGTGC AC[C/gap]AGGAT GCCTGACACCAT GCTGCCCG	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.2E-91	
5200	cg42527756	322	CAAGTACTGGAG C CAGCTAGCAAGC T/C]TACTCCCCA CTCTCCTCACTT ATCTC	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q95221 PIUS - ORYCTOLAGUS CUNICULUS (RABBIT), 425 aa.	2.4E-90	3

5201	cg43937263	240	CCCCTGGTGT CGATGGTGTGGA A/C/gap/ATTGGG GTGAGGGGCAA AATGCCTA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60831 JM4 PROTEIN, COMPLETE CDS (CLONE IMAGE 546750 AND LLNLC110F1857Q7 (RZPD BERLIN)) - HOMO SAPIENS (HUMAN), 178 aa.	2.4E-90	
5202	cg43937263	263	AACATTGGGGTG AGGGGCAAAATG C/C/gap/TAAGCA GAGCTGGAGGG AGGCAAT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60831 JM4 PROTEIN, COMPLETE CDS (CLONE IMAGE 546750 AND LLNLC110F1857Q7 (RZPD BERLIN)) - HOMO SAPIENS (HUMAN), 178 aa.	2.4E-90	
5203	cg44015091	194	TATGAATTTCTC ATGGAGATAGCA T/C/JTTACATCAC AGAGCTGTTGTG AAAA	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa.	4E-90	9
5204	cg44015091	210	GAGATAGCATTT ACATCACAGAGC T/G/AJTTGTGAAA ATAAAATAAGAA TGTAC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa.	4E-90	9
5205	cg44015091	231	AGCTGTTGTGAA AATAAAATAAGA A/T/CJGTACAGCA CACCTGGAATAT AAAA	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa.	4E-90	9
5206	cg44015091	256	GTACAGCACACC TGGAATATAAAA A/gap/AICATCCC AATAACTTACTT GGAGCCC	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32456 RNA CYCLASE HOMOLOG - HOMO SAPIENS (HUMAN), 265 aa.	4E-90	9
5207	cg43983913	274	TTTTTATTATT TTTTTTTTTTTTT GTGGCACAGAC GCGGGCTTTATT AAC	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11

5208	cg43963913	378	CGCAACGGTTAA ACCTGGCTCGC GA[C/T]TAGCGC AGGCGCCTGGG GAAAAGC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11
5209	cg43963913	511	CCGTGGCTTCAC ACGCACCGGAA GG[G/gap]AATCT GGTCAGCCCT CCCTCCAAA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11
5210	cg43983527	1599	GCGTGCCTTTT GTGGACACAGG AG[C/gap]TCCTC CAGGACAGGC TGGATCCC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa.	6.5E-90 (11q23.3)	3
5211	cg43003890	733	AGGAAAGCGATG GGCCCTGCCCT GC[A/C]CAGGTG GAGAGGGAGGG AGAGGGGA	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14813 HYPOTHETICAL 22.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 210 aa.	1.3E-89	11
5212	cg43990642	1182	CCTGCCCATCCT CCCATGAGAGAC TTC/GTTGTTAGT CAACACATCTGT AAATA	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O93501 NO27 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 248 aa.	2.4E-89	1
5213	cg43990642	2175	TGTATTTCTGGT TCATTATAACAAA [C/T]TGTTGCTT AAATCCAAAAA AAAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O93501 NO27 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 248 aa.	2.4E-89	1
5214	cg43916722	301	CCTGTGAGCATA TAAACACACAAA TIG/A]TATGCTG AAGTTGAAGATT AAGAT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAC78841 MYOTUBULARIN RELATED PROTEIN 6 - HOMO SAPIENS (HUMAN), 465 aa (fragment).	2.8E-89	13



5215	cg43059113	186	GATGCAGCTCAGG GGTACAAGGCA GTG/TTACAGG GTAGAGTGCAGC CCAAGCC	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa.	7.4E-89	3
5216	cg43922090	577	AAAAAAGGACCC AACTCTTACTTTA [G/A]GAGTATTAG GCCTGGACITCC CCIG	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa.	5.2E-88	3
5217	cg43922090	628	CCCATGCAATAA AGCAAGTTTAT A/T[gap]ACAGTC CCCATATTTTTT CTAACA	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa.	5.2E-88	3
5218	cg43922090	923	TTGCTGTCTGTC CTCCAGAACCCG T[G/gap]CCAAGG CCTCCGAGTGCC CAGITAC	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa.	5.2E-88	3
5219	cg43922090	988	AGTTACTGAGGC AGCTGGGGAAAA A[C/T]GTTGAGTA AACATGATTCTA CAATT	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41257 LRR FLI-I INTERACTING PROTEIN 2 - HOMO SAPIENS (HUMAN), 721 aa.	5.2E-88	3
5220	cg43960450	1307	GGGGATTACTA TTGGTGGGGCG TG[C/gap]CAGAC CCTCCCTTGCTT CAGCCAGA	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
5221	cg43960450	1308	GGGATTACTAT TGGTGGGGCGT GC[C/gap]AGACC CTCCCTTGCTTC AGCCAGAC	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8

5222	cg43960450	307	TTGGTGTGTTA GTAGGCAGGATT G[C/gap]CTTACA CTGGGGAAGAAA GACCAGC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
5223	cg43960450	308	TGGTGTGTTAG TAGGCAGGATTG C[C/gap]TTACAC TGGGGAAGAAA GACCAGCT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
5224	cg43955651	110	GACAACACTCT GAGCCTGCAGA GG[gap]CTCACC GCCACACCCACT TCTGCCGC	gap	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.1E-87	2
5225	cg43955651	137	CACGGCCACAC CCACTTCTGCCG CA[G/gap]GGACT GTCTGTTGAGGA GCCGAACC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.1E-87	2
5226	cg43955651	139	CGGCCACACCC ACTTCTGCCGCA GG[G/gap]ACTGT CTGTTGAGGAGC CGAACCGT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.1E-87	2
5227	cg43931874	307	CTTGGAGGAGG GCTGCCAAGTGT G[G/gap]CCAGGG GACCCGGCCTC AGGTCTGT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54745 P65 PROTEIN - RATTUS NORVEGICUS (RAT), 613 aa.	2.4E-87	

5228	cg42556108	180	TGGGCTAGAGG GAGGCAGACAT GGG[G/gap]ACCA TGAAGACCCAAA GGGATGGCC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49913 ANTIBACTERIAL PROTEIN FALL-39 PRECURSOR (FALL- 39 PEPTIDE ANTIBIOTIC) (ANTIMICROBIAL PROTEIN CAP-18) (LL-37) - Homo sapiens (Human), 170 aa.	2.9E-87	3
5229	cg43992520	165	TAAGCCTGCAGA GCTGTTTTTTTT [T/gap]CTACACA CGACAAATACTT TGATAT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa.	6E-87	11
5230	cg43992520	428	GGGAAGGGGGC CAAGAAAAAAG AA[T/C]GGCCACT CTCCTTCTGTC CTTCCC	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa.	6E-87	11
5231	cg43992520	530	AGAAATCAATTG CACATCTCTAGT T[C/gap]GCAAGC GTCAAAGTCACA ACAAGTC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa.	6E-87	11
5232	cg43993006	58	CGGCCGTCGA CTTTTTTTTTTT T[A/T]TAAGGTGT GAGCTTTTATTG CTTAA	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43731 ER LUMEN PROTEIN RETAINING RECEPTOR - HOMO SAPIENS (HUMAN), 214 aa.	7.7E-87	22
5233	cg43970868	855	TCCTGTCCAGC CCTGCCTCCAGG G[C/gap]TCCTGG GCTGCCAGGGA CCTTCAGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19508 Y39A1C.2 PROTEIN - CAENORHABDITIS ELEGANS, 1066 aa.	9.8E-87	12

5234	cg43975606	1106	GAGAAATAGAAA GTCTTCAGTGAT G[G/gap]CCTACG CCAAAGCACAGG ATGGGGC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99871 X-LINKED PROTEIN STS1769 - Homo sapiens (Human), 295 aa.	9.8E-87	X
5235	cg43975606	1132	CCTACGCCAAAG CACAGGATGGG GC[G/gap]GGCAG GAAGCCCTCTCC CAAGATCG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q99871 X-LINKED PROTEIN STS1769 - Homo sapiens (Human), 295 aa.	9.8E-87	X
5236	cg43068353	118	TGCTAGTGGTCC CTGCAGGGCGCC GC[G/gap]GCGAC CGCCTCAGGGG GCCGTTGTT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa.	1E-86	2
5237	cg43918822	1227	TAGGGATCACGC ATACCCCAGACA G[G/gap]GCAGGC CCATCCTCAGGA GCTGGAG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15
5238	cg43918822	1266	CAGGAGCTGCA GTCACACTCAGC CC[G/gap]GCCTG AGGCAAGGGAT GCAGGGCCT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15
5239	cg43918822	220	ACATTCTTTATTC TATTGCTTCAAA G[C]ACAGTTTGT GAGAATGGAAGA TAAC	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15
5240	cg43918822	500	AGAGTCTCCCAC ATCTGCGAATGG G[G/gap]CCAATG GCACTCACTGTC TCTTCAG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15

5241	cg43918822	508	CCACATCTGCCA ATGGGGCCAATG G[C/gap]ACTCAC TGCTCTCTCAGG CCCCAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CA04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15
5242	cg44018226	342	GGCCAGTAGCT GCTGTGACCGA GTC[A/gap]CCAA GATGACCACAGC AGGACCCCT	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa.	1.6E-86	
5243	cg44018226	426	GTACAGTCGTGA AGGCAGTGTGTG C[C/gap]TCTCGG CCGGCACAGGA GGGGCCCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa.	1.6E-86	
5244	cg44018226	638	CTTCCCTTCAG ATGTTATCTTG G[G/gap]CCACCC GGCACTATTTT GGAATAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa.	1.6E-86	
5245	cg43250258	617	TGCATTTCACAG ATAAGCAGGATT C[T/gap]ACATCC GGCCCCCAGTG GGTCTCGG	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34116 CGI-121 PROTEIN - HOMO SAPIENS (HUMAN), 175 aa.	2.6E-86	2
5246	cg43312336	2475	AGAGTTCAGTG TCGCAGTCGCAT A[T/A]TACAACCA TGTTTCACACAG CCCTG	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:043532 RIG-LIKE 7-1 - HOMO SAPIENS (HUMAN), 171 aa.	7E-86	11
5247	cg43921099	211	TAAAGCTGGGTG TTGTGAGGCAAA G[C/gap]CCTTCC CTGCTGCCAGG GGTGGGAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:043760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	

5248	cg43921099	213	AAGCTGGGTGTT GTCAGGCAAAGC C/C/gap]TTCCT GCTGCCAGGGG TGGGAGCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	
5249	cg43921099	293	CCCTCACACCAC GGGAGGCAGCC CA[G/A]AGGCCA CCGGCACAGGG TGGTGGCC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	
5250	cg43921099	317	AGAGGCCACCG GCACAGGGTGG TGG[C/gap]CCCC AGATCATACAGC AGTGGGCAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	
5251	cg43921099	518	GTCAGTAGCACA TGGGCACCTGCT G[G/gap]CTTCTA GCCACTGCAGG CGGGGCTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	
5252	cg43921099	612	CTAAAGTGCCC TGGAGGAGTGA GC[G/A]GCTGAC TGAAGCCCCTCTG GGCACAG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43760 SYNAPTOGYRIN 2 - HOMO SAPIENS (HUMAN), 224 aa.	9.7E-86	
5253	cg43966448	1167	TACGCCTTTCAT CCCTCCTTCTAG G[G/gap]CCTATG GCAGTTCCTCCA GGATGTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22
5254	cg43966448	1205	CTCCAGGATGT GTGGCGAGAGC CT[G/gap]GGCCA GCCCACAGCGTT CCTAGTCA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22

5255	cg43986448	1207	CCAGGATGTGT GGCGAGAGCCT GG[G/gap]CCAGC CCACAGCGTTCC TAGTCAGG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22
5256	cg43986448	1335	CTTCCAGCTGC TGTTTTGTAAAAA [G/A]AAAAAGAAA AAAGAAGCCCAA ACTA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22
5257	cg43986448	1551	AGAAAATGATTG ATGGCTGGGG AA[C/gap]CCTGG AGAGCCTCGACT CCGGAAGT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22
5258	cg43986448	859	TCCTGGTCCCT TGCCCGCGTGG GA[C/G]CCCAATA GAACTCAGCCCT TCCATG	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA18439 DJ1119A7.1 PROTEIN - HOMO SAPIENS (HUMAN), 166 aa.	1.4E-85	22
5259	cg43923303	170	AAGTGTGGCACC AAAAGGTGGTAG G[G/A]GCGGCTG GGGAGGGAGGA CCAGGAC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O43709 PUTATIVE METHYLTRANSFERASE (EC 2.1.1.-) - Homo sapiens (Human), 220 aa.	2.3E-85	
5260	cg43948718	278	GATCAGTTTGT ACAAGAGTTTTT T[A/gap]AAAAAAA TCAAATCACAAC AAAGCT	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa.	3.4E-84	17
5261	cg43948718	378	CCAGTCCTGCCT CTTCACAAACAC T[G/A]ATTCGGCT CTCCTAGGCTTC CGCCT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa.	3.4E-84	17

5262	cg43948718	466	AAGTTAAGAGTG AGGCTGCTTCAG A[G/gap]CCCCCTG GCCCATGTGTCC ATCCAGA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa.	3.4E-84	17
5263	cg43948718	494	CCTGGCCCATGT GTCCATCCAGAC T[C/gap]CCAAGT GGAGTGTAGG CTCCCAGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa.	3.4E-84	17
5264	cg43948718	496	TGGCCCATGTGT CCATCCAGACTC C[C/gap]AAGTGG AGGTAGGGCTC CCAGGGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20432 COSMID F45E12 - CAENORHABDITIS ELEGANS, 246 aa.	3.4E-84	17
5265	cg43934734	352	ACCACCCAAGGT CCTTTCAGGACC C[C/gap]AGGCCT GGCGGCTGTAG GAGAGAGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.1E-84	20
5266	cg43934734	470	CTCCAGACAGGC CGGTGAGGCTA CT[C/T]GACACCC TCACAAAGGGGA AACCCT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.1E-84	20
5267	cg43934734	547	CCCGATGCGGG AGGTTTTGGGCT AG[C/gap]CCTCC CCAGATCCCCG GCCTGAGGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.1E-84	20
5268	cg44032523	19	TTTTTTTTCATT AAAAAA[gap]/A/C CATTATAGTCAT TTCATGTTGGT	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE), 669 aa.	9.1E-84	



5269	cg44032523	22	TTTTTTTTCATT AAAAAACCA/GTT TTATAGTCATTC ATGTTGGTTGG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE), 669 aa.	9.1E-84	
5270	cg43945523	1372	AGATTAGCATTT TTCAACTGCTCA GTT/CJTTCCTT CAATCTTGGAGA CATTG	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q63918 SERUM DEPRIVATION RESPONSE (SDR=SERUM DEPRIVATION RESPONSE) - MUS MUSCULUS (MOUSE), 418 aa.	3.1E-83	2
5271	cg43919539	267	TCCTTTAAGAAG CCATTGATGGAC C/gap/CJTTCATTG ATGGAAGTTCT GTAAGTG	gap	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa.	3.5E-83	1
5272	cg43919539	4091	CCTCTCGGCTTA CAAGCAGGTCCT GJA/GJGCTCAAAA GGATGCAACCTT GACCA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa.	3.5E-83	1
5273	cg43919539	609	AATAAATTTTCT TTTGTTGTGTT CT/GAATTTTACA GAAAAAATACT GAC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa.	3.5E-83	1
5274	cg43919539	844	GTCCAGGCCTAG GGGATGCTCTTC TTC/GJGAGCCTG TGCTGGTCTAGG AAGCCT	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa.	3.5E-83	1
5275	cg43919539	879	CTGGTCTAGGAA GCCTCTCTTTA G/G/gap/AATCAT TTTTTTGTCCCC CGTGAAC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15053 HYPOTHETICAL PROTEIN KIAA0040 - Homo sapiens (Human), 153 aa.	3.5E-83	1

5276	cg43989507	110	ATGCCCCCAGGT GAAGATGGTTG C[G]AGCTGTTCA GCAGCCACGTCT CCTGC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P36639 7,8-DIHYDRO-8- OXOGUANINE TRIPHOSPHATASE (EC 3.1.8.-) (8-OXO-DGTPASE) - Homo sapiens (Human), 156 aa.	3.9E-83	7 (7p22)
5277	cg43989406	1748	TGTTGCCAAAAT GGTGGCCTGGC TT[G]gapJCTTCT GAACGTTTGGTT CAAATGT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E47283 DNA FOR ORF1 AND ORF2 FROM CHROMOSOME X - HOMO SAPIENS (HUMAN), 157 aa.	5E-83	X (Xp11.4)
5278	cg43948335	1456	GAAGATTCAACA CTCTGGAAGCT T[G]TCAAAGATT ACTGTTACCGA GACAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P38714 ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.19) (ARGININE- TRNA LIGASE) (ARGRS) - Saccharomyces cerevisiae (Baker's yeast), 643 aa.	6.5E-83	6
5279	cg43970119	234	AATAATTATCTTG CGTAAAGAGAAA [A]GIGTAGAGCA CAATATATATATA TCAC	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88719 CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE (EC 2.7.7.43) (ACYLNEURAMINATE CYTIDYLTRANSFERASE) (CMP- SIALATE PYROPHOSPHORYLASE) (CMP-SIALATE SYNTHASE) - MUS MUSCULUS (MOUSE), 432 aa.	1E-82	12
5280	cg43120215	256	AGGCCACCAGG AACTGTTTTTAAA G[C]AJATAGGC TGCACTAGGAGG AAGTTT	C	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P78524 P126 (P70) - HOMO SAPIENS (HUMAN), 1137 aa.	1.3E-82	7
5281	cg43120215	50	TTAATATCTAAGA TAAAAA gap/A]CCCAACCA CCAAACAAACCC ATTG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P78524 P126 (P70) - HOMO SAPIENS (HUMAN), 1137 aa.	1.3E-82	7

5282	cg43921918	274	TGAAAGAACAAA CCAGAAGAATTT TTT/AJTTCAGT TAGATTTTGGAA CTTT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:060613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5283	cg43921918	275	GAAAGAACAAC CAGAAGAATTT TTT/AJTTCAGT AGATTTTGGAA CTTT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:060613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5284	cg43921918	276	AAAGAACAACC AGAAGAATTTT TTT/AJTTCAGT ATTTTGAACCT TTT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:060613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5285	cg43921918	282	CAACCAAGAAGA ATTTTTCAG TTT/AJTTCAGT GAAACTTTTAT TAT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:060613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5286	cg43921918	404	GTATGTATCTGA TCCACACAAATC C/C/TTAGAAAGG TTTCTGTGTAG CTTC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:060613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5287	cg43921918	718	CTGCTTGTAA CCTCTCTAATTA [G/A]AAATCTGT GTCGTAAACT GGAC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:060613 15 KD SELENOPROTEIN PRECURSOR - Homo sapiens (Human), 162 aa.	1.5E-81	1
5288	cg43283313	961	GCGTCCGCTCC CCGGTCAGGAG CGC[A/G]GCCGA CGAGTACAGTTG CTGCTGCT	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:043658 CANDIDATE TUMOR SUPPRESSOR P33ING1 - HOMO SAPIENS (HUMAN), 279 aa.	1.9E-81	4

5289	cg43933199	470	TTTGGGGGGGTT GTGCTGGGGGG GA[gap]/GJGGGG GTTCAAATATTTA TTGTATTT	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O75293 NEGATIVE GROWTH- REGULATORY PROTEIN MYD118 (MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118) - Homo sapiens (Human), 160 aa.	1.9E-81	19
5290	cg43933199	475	GGGGGTTGTGC TGGGGGGGAGG GGG[gap]/GJTTC AATATTTATTGTA TTTTTTGT	gap	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O75293 NEGATIVE GROWTH- REGULATORY PROTEIN MYD118 (MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD118) - Homo sapiens (Human), 160 aa.	1.9E-81	19
5291	cg44030987	83	CGTAAGCAGAAT TAACCAGACAGT TTT[A]CAAACTC GAACCTTTGTTTA ATTAA	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA76495 TYPE II MEMBRANE PROTEIN SIMILAR TO CD89 - HOMO SAPIENS (HUMAN), 149 aa.	1.9E-81	
5292	cg43298483	100	CTAGGCTGGGG CTGCCCGGCTCA GC[C/gap]/AGCGG GTCTAAACAGTG TGTCAGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00423 HUEMAP - HOMO SAPIENS (HUMAN), 717 aa.	2.5E-81 (12q13.3 )	12
5293	cg43298483	215	AGTCGGCCCCCTA GTCGTGGGGGA TT[G/A]GGCCAG GGAAGGGCAGG GCGGGGCG	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00423 HUEMAP - HOMO SAPIENS (HUMAN), 717 aa.	2.5E-81 (12q13.3 )	12
5294	cg43298483	340	GGGTTGAGAG GGCGTGGCGGG CGC[C/gap]/GGCC CCGCGCCCCCA GCGCCCCAGCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00423 HUEMAP - HOMO SAPIENS (HUMAN), 717 aa.	2.5E-81 (12q13.3 )	12

5295	cg43076394	184	ATTATATAATAA C ATTCATTATGACA C/TJTGATTCCAA ATTGTATGTACG AAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa.	6.6E-81	16
5296	cg43076394	227	GTACGAATTGGC C TTGACATAATAA A/C/TATAACAT AAGGGCAATTTA AACAT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa.	6.6E-81	16
5297	cg43076394	261	AAGGGCAATTTA G AACATTGGCAGT A/G/AJTTTATGTA AGTCAATTCAAG GTCAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa.	6.6E-81	16
5298	cg43076394	354	TCCTTAGGAAGC T AGCCCTGTAACA A/T/CJGTACATT GTAGATCAGGG GCTAAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa.	6.6E-81	16
5298	cg43076394	481	AAAGTAGATTTT A ATTACAGAGCAA A/TJTTTCTATC AATTCATGCTTT AA	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q99547 M-PHASE PHOSPHOPROTEIN 6 - HOMO SAPIENS (HUMAN), 160 aa.	6.6E-81	16
5300	cg43320682	299	CTGTCAAGCAGA G TCCTGAGGGTTA T/GA/JGTTAAGCC TGATAACAGCCT CTTAA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45773 HYPOTHETICAL 18.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 162 aa (fragment).	6.6E-81	
5301	cg43321624	432	CAAGGGAGGGG gap ACAGGCACATGG AGIgap/CJTACCC GAAGTAGGGCA GGGTGTAGT	gap	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60377 P1.11659_5 - HOMO SAPIENS (HUMAN), 188 aa (fragment).	1.1E-80	9

5302	cg42651270	281	CCGGTGAGGCC AGGGGCAGCAG TGC[G/A]GCTCA GCAGGTGCCGAG GCAGGCCTTA	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75865 R32611_2 - HOMO SAPIENS (HUMAN), 160 aa (fragment).	1.4E-80	
5303	cg42651270	88	TATTGAGCAGCT ACTGGGCAGTGA C[G/T]CTGCCGA GGCGGGAATCC CACCACA	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75865 R32611_2 - HOMO SAPIENS (HUMAN), 160 aa (fragment).	1.4E-80	
5304	cg42651270	92	GAGCAGCTACTG GGCAGTGACGC TG[C/gap]CGAGG CGGGAATCCAC CACAGTCC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75865 R32611_2 - HOMO SAPIENS (HUMAN), 160 aa (fragment).	1.4E-80	
5305	cg43969140	222	ATTCCAATTGCA GGGCCCCAGCA CA[G/C]GGCTGG GCAGGTGAGATA GGGAGGG	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
5306	cg43969140	274	TGGAGGAAGTAA TCTGGCCCCAGG GC[C/gap]TCAGA GCTGTGAGATGA TATTGGGT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
5307	cg43969140	789	GGCTGCAGCGG CTCTGCTGAAAC TG[C/gap]GGACC CCGCCAGACGC CCACTCTCTCC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	

5308	cg43270152	81	TCAATTTGGCTC TTCTTGGCTAAA A[A/gap]TTCTCTG GAGGGTGGTGG TGATGAT	A	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SWISSNEW- ACC:P39877 CALCIUM-DEPENDENT PHOSPHOLIPASE A2 PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) (PLA2-10) - Homo sapiens (Human), 138 aa.	4.6E-80	1
5309	cg43338199	139	TGCCCCCTTCCT AGGGTGCGGT GG[C/gap]CTCCA GCCAGGGGGGC TTCCAGGTT	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:O60894 MRNA ENCODING RAMP1 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.6E-79	2
5310	cg43338199	140	GCCCCCTTCCTA GGGTGGCGGT GC[C/gap]TCCAG CCAGGGGGCT TCCAGGTTA	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:O60894 MRNA ENCODING RAMP1 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.6E-79	2
5311	cg43817480	768	TCCTTTAAAAG GAACAAAACTTT A[G/T]TATTTAAT TAGTTGATTTATT TAAT	G	T				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:Q15649 THYROID RECEPTOR INTERACTING PROTEIN 3 (TRIP3) - Homo sapiens (Human), 152 aa (fragment)	1.6E-79	17
5312	cg42708544	123	CACACACACACA CACACACACACA C[A/gap]CGGATT CCCCATCAAGGG GACATT	A	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa.	2.6E-79	
5313	cg42708544	124	CACACACACACA CACACACACACA C[gap]AIGGATTC CCCATCAAGGG GACATTG	gap	A				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa.	2.6E-79	

5314	cg42708544	341	GAAGACTGCAGC AAAGACATCCAA A[G/gap]CCAACG GCAAGGGAAGC GTCAGCGG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa.	2.6E-79	
5315	cg42708544	710	GCTACTCAGGAG GCTGAGCGGG AG[A/G]ATCGCTT GAACCCGGGAG GGGGAGG	A	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14684 PIG12 - HOMO SAPIENS (HUMAN), 153 aa.	2.6E-79	
5316	cg44024149	880	ATCCCTCACCCA TCCTAGAGGCCA G[G/gap]CAGGAG CCCTTCTATACC CACCCAG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.3E-79	1 (1p35)
5317	cg44024149	986	GTGCTTAACCAA AGAAGCTGTACT C[C/T]GGGGGGT CTCTTCTGAATA AAGCAA	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.3E-79	1 (1p35)
5318	cg43963131	186	CTGGGATGGATG AGTAAGAGGAG GA[A/C]GGTACA CTAGAGGCTTTG GTAAAC	A	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa.	6.8E-79	6
5319	cg43963131	228	GGTAAACATCT TCTCTCCAGAGG G[gap/G]TGAAGA TAAATAAACCTTA CAGAGA	gap	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa.	6.8E-79	6



5320	cg43963131	318	TGGTAGGGGCA TCCAGGGGTGTC C[C/gap]TTCCAA TGTAAGAGACAA ACTGTG	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa.	6.8E-79	6
5321	cg43963131	331	CCAGGGGTGTC CCTTCCAATGTG AA[A/gap]GACAA ACTGTTGCATCT TGCATCCT	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa.	6.8E-79	6
5322	cg43963131	369	CATCTTGCATCC TCATGCAAGGAA G[G/gap]AAGCAC ACTGCCTGGTGA GCCTGTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q04490 P5-1 PROTEIN - HOMO SAPIENS (HUMAN), 143 aa.	6.8E-79	6
5323	cg43287619	186	CAATTAGAAAG AAACACACITTA A[G/A]AAATCAAA ATTCTCAATTCA GGCAG	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa.	6.8E-79	12
5324	cg43287619	517	TGGAGGCCGA GGTGGGTGGAT CAC[A/G]AGGTC AGGAGATCGAGA CCATCCTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa.	6.8E-79	12
5325	cg43287619	595	TAAAAAATACAA AAAATTAGCCGG G[C/T]GTGGTG CGGGCGCCTGT AATCCCA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa.	6.8E-79	12
5326	cg43287619	611	TTAGCCGGGCGT GGTGGCGGGCG CC[C/T]GTAATCC CAGCTACTCGGG AGGCTG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P00695 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa.	6.8E-79	12

5327	cg43287619	615	CCGGGCGTGGT GGCGGGCGCCT GTA/GJTCCAG CTACTCGGGAG GCTGAGGC	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P00895 LYSOZYME C PRECURSOR (EC 3.2.1.17) (1,4-BETA- N-ACETYLMURAMIDASE C) - Homo sapiens (Human), Pan troglodytes (Chimpanzee), and, 148 aa.	6.8E-79	12
5328	cg43918538	1513	GGCCCCCAGG TGGAGTGCCTGA CAT/CJAGGGCT CGCTCCAGAGG CGTCTGAC	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa.	8.6E-79	16
5329	cg43918538	592	TTATTTTACTAT TAAAAA A/gapJTCAAAGG ACACACTGGGAA TTGAA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa.	8.6E-79	16
5330	cg43918538	592	TATTTTACTATT AAAAA gap/AJTCAAAGG ACACACTGGGAA TTGAA	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa.	8.6E-79	16
5331	cg43918538	592	TATTTTACTATT AAAAA gap/AJTCAAAGG ACACACTGGGAA TTGAA	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20633 ARF-LIKE 2 BINDING PROTEIN BART1 - HOMO SAPIENS (HUMAN), 163 aa.	8.6E-79	16
5332	cg43250517	208	TTTCAGATGATG GGGTCTGAGATG TTC/GTCCCTCAGG CTGCATCAGCTG TCTTC	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34037 CGI-41 PROTEIN - HOMO SAPIENS (HUMAN), 475 aa.	1.4E-78	
5333	cg43267341	968	TTAGCTTTTTT TTTTTTTTTTTg ap/TJAATTCAATC TGAATCAGAAA GCGG	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	

5334	cg43287341	1035	GTCTTGTCGCC TCCCACTCATC C[C/T]TGGCTGG TCCCTGTTGCC TATAG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5335	cg43287341	1056	ATCCCTGGTCTG GTCCCTGTTGC C[T/C]ATAGCCCT TTACCCTGAGCA CCACC	T	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5336	cg43287341	1083	TAGCCCTTTACC CTGAGCACCACC C[C/gap]AACAGA CTGGGGACCAG CCCCCTCG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5337	cg43287341	1092	ACCCTGAGCACC ACCCCAACAGAC T[G/gap]GGGACC AGCCCCCTCGC CTGCCTGT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5338	cg43287341	1154	AACCCCTTTAGA TGGGAGGGAA GA[G/A]GAGGAG AGGGAGGGGA CCTGCCCC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5339	cg43287341	1167	GGGAGGGAAG AGGAGGAGAGG GGA[G/gap]GGGA CCTGCCCTCC TCAGGCATC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	

5340	cg43267341	1170	GAGGGAAGAGG AGGAGAGGGA GGG[gap]ACCT GCCCCCTCCTCA GGCATCTGG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5341	cg43267341	1198	CTGCCCCCTCCT CAGGCATCTGG GA[gap]GGCCC TGCCCCCATGG GCTTACCC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5342	cg43267341	1200	GCCCCCTCCTCA GGCATCTGGA GG[gap]CCCTG CCCCCATGGCT TTACCCCT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:E1216178 SEQUENCE 18 FROM PATENT WO9625492 - UNIDENTIFIED, 154 aa.	1.4E-78	
5343	cg42535274	74	CCTGCTGCCACC ACGCAGCCTC GG[gap]CTCCC AGGCGGACAC GGCCACCGC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43791 SPOP - HOMO SAPIENS (HUMAN), 374 aa.	1.8E-78	
5344	cg43999987	1703	ACACAGCCTGTG GATCCTGGGC ATC/TTGGAAG GGCACACATCA GCAGCC	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q09981 HYPOTHETICAL 107.4 KD. PROTEIN F30H5.1 IN CHROMOSOME III - CAENORHABDITIS ELEGANS, 961 aa.	4.8E-78	15
5345	cg43949675	116	ACAAATCACAGC TGATAGACAGCG A[gap]JCGCTTC CCCATAGAGACC GTGCTCC	gap	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	
5346	cg43949675	156	ACCGTGCTCCAA CTCGGGCCTGG GG[gap]C/ACTGC TCGCTGCTCCCA GGAAGGGG	gap	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	

5347	cg439498675	238	AGAGTCCAGGGT GGAGCGCGCCA CC[C]gap]TCAGC CAGAGCAGCCA CGACAGCCA	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	
5348	cg439498675	910	CCGTCCCCTCAG AAGAACGAAACGT G[G]gap]CGCCGC CTCCTCTCGGGA GCTCTCT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	
5349	cg43259701	605	GGACGAGTCGG ACCGAGGCTAG GAC[G/A]TGGCC GGCGCTCTCCA GCCCTGCAG	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00496 IPL (IPL) - HOMO SAPIENS (HUMAN), 152 aa.	1.3E-77	11
5350	cg44003673	110	GGGAACACCCC ACACCCACACCC TG[ap/C]CCCCC CATACCCCTTCC TCCAGGAG	gap	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa.	1.6E-77	
5351	cg44003673	216	TCGCCAGTGTCT GCTGCCCTCCTCC C[C/T]GCAAAGTC TCCCACAAAGCAC AGGAC	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25021 CALCIUM-REGULATED HEAT STABLE PROTEIN CRHSP-24 - HOMO SAPIENS (HUMAN), 147 aa.	1.6E-77	
5352	cg44923000	291	TTTGTTCTTTTA TATATACACATA T/CJTATCTCAAA ACATAGTATTTT TA	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA22102 Y75B8A.14 PROTEIN - CAENORHABDITIS ELEGANS, 272 aa.	4.3E-77	12
5353	cg44923000	294	GTTTCTTTTATAT ATACACATATTTT A/TTCTCAAAACA TAGTTATTTTAC TT	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA22102 Y75B8A.14 PROTEIN - CAENORHABDITIS ELEGANS, 272 aa.	4.3E-77	12

5354	cg44923000	665	AGGCATGAGGCT GATAAAGAACGA A[G]gap]TTTTACT TTTTTTCATTAAA ATAAG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA22102 Y75B8A.14 PROTEIN - CAENORHABDITIS ELEGANS, 272 aa.	4.3E-77	12
5355	cg43112852	1152	CCTGACAAGCAC T CAGATTCCATTG TTTATCACGTTT TTAGAGATTAAAT TCCA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78730 PALBH (EC 3.4.22.17) - HOMO SAPIENS (HUMAN), 813 aa.	1.1E-76	
5356	cg43112852	1153	CTGACAAGCAC T AGATTCCATTGT TTTATCACGTTT TAGAGATTAAAT CCAT	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78730 PALBH (EC 3.4.22.17) - HOMO SAPIENS (HUMAN), 813 aa.	1.1E-76	
5357	cg42520895	97	AAGAAGGGCTCA G GCGCTCCCG CC[G]gap]GGCCG TGGACAGAGGG GCACAGTTT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB51858 ATP-DEPENDENT METALLOPROTEASE YME1L - HOMO SAPIENS (HUMAN), 716 aa.	2.4E-76	
5358	cg43298234	1052	GCTCCTGCCTAC G ATCCAGGCAGAA A[G]TATAGGCAG GGGCTCTTGGAA GACGT	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5359	cg43298234	1110	TGTGACCTCCGA G GCCCTCCTGGTG G[G]A]AAGACAG CTGGAAGGCTG GGAGGA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5360	cg43298234	1147	AAAGGCTGGGA C GGAGAAGGGAG GGG[C]T]TGGGG GTTCCAGGAGC CATGCGTG	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7

5361	cg43298234	1260	CTGGAGTGGG GTGTGTTAGAGC CC[C/gap]TCACC GGGACTTGCTGT GCGGATGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5362	cg43298234	1287	CACCGGACTTG CTGTGCGGATG GG[G/gap]CCTGG GCCTCCTTCCTA CAGGGGCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5363	cg43298234	564	CACCGACACGCT GCTGTGAGGGT CC[G/C]GGTGAG ATGGAGTGGGTC ACACCTG	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5364	cg43298234	644	AAGAAAGTTCCC TGGGGATGGGA GA[G/T]CGGGTG GGTGCTGCCAAT CTCCAGC	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5365	cg43298234	825	CAGTGGAGGAAA ATGTGATAAGGC CIA/GGAGCTTGT GTGCTGGGCAC AGAAAT	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5366	cg43298234	897	CGCAGGCTGGG CCGGAGCCTCT GCC[C/T]GCAGG TTTCTATGCTGTT TCTTAGC	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60896 MRNA ENCODING RAMP3 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.3E-75	7
5367	cg43957018	539	GGAGAGCATCA GGGAGGCCCTT AG[G/gap]CTGTT GCTCTGGGCAG GGGTGGGG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD44697 MUM2 - HOMO SAPIENS (HUMAN), 145 aa.	2.1E-75	17

5368	cg43973471	128	TCCTGAGAACAA ACAAGTAGGCCT G[C]/TTCCTCTCA CCACGTGCTTGT TTATT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14834 DIM1P HOMOLOG - HOMO SAPIENS (HUMAN), 142 aa.	2.1E-75	
5369	cg43918219	387	GAGACAGTGTCTG GGCAATGGGG GG[C]/gap]CCGCA GGGCTTCTTGT GGGCTGCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q21992 SIMILARITY TO LUPUS LA PROTEINS - CAENORHABDITIS ELEGANS, 1356 aa.	8.2E-75	5
5370	cg43918219	56	ATGGTCGATTTT GTCCTTTTCTTC [T]/gap]TTTTTCC CCATTTTTTCAA GGATG	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q21992 SIMILARITY TO LUPUS LA PROTEINS - CAENORHABDITIS ELEGANS, 1356 aa.	8.2E-75	5
5371	cg43918219	62	GATTTGTCITTT TCTCTCTTTTTT /gap]CCCCCATTTT TTCAAGGATGGA AAGG	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q21992 SIMILARITY TO LUPUS LA PROTEINS - CAENORHABDITIS ELEGANS, 1356 aa.	8.2E-75	5
5372	cg43311348	334	TTTTCTGAAAA AGACAGGGCCG GG[C]/gap]CCACC CAGGTCCACTT CCACTCAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76055 WUGSC:H_DJ130H16.4 PROTEIN - HOMO SAPIENS (HUMAN), 149 aa.	1.2E-74	22
5373	cg43311348	336	TTCTGAAAAAG ACAGGGCCGG CC[C]/gap]ACCCA GGGTCCACTTCC ACTCAGCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76055 WUGSC:H_DJ130H16.4 PROTEIN - HOMO SAPIENS (HUMAN), 149 aa.	1.2E-74	22
5374	cg43311348	66	TTTTTTTTTTTT TTTTTTTTTTTT/A TTACCTCTTCAG GATTATTGGGT CAG	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76055 WUGSC:H_DJ130H16.4 PROTEIN - HOMO SAPIENS (HUMAN), 149 aa.	1.2E-74	22



5375	cg44012742	1535	GGGTGACCACA CTGTACTTGGGG CTG[gap]GGCCC TCTGCCCTGTG TCCCATC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa.	1.8E-74	
5376	cg44012742	1537	GTGACCACACTG TACTTGGGGCTG GIG[gap]CCCTCT GCCCTGTGTCC CCATCTG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa.	1.8E-74	
5377	cg43272466	714	CCAACCCATGAG CACTCAATTCCA CIA/GICAGGGG AATACCTCAAGC AGAGAG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa.	1.9E-74	10
5378	cg43272466	762	CTCAAGCAGAGA GAGGGCTTCAG GCIG[gap]ACCCC ACTTCTGGCTCT TTCCAGTC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa.	1.9E-74	10
5379	cg43272466	766	GGGCTTCAGGC CACCCCACTTCT GGC/TTCCTTCC AGTCCTAGCAGG TAAAG	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa.	1.9E-74	10
5380	cg43984390	37	TTATGTTTACCA GTTTATTACAAA CIG/ATTATTAGA AAAGGATACAAA TAAGT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29636 HYPOTHETICAL 15.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 134 aa.	1.9E-74	20
5381	cg43984390	811	GGCCAAGGACG GAATGACAGAAG AGT/GTGTATTAG TAACCATATG GCTGTT	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29636 HYPOTHETICAL 15.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 134 aa.	1.9E-74	20

5382	cg42670378	154	TTATTTTAAATGA GAAAAA A/gap]CCCTCACA ACGTGAGATTCC TTTAC	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD31392 GLYPICAN-6 - HOMO SAPIENS (HUMAN), 555 aa.	1.9E-74	
5383	cg43969639	965	CCACTCTGCAGT AAGGTGTTTCAA A/A/TTCAGAAAT GCACAAATGAAA AGTTA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
5384	cg43969639	994	AAATGCACAAA TGAAAGTTAAC TTC/TTCCTACAGC ATGGTGTGGCAG GGGAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
5385	cg43969639	995	AAATGCACAAAT GAAAGTTAACT C/C/TTCACAGCA TGGTGTGGCAG GGGAA	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
5386	cg43969639	996	AATGCACAAATG AAAAGTTAACTC C/C/TTCACAGCAT GGTGTGGCAGG GGAAAT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
5387	cg43969639	1238	GCCTAATAGGTA TACTCTGGAAGC C/G/A/TACAGGA AGCTACAATCAA ATCAA	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3

5388	cg42332174	1186	GAAAAGCTTATT CATGGCGGTGC AG[G]gap]CTGCA GCCTTTCCCTCA GACCAGGA	G	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5389	cg42332174	235	AAATTTCTTCATG TCTTCTAACGTG gap/A/AAAAAAAAA AAAATCCCATCC AATTA	gap	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5390	cg42332174	247	TGCTTCTAAGC TGAAAAAAAAAAAA A[A]gap]TCCCAT CCAATTAACAAA CTTTCT	A	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5391	cg42332174	247	GTCTTCTAAGC GAAAAAAAAAAAA A[A]gap]TCCCAT CCAATTAACAAA CTTTCT	gap	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5392	cg42332174	37	CAGGATTATTTA TAATGTTTTCCTT T/CJTTTTTTTAG CTGAAATGTATT TTTA	T	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5393	cg42332174	39	GGATTATTATAA TGTTTTCCTTTT T/CJTTTTTTAGCTG AAATGTTATTTTA TT	T	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92527 ANKYRIN MOTIF - HOMO SAPIENS (HUMAN), 151 aa.	1.4E-73	
5394	cg44007500	48	TTTTTTTTTTTT TTTTTTTTTTTTTT AJATTGTATAAAA TTTAAATTTTATG A	T	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45717 HYPOTHETICAL 17.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 153 aa (fragment).	1.4E-73	

5395	cg43981873	942	GGTTTGTGAAA CGGCCGTCCCA AA[G/A]CTGGCT GGATTCTCTAGAA GAGTCTG	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5396	cg43981873	1135	GCCTGCAGGGTT TCCTTGGGCGC GG[C/gap]CCCAA AATTGCCCTTCAA AACAAACC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5397	cg43981873	1161	CCCAAAATTGCC TTCAAAACAAAC C[C/gap]GGGACG GTTGAAAGCCTT CGAACCG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5398	cg43981873	1201	CTTCGAACCGTG CAGGGGATGCC TT[gap]/G[GGCCC TGGCCCTTCGCT TCCTCTCT	gap	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5399	cg43981873	811	TGCTCAGAAAGG AAGAGGCAGGC GC[C/gap]AGGGG GAACCCCTTCG TGTTTGT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5400	cg43981873	824	AGAGGCAGGCG CCAGGGGGAAC CCC[C/gap]TTCG TGTTTGTGACC CTCCCTTTT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
5401	cg44004729	287	TTTTCTTGCTTGA CACTTTATTCTC[ G/CTGAGAGGG GAGGACAGCAG AGGGAG	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P22749 NKG5 PROTEIN PRECURSOR (LYMPHOKINE LAG-2) (T- CELL ACTIVATION PROTEIN 519) - Homo sapiens (Human), 145 aa.	1.7E-73	

5402	cg44004729	379	GCAGAGGAGCCG GCAGAGGTTGCT GA[G]GTTCCC GGGATCTGAGG ACAGGAGC	G	C			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P22749 NKG5 PROTEIN PRECURSOR (LYMPHOKINE LAG-2) (T- CELL ACTIVATION PROTEIN 519) - Homo sapiens (Human), 145 aa.	1.7E-73	
5403	cg43942549	2079	AGAAGAAAGCAA GCAAGGCCGCTT C[G]GAGTGGCGC TAAGTGGACAGG CGACTGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q94218 CODED FOR BY C. ELEGANS CDNA CM10H5 - CAENORHABDITIS ELEGANS, 589 aa.	2.8E-73	4
5404	cg43933021	240	CTTTTTTTTTT CGAAGTCCCTC T[Gap]TTTTTTT CCTTCAGTGTGG TGCTT	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38506 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa.	2.8E-73	13
5405	cg43947751	220	GGATCCTTTCGA GATCATGCTCCC AIC[Gap]ATCTATT AAAAGATACATA AGCTT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P91088 CODED FOR BY C. ELEGANS CDNA YK134H12.5 - CAENORHABDITIS ELEGANS, 470 aa.	8.6E-73	6
5406	cg43048518	226	GTGGATGTCATT GAGGCTTGGGA GG[C]GAGTCCCAG TCTGGCGGGAG AGAAATCCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P50416 CARNITINE O- PALMITOYLTRANSFERASE I, MITOCHONDRIAL LIVER ISOFORM (EC 2.3.1.21) (CPT I) (CPTI-L) - Homo sapiens (Human), 773 aa.	2.5E-72	19
5407	cg43048518	229	GATGTCATTGAG GCCTTGGAGGC CC[C]GAGTGTCT GGCGGAGAGAG AATCCACAC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P50416 CARNITINE O- PALMITOYLTRANSFERASE I, MITOCHONDRIAL LIVER ISOFORM (EC 2.3.1.21) (CPT I) (CPTI-L) - Homo sapiens (Human), 773 aa.	2.5E-72	19
5408	cg43932428	386	ACAGCAGGAATG GGCTGGGGAGG GT[C]GAGTCCCCG CAAGCTGGACCC CTTGTTCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.5E-72	

5409	cg43932428	426	CCCCTTGTCCG TTCGGCCCGTGA G[G]gap]AGAACG GAACTGGCGGC CAAGGGGA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.5E-72	
5410	cg42372763	150	ACTGGGAAAGAT CCGAGGTCAGG AAT/GIAGGCC GTCAATCAGAAG CGCTGAA	T	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75128 KIAA0633 PROTEIN - HOMO SAPIENS (HUMAN), 1316 aa (fragment).	3.3E-72	7
5411	cg43981956	854	GAGTGGCGGGA AATGGGGGCA TCAIC/GICATGCC TGCCGTCGGTT CCTGCGC	C	G			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q63625 CTD-BINDING SR-LIKE PROTEIN RA9 - RATTUS NORVEGICUS (RAT), 1473 aa.	1.6E-71	
5412	cg43292786	825	AAGAAACACAA CTGTACTTTAA AT/CJATGTACAA AGAAAAAATTT CTTA	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA82970 AP-4 CLATHRIN ADAPTOR-RELATED COMPLEX SIGMA4 SUBUNIT - HOMO SAPIENS (HUMAN), 144 aa.	1.8E-71	
5413	cg43951096	1405	TCTGGTTATCTA CCTATAAATTTCA IT/CJGGTATTCT TTAAACACTGAA GTAC	T	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2E-71	17
5414	cg43951096	1423	AATTCATGGTA TTCTTTAAACAC IT/AJGAAGTACTA AAAGCACTGATG ATT	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2E-71	17
5415	cg43951096	456	CCCATGTGAAAA GTTCCATGCAG TIT/gap]ACAAAG GCAGCAGCACAT GCTGTTT	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23382 ZK1058.4 - CAENORHABDITIS ELEGANS, 442 aa.	2E-71	17

5416	cg43934599	582	GGCCAGGCCAG AAGAGTAAGGC AA[C/T]TCAGGAT ACTCCATTATT GAATC	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34127 CGI-132 PROTEIN - HOMO SAPIENS (HUMAN), 137 aa.	3.7E-71	10
5417	cg43283970	1054	CGGCCCTGCCG TTTAACCCGGCC CT[A/C]JAGAAGAG TGAACACAGAATC CAAATC	A	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA82971 KIAA1019 PROTEIN - HOMO SAPIENS (HUMAN), 1887 aa (fragment).	8.1E-71	21 (21q22.1)
5418	cg43271682	112	CGTTGCCCCCCCA CCGCCCCCGCC CC[A/G]CATGCTC TGACTCCTTTGG GGCTG	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
5418	cg43271682	650	TCAGTCCTGGCC TGGCAGGAGT CT[G/gap]GCGGA GCCTCTGAGGTG ACGAGACC	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
5420	cg43271682	651	CAGTCCTGGCCT GGCAGGAGTC TG[G/gap]CGGAG CCTCTGAGGTGA CGAGACCA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
5421	cg43271682	90	AGCGCCCCCTC CCTAGCCCTAC GTT[C/G]CCCCC CCCCGCCCCCG CCCCACAT	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
5422	cg43271682	96	CCTCCCTTAGCC CTACGTTGCCCC C[Gap/A]CCCCCG CCCCGCCCCAC ATGCTCTG	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1

5423	cg44032365	203	AACAAAAATTTAA AAAATCACCTAT T/gap]ATCTTACC ACACAACCACTG TTATG	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q15170 (PP21) - HOMO SAPIENS (HUMAN), 157 aa.	3.3E-70	
5424	cg43918399	1015	TGCTGTTCTACT ATTTAACTACTG [G/gap]CAAAGCC ACTTGCATTTTC ATTAG	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43415 HYPOTHETICAL 15.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 136 aa (fragment).	4.2E-70	4
5425	cg43045396	102	TAGGGATACAAG AGGCACCAAGG CC[T/A]GGGGG TGGGGTGGGG GACACTAC	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5426	cg43045396	216	AGCTCAGAACTA TGACATATTCCT C/A/gap]GGGGAG CCTGCATCCCTT CCTGAAA	A	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5427	cg43045396	222	GAAGTATGACAT ATTCCTCAGGGG A/G/gap]CCTGCA TCCCTTCCTGAA AGTAGGA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5428	cg43045396	266	AGTAGGAGCAAG CCAGCTGCCTTC A/C/TTCCTCGGAC ATAAATTCTGGT GCAGA	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5429	cg43045396	63	ATGACTTCGAAA CCGTGCAATGC C/A/G]AACTATGG AGCACTAGGGAT ACAAG	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15



5430	cg43045396	64	TGACTTCGAAAC CGTGCAATGCC A/GJACTATGGA GCACTAGGGATA CAAGA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5431	cg43045396	65	GACTTCGAAACC GTGCAATGCCA A/GJCTATGGAG CACTAGGGATAC AAGAG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5432	cg43045396	71	GAAACCGTGCAA ATGCCAACTAT G/GCJAGCACTA GGGATACAAGAG GCAQCA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P29762 RETINOIC ACID-BINDING PROTEIN I, CELLULAR (CRABP-I) - Homo sapiens (Human), 136 aa.	4.2E-70	15
5433	cg43917991	400	CCTGAGAGGGT GACAGTCACAGC TA/CJAAAGAGA GGGCCGAGCTC CTGGTGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 ERECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	6.9E-70	11
5434	cg43967210	379	ACCTCAAGAGAG AGCTAAATCATT TTCJAGGTTTGG GAAAAATTTTATT GCAT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q44780 CODED FOR BY C. ELEGANS CDNA YK355D7.5 (CODED FOR BY C. ELEGANS CDNA YK373A5.5) - CAENORHABDITIS ELEGANS, 885 aa.	8.1E-70	3
5435	cg44922306	482	ATAAAGATAATT GAACACAGTAAT G/Agap/AAAAAA AAAGAAAGAAAC AGTATGG	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q01469 FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (PSORIASIS-ASSOCIATED FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABP) - Homo sapiens (Human), 135 aa.	1.8E-69	17

5436	cg44922306	491	ATTGAACACAGT AATGAAAAA ATA[gap]GAAAGA AACAGTATGGAG ATTGCT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q01469 FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (PSORIASIS-ASSOCIATED FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABP) - Homo sapiens (Human), 135 aa.	1.8E-69	17
5437	cg44922306	491	TTGAACACAGTA ATGAAAAA A[gap]A/GAAAGA AACAGTATGGAG ATTGCT	gap	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q01469 FATTY ACID-BINDING PROTEIN, EPIDERMAL (E-FABP) (PSORIASIS-ASSOCIATED FATTY ACID-BINDING PROTEIN HOMOLOG) (PA-FABP) - Homo sapiens (Human), 135 aa.	1.8E-69	17
5438	cg42500321	110	CCAGGGCCTGA CTTGGCAGTGGC CC[C]gap]AGGCT GCATGGGCTCA GGTAGGCTC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41588 TESTISIN - HOMO SAPIENS (HUMAN), 314 aa.	2E-69	16
5439	cg40985789	549	GGCGTTTCCAA GTCAATTTATTCA [A/G]AATTTGTG TTTGTTTCCTGA ATCA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P04765 EUKARYOTIC INITIATION FACTOR 4A-I (EIF-4A-I) - Homo sapiens (Human), and Mus musculus (Mouse), 406 aa.	2.6E-69	17
5440	cg43292800	285	TTATTCAGAATC ATAAGGGTTTT TTATJAAAAAAT CTTACCATTATG AAAGT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75449 P60 KATANIN - HOMO SAPIENS (HUMAN), 491 aa.	3E-69	6
5441	cg43930848	1334	GGTGGGGGTAA TTGTCTCTTGGT GG[G]gap]CCCAG TTAGTGGGCCTT CCTGAGTG	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75817 RIBONUCLEASE P PROTEIN SUBUNIT P20 - HOMO SAPIENS (HUMAN), 140 aa.	7.9E-69	7 (7q21)

5442	cg43323149	1471	TCCGTCCTTTTA GTTTAAATTATT [G/A]GTTAAACTG ATGGCAGCAATC CATG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P50636 GAMETOGENESIS EXPRESSED PROTEIN GEG-154 - Mus musculus (Mouse), 429 aa.	1E-68	1
5443	cg41400057	183	AATGGTAGTCAC TGTAAGAACTGC TT/CJCTCTAAC ACAGGTCTAGCC TGACT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49901 SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS) - Homo sapiens (Human), 116 aa.	2.7E-68	9
5444	cg43955219	625	CATCTCTCCAC TGATGGCCGTG C[C/gap]TAGACC GATGGCAGCCAT CGAATAT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 III ALU SUBFAMILY SQ WARNING ENTRY IIII - Homo sapiens (Human), 593 aa.	6.4E-68	
5445	cg43955219	691	GGGTGTTTCCA CCCCCTGCAG CA[A/C]CTAAGAT GGTGGGGAGA GGGGGT	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 III ALU SUBFAMILY SQ WARNING ENTRY IIII - Homo sapiens (Human), 593 aa.	6.4E-68	
5446	cg44004331	138	CAGACAGCAGG ACTCCAAAGAGG GT[C/G]GGCTC CTAGGCTGCCCC GGACTAG	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	7.1E-68	
5447	cg44004331	234	GAGGGGACCC TGACCTGCCTCT GG[C/gap]CGCCG AACCCGGGCC CTCCCTCTGG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	7.1E-68	
5448	cg44004331	296	ATCTCAGAAAC AAAGGCTGTCCC TIG/TCTTTTGT AGCCCTAGACCA GGTCT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	7.1E-68	

5449	cg44004331	35	TTTATGATTTGT CTACATTTTATT C/TTTTCACTCAA CAGAATAGAAGT TTT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	7.1E-68	
5450	cg43980385	286	ACTGCTCAGCCT GGTGGTGGCTG GA/GCJCTCAGA AATTGGGAGTGA CACAGGA	G	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20
5451	cg43969533	35	TTTTTTTTTT TTTTTTTTTTT A/GATTTTAA AGCCATTATTTT A	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-67	7
5452	cg43969533	37	TTTTTTTTTT TTTTTTTTTTG /TTTTTAAAAAG CCATTATTTTAA A	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39844 HSPC028 - HOMO SAPIENS (HUMAN), 419 aa.	1.6E-67	7
5453	cg43951170	241	TCTAATCTGGG TTCTGCACCATC A/GA/GAAGAGA ATATCCTACAGG ACAGTT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27777 RNA POLYMERASE I 16 KDA SUBUNIT - HOMO SAPIENS (HUMAN), 133 aa.	1.9E-67	13
5454	cg43951170	260	CCATCAGGAAGA GAATATCTTACA G/GTACAGTTCT CCTTGATACTG CATAA	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27777 RNA POLYMERASE I 16 KDA SUBUNIT - HOMO SAPIENS (HUMAN), 133 aa.	1.9E-67	13
5455	cg44921579	625	GGCTAGAAGAT GAACCCCTGGAG A/T/CJGGCCACTA AGGAGAATTGAA AAAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75477 KE04P - HOMO SAPIENS (HUMAN), 346 aa.	3.1E-67	

5456	cg44030323	422	AGCCTGGGTCA GAGGCCTGGTG GGC[C/gap]AGCC CAGTGGGACTAG GCAGGAAGC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27747 CGI-38 PROTEIN - HOMO SAPIENS (HUMAN), 176 aa.	3.9E-67	
5457	cg43999983	875	GATTTCACCTG TAATCATAAACTT [G/T]TAACATCA AACTCGACAGCT AACC	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43446 HYPOTHETICAL 34.0 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 299 aa.	1E-66	
5458	cg42506346	532	TCAGAGATGAAA AGTCACCTCAGT T[ga]/TAAAAGC AAAAAGGAAGAT AGAAAAT	gap	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45744 HYPOTHETICAL 66.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 577 aa (fragment).	3.5E-66	2
5459	cg44928538	1092	CCCGCCCCACTA TGGGCCTACCAT T[A/T]ATAGTGA TAACCTGGAGGT TAAA	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA34673 CFKBP/SMAP - GALLUS GALLUS (CHICKEN), 577 aa.	3.5E-66	7
5460	cg44928538	917	GGTTAAACATT TTAGAAATATTCT [A/T]GAGATGG CAGGAGAGTCAA AGGGC	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA34673 CFKBP/SMAP - GALLUS GALLUS (CHICKEN), 577 aa.	3.5E-66	7
5461	cg44911411	1159	GGGTTTCTGCC ACTTCGGGTCT A[G/gap]GCCCTG CCCCAAATCCAG CCAGTCC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
5462	cg44911411	1160	GGGTTTCTGCCA CTTCGGGTCTA G[G/gap]CCCTGC CCCCAAATCCAG CAGTCCT	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	

5463	cg44911411	1166	CTGCCACTTCGG GGTCTAGGCCCT G[C/gap]CCCAA TCCAGCCAGTCC TGCCCCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
5464	cg44911411	714	TTCTGGATCCCA CAGTGTATGGGA G[C/gap]CCCTGA CTCCTCACGTGC CTGATCT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
5465	cg43984044	948	CCTTCCCTCCT GGATTCCGGTA G[C/G]AGAGGCA GCGCCGCAGGA GGCGGGT	C	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00455 TTF-I INTERACTING PEPTIDE 20 - HOMO SAPIENS (HUMAN), 385 aa (fragment).	7.3E-66	19
5466	cg43984044	960	GGATTCCGGTA GCAGAGGCAGC GC[C/gap]GCAGG AGCGGGTGCC CGTTTGTC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00455 TTF-I INTERACTING PEPTIDE 20 - HOMO SAPIENS (HUMAN), 385 aa (fragment).	7.3E-66	19
5467	cg43969609	192	AAAAAACCAAC AAAGATTTTTT [C/T]TGATTTG CAGGACAAAGTAC AACT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42992 UBIQUITIN-SPECIFIC PROTEASE 3 - HOMO SAPIENS (HUMAN), 521 aa.	7.3E-66	
5468	cg43969609	195	AAACCAACAAA GATTTTTTTCTT [G/T]TATTGCAG GACAAGTACAAC TGAA	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42992 UBIQUITIN-SPECIFIC PROTEASE 3 - HOMO SAPIENS (HUMAN), 521 aa.	7.3E-66	
5469	cg43969609	329	CTTTGTTATATT TACAGGCAAAA G/AJAATGATTCC TCAGCAGTCATT GTGA	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42992 UBIQUITIN-SPECIFIC PROTEASE 3 - HOMO SAPIENS (HUMAN), 521 aa.	7.3E-66	

5470	cg42871015	100	CAATGAATTATT ACCTCAAATATC A/gap/JAGAGGCC CTGAGGTAGGGT GGCTCC	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O08616 BETA-ALANINE- PYRUVATE AMINOTRANSFERASE PRECURSOR - RATTUS NORVEGICUS (RAT), 512 aa.	2.5E-65	5
5471	cg43919145	346	AAAATTGCACTA AAGCTCTGTAAA G/gap/AJAAAAAA TATAATAAATGTC TTATAC	gap	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB52430 DJ703H14.1 PROTEIN - HOMO SAPIENS (HUMAN), 485 aa (fragment).	3.2E-65	1
5472	cg43919145	352	GCACTAAAGCTC TGTAAGAAAAA A/gap/AJTATAATA AATGCTTATAC AAATT	gap	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB52430 DJ703H14.1 PROTEIN - HOMO SAPIENS (HUMAN), 485 aa (fragment).	3.2E-65	1
5473	cg42703392	20	TTTTTTTTTT TTTTTTG/TJCA GAAGTAGGGTTT TGTTATTAA	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q60778 NUCLEAR FACTOR OF KAPPA LIGHT CHAIN PROTEIN ENHANCER IN B-CELLS INHIBITOR, ALPHA (IKB-BETA) - MUS MUSCULUS (MOUSE), 359 aa.	4.2E-65	
5474	cg43946737	229	GGCGCGGAGG AGGCTGGCTGG GGC/C/gap/ATCA CGGAGTGCCCAT CCTGCACTG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB42836 DJ22E13.1A.1 (C- TERMINAL PART OF NOVEL PROTEIN DJ22E13.1) (PARTIAL ISOFORM 1) - HOMO SAPIENS (HUMAN), 134 aa (fragment).	1.1E-64	22
5475	cg43923225	1058	AAAGTGACCCTA TAGCGCAGGGA GC/GA/JGGGTAG TTCCTTGGCTTT ATGCATT	G	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa.	2.2E-64	1
5476	cg43923225	1150	GATGGTTGTTAT TGAGGATGGGG TG/C/gap/JCCATT GGCTAGGGGCC GGCTCTTTG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa.	2.2E-64	1

5477	cg43923225	258	ATTTTATTAA TCTTTAATTTT /TAAAAAAACC CATTACAGTAC ATT	A	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa.	2.2E-64	1
5478	cg43923225	458	GGGGAAGAGG CCAGAGAAAGGA GG[A/gap]GGCAG TCAGATCTTAGA CCTGTCGC	A	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA81907 HRPET-1 - HALOCYNTHIA RORETZI (SEA SQUIRT), 378 aa.	2.2E-64	1
5479	cg43929282	128	TGATCATCACAT GAGCCCTCTTCT CIC/TATATACAC ATTTGTTAGTGT GAAAA	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20678 HYPOTHETICAL 97.3 KD PROTEIN F52E4.7 IN CHROMOSOME X - CAENORHABDITIS ELEGANS, 848 aa.	2.9E-64	
5480	cg43929282	301	TAAAGGAAAT TCCCATCCAGTC AT/CJTGAGAAAT GCTAAAGGCATT TTATG	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20678 HYPOTHETICAL 97.3 KD PROTEIN F52E4.7 IN CHROMOSOME X - CAENORHABDITIS ELEGANS, 848 aa.	2.9E-64	
5481	cg44924736	1579	TTTTTTTTTTC ACATTACCGAAA G/gap]GCCAAGT AATGTGGTGTGA TTACTA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q27244 T09F3.2 - CAENORHABDITIS ELEGANS, 384 aa.	5.6E-64	3
5482	cg44924736	1580	TTTTTTTTTTC CATTACCGAAAG G/gap]CCAAGTAA TGTGGTGTGATT ACTAT	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q27244 T09F3.2 - CAENORHABDITIS ELEGANS, 384 aa.	5.6E-64	3
5483	cg42381630	643	GTTCAATTAAT CTCCCAATAAAG C/gap]TTTACAGC CTCTGCAAAAA AAAAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.9E-64	



5484	cg42381630	662	ATAAAGCTTTAC AGCCTTCTGCAA A/A/GjAAAAAAAAA AAAAAAAAAAAAA AAAAA	A	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.9E-64	
5485	cg44001502	1002	GATTATTTATTG TAATACCTCACA G/AJACGTTGTAC CATATCCATGCA CATT	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14849 MLN84 MRNA - HOMO SAPIENS (HUMAN), 445 aa.	7.6E-64	
5486	cg44001502	1009	TTATTGTAATACCT TCACAGACGTTG T/CJACCATATCC ATGCACATTTAG TTGC	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14849 MLN84 MRNA - HOMO SAPIENS (HUMAN), 445 aa.	7.6E-64	
5487	cg42367764	486	ATTCCACACCTC TCTTCCCCAGCC G/gap/GJCAACGG GGGTGCCAGGA GCCCCAGG	gap	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14210 E48 ANTIGEN PRECURSOR - Homo sapiens (Human), 128 aa.	9.7E-64	8
5488	cg42367764	622	AGGATGAAGCCA CCCCACAGAGG ATTG/gapJGAGCC CCCAGCTGCATG GAAGGTGG	G	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14210 E48 ANTIGEN PRECURSOR - Homo sapiens (Human), 128 aa.	9.7E-64	8
5489	cg43132517	389	GGTTAATAAATT ACTAGGTCTATT TT/CJGAATAACA AATTGAGTACTT TTATT	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.6E-63	
5490	cg43132517	419	TATTTGAATAACT AAATTGAGTACTT T/CJTTATTAGACC TAAGTGAACCTT TAT	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.6E-63	

5491	cg43132517	424	TGAATAACAAAT TGAGTACTTTTAT [T/G]AGACCTAAG TGGAACCTTTATC TGAA	T	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.6E-63	
5492	cg43132517	442	CTTTATTAGAC CTAAGTGGAACCT TTT/C]ATCTGAAT CTGAATTTTCCA AGGGG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12799 T-COMPLEX PROTEIN 10A - HOMO SAPIENS (HUMAN), 416 aa.	2.6E-63	
5493	cg43969715	284	CAGTTTCTTCA CAAAACAGCATT C[G/A]AAGGAGA AGGGAAAGTTCC CACATT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60688 HYPOTHETICAL 13.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 119 aa.	3.3E-63	22
5494	cg43933863	284	ACGTATTAGGAA CAAAATTAAGAGT TTT/A]TTTTGGG TTTTAACTGCA CTTTA	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25962 ZINC RING FINGER PROTEIN SAG - HOMO SAPIENS (HUMAN), 113 aa.	1.1E-62	
5495	cg43933863	286	GTATTAGGAACA AATTAAGAGTTTT [T/A]TTGGGTTT TAAACTGCACCT TATT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD25962 ZINC RING FINGER PROTEIN SAG - HOMO SAPIENS (HUMAN), 113 aa.	1.1E-62	
5496	cg43950549	1039	GGACGGGCTGA ACCAGCGCTACT TC[C/gap]GCAAG CGTGCCCTCTAC CTGGCCCCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30082 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.4E-62	
5497	cg43988710	64	ATCTTGTGGGA CTCTTTTGCCTA A[G/C]CTGGTTCC CAAATCATGGAG GGAAA	G	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34051 CGI-56 PROTEIN - HOMO SAPIENS (HUMAN), 317 aa.	1.4E-62	

5498	cg43308257	1097	CGACGTTTGGG CAGTGTTCCCTG T(gap)CCCCGTG GGCCGGGAGC GAGTAAAG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa.	2.9E-62	
5499	cg43308257	1135	GGAGCGAGTAAA GTCTGGCCAG GCJA/TAAAAA AAAAA AAAAA	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa.	2.9E-62	
5500	cg43308257	439	TGAGCGAGAGT CTACAGTGAGAT C/C/TTGGACAAG AAGTTCACAGTG ACGT	C	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa.	2.9E-62	
5501	cg44015973	1734	AAGAAGAGGCCT CCATTTTTTTT T(gap)CTTTTTT ATTGGTGTAGTT ACGA	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa.	3E-62 (3p24.2)	
5502	cg44015973	2224	GTAAAAGTAAA ACTTTACCATGC C(gap)TTTTTTT TTTTGTGGCC TAACAT	gap	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa.	3E-62 (3p24.2)	
5503	cg44015973	2225	GTAAAAGTAAA ACTTTACCATGC C/T(gap)TTTTTT TTTTGTGGCCT AACATT	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa.	3E-62 (3p24.2)	
5504	cg44015973	2236	AACATTACCATG CCTTTTTTTTTT T(gap)GTGGCCT AACATTGAGGCC TTAAA	T	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14202 DXS6673E PROTEIN - Homo sapiens (Human), 1358 aa.	3E-62 (3p24.2)	

5505	cg43981475	211	CTGGGAAGAAG CTTGTGTCGTT TTT/gap/GATTGT CCTCTGCCAGCA GATCTGC	T	gap				SILENT- NONCODI- NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34088 CGI-93 PROTEIN - HOMO SAPIENS (HUMAN), 291 aa.	4.8E-62	
5506	cg43981475	415	TCGGCTCTTTTC TGGCCCTGGAG GC[C/gap]ATGAG GCTGAAGAAGAG CCCAGGAG	C	gap				SILENT- NONCODI- NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34088 CGI-93 PROTEIN - HOMO SAPIENS (HUMAN), 291 aa.	4.8E-62	
5507	cg43950850	41	CAATGAGACTTT ATTGGCAGTGGG C[C/gap]AGATTT GGGTAGTCTGCT AACTCTA	C	gap				SILENT- NONCODI- NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I- B14.5B) (Cl-B14.5B) - Homo sapiens (Human), 119 aa.	7.8E-62	11
5508	cg43961684	192	CAAAATAAAAAG ATCCACGTCCT TT/TTTCTCTAC ACAAAACGCGTT TTTAA	A	T				SILENT- NONCODI- NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa.	1.2E-61	18
5509	cg43961684	44	TTTTTTTTTTT TTTTTTTTTTT[G /TJGTTCAGAA AGAGAAATTTAA TCT	G	T				SILENT- NONCODI- NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa.	1.2E-61	19
5510	cg43961684	46	TTTTTTTTTTT TTTTTTTTTTTGT G/TJTTCCAGAA GAGAAATTTAAT CTAA	G	T				SILENT- NONCODI- NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa.	1.2E-61	19
5511	cg43961684	466	CATTGTGGGCTC AGTGGGGGGCT CC[C/gap]AGGCC CCAGCAGGCC CACAGAGGG	C	gap				SILENT- NONCODI- NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88287 WIZS - MUS MUSCULUS (MOUSE), 955 aa.	1.2E-61	19

5512	cg43983897	339	CAAGATACCGAC TTTCTGGCCCTG G[C/gap]CCTAAT CCTAAACTCTCC TCCITTG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q19300 CODED FOR BY C. ELEGANS CDNA YK20F8.5 - CAENORHABDITIS ELEGANS, 929 aa.	1.8E-61	6
5513	cg43983897	341	AGATACCGACTT TCTGGCCCTGGC C[C/gap]TAATCC TAAACTCTCCTC CTTGGCA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q19300 CODED FOR BY C. ELEGANS CDNA YK20F8.5 - CAENORHABDITIS ELEGANS, 929 aa.	1.8E-61	6
5514	cg43983897	377	CTCTCCTCCTTT GCAAGCTGACAA A[G/T]CAAGGATT TGTATGTCTCGA GAGGC	G	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q19300 CODED FOR BY C. ELEGANS CDNA YK20F8.5 - CAENORHABDITIS ELEGANS, 929 aa.	1.8E-61	6
5515	cg44926530	1746	ACACTGACAAAT TCCTAAGTTAAT G[G/gap]CTTTAG CCCAACATTTTT AGTCAGT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa.	2.1E-61	X
5516	cg44926530	213	AGGGCACAAAAG CCAGCAGCATAA A[gap]AIGAAACA TGAATAATGACT GAGAAAT	gap	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa.	2.1E-61	X
5517	cg44926530	368	CAACATGCACA TAGTATTCCTAG A[A/T]GAATATTG CCTTAATATTGT CAATA	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P51808 PROTEIN 91/23 - Homo sapiens (Human), 116 aa.	2.1E-61	X
5518	cg42701870	133	TTGCTTTGAGAG TGTATGCATGTA TTGATATATATA TGATAAATGATT ATAAC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q07325 GAMMA INTERFERON INDUCED MONOKINE PRECURSOR (MIG) - Homo sapiens (Human), 125 aa.	3.4E-61	4

5519	cg43918476	1426	TGAAATAACTGG GTTTAAAAAAA A[A/gap]GTTTAA ATGAAGCCCAAG TTTAAA	A	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34122 CGI-127 PROTEIN - HOMO SAPIENS (HUMAN), 121 aa.	6.3E-61	2
5520	cg43918476	174	TATTGTGACAGC AAATGCACATAG TTG[gap]CTGTAG GTAAGGCATGCT ACTAGGA	G	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34122 CGI-127 PROTEIN - HOMO SAPIENS (HUMAN), 121 aa.	6.3E-61	2
5521	cg43298020	572	CTTGAATAAAAC ACAAAGCCTCCGT TTATTAATAAAAA AAAAATAAAAAA AAAGA	A	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa.	7E-61	
5522	cg43982373	27	GTCGACTTTTGT TTTTTTTTTTTG /TTGAGCAACAG AGATAGTCTTTA TTC	G	T				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38195 MINDIN PRECURSOR - RATTUS NORVEGICUS (RAT), 330 aa.	8.8E-61	4
5523	cg43285334	364	AAGAGGTTCTT CTAGGAGGCC CG[C/gap]CCCTC CAAATGGTCATT TCTCTTT	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.9E-60	1
5524	cg43285334	367	AAGGTTCTTCTA GGAGGCCCGC CC[C/gap]TCCAA ATGGTCATTCT CTTTCTG	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.9E-60	1
5525	cg43285334	795	GTCAAAGCCTTG GGCGCAGCAT GC[C/gap]TACGG TTCCTAACCCCTG GGCTTTTG	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.9E-60	1

5526	cg43919808	592	AACTCAGGAGGC AGAGGCTGCAGT G/A/G]GCTGAGA TTGCACCACTGC ACTCTA	A	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O18216 Y53C12B.2 - CAENORHABDITIS ELEGANS, 277 aa.	2.3E-60	2
5527	cg43919831	1543	TTGCATTTTATT CAAATGTTATCT[ C/gap]TTTTTTC TTTGAGAAATAA ACTGT	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P91125 CODED FOR BY C. ELEGANS CDNA YK110H1.3 - CAENORHABDITIS ELEGANS, 299 aa.	9.5E-60	1
5528	cg43919831	1827	TATATGTAAATTG TGTTGTTAAAGAG[ C/G]TGATACTGA TTTTCATATGACA ATG	C	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P91125 CODED FOR BY C. ELEGANS CDNA YK110H1.3 - CAENORHABDITIS ELEGANS, 299 aa.	9.5E-60	1
5529	cg42686005	108	CAAAGAGAACAG GAATGGCTGACT C/T/C]GCATAAAT TGGCCGAAGATT ATCCA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P22486 GALANIN PRECURSOR - Homo sapiens (Human), 123 aa.	1.3E-59 (11q13.3 )	11
5530	cg42686005	174	TTCAGGTTACAG CACACAGACAAA C/G]ATGCCAG GAGGCTCTCAG GACCGCT	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P22486 GALANIN PRECURSOR - Homo sapiens (Human), 123 aa.	1.3E-59 (11q13.3 )	11
5531	cg43985327	68	TTTCTCTTTGTCC AGTTCTTTTATT[ G/T]GGGGCAGG GCACCAAGAAGA GGCC	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.1E-59	1
5532	cg43985327	80	CAGTTCTTTTATT GGGGCAGGGC A/C/gap]CAAGAA GAGGCCCTCCG CTCCCCAA	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.1E-59	1

5533	cg43958640	105	GGAGCCCCACG AATGTGAGGCCT GG[C/gap]CCCTT CCTCCAGGCCTC CAGGCCCC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43653 PROSTATE STEM CELL ANTIGEN - HOMO SAPIENS (HUMAN), 123 aa.	2.7E-59	
5534	cg43958640	99	ATTGAGGGAGCC CCACGAATGTGA G[G/gap]CCTGGC CCCTTCCTCCAG GCCTCCA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43653 PROSTATE STEM CELL ANTIGEN - HOMO SAPIENS (HUMAN), 123 aa.	2.7E-59	
5535	cg43976473	190	GACGGGGCCCC CCATGCTGTCCG GG[C/gap]CCAGG GCTGCTGTCCGC AAAGAGCG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa.	3.5E-59	11
5536	cg43939569	895	TCTTTGTACACG AACTTCATCCTC C[C/gap]GGGAAG CGGGCTGGACA GGGCTGGG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa.	3.5E-59	17
5537	cg43939569	357	AGAAAGGAGAAA GGAGAGTTACAA G[A/T]TGCCAACT CCACCATTACCC CTCCT	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa.	3.5E-59	17
5538	cg43253949	531	GTCGACTGTTGC TTGCTGGTCGCA G[A/gap]CTCCCT GACCCCTCCCTC ACCCCTC	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-59	12



5539	cg43253949	628	CCAGCCCTAGT GTCAGGGCGG GGC[gap]CTGGA GCAGCCCGAGG CACTGCAGC	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-59	12
5540	cg43253949	710	CTGCCAGTCCG GTCGCTGGCTTC GIC[gap]GCCGCC ATGGCAATGAGA CAGACGC	C	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-59	12
5541	cg43253949	710	TCGCCAGTCCG GTCGCTGGCTTC GC[gap]C/GCCGC CATGGCAATGAG ACAGACGC	gap	C				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB38041 UNR-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 350 aa.	4.3E-59	12
5542	cg44011422	883	AGGCCACCCCTG CCTCTACCCCAAC CA[G/gap]GGCCC CGGGCCCTGTTA TGTCAAAC	G	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
5543	cg44011422	885	GCCACCCCTGCCT CTACCCCAACCAG G[G/gap]CCCCGG GGCCTGTATGT CAAACCTG	G	gap				SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)

5544	cg44011422	895	CTCTACCCAAACC AGGGCCCCGGG GC[C]gapJTGTTA TGTCAAACTGTC TTGGCTGT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
5545	cg44011422	806	CAGTGGCCAAAGA TCACAGTGGCCA C[G]gapJGCCACG GCCACAGTCATG GTGGCCA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
5546	cg44011422	807	AGTGGCCAAAGAT CACAGTGGCCAC G[G]gapJCCACGG CCACAGTCATGG TGCCAC	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
5547	cg44011422	834	CACGGCCACAGT CATGGTGGCCAC G[G]gapJCCACAG CCACTAATCAGG AGGCCAG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM- BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
5548	cg44005977	604	AAATCTGTGGT ATAACAATGTAC T[G]C]ATGTTCTG TAGCTCTTTACT GAAGG	G	C			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76071 WD40 PROTEIN CIAO 1 - HOMO SAPIENS (HUMAN), 339 aa.	4.4E-59	

5549	cg43063845	740	GTATTCGGATT AGCAACCCAGGA A[A/C]CCATCACT TCTGAAGACTCT AAACT	A	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O57683 146KDA NUCLEAR PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1307 aa.	5.4E-59	
5550	cg44914411	778	GTCCCCCAGGCT GGAGTGCAGTG GC[G/A]CGATCAT GCTCACTGCAGC CTCAAT	G	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment).	7.2E-59	22
5551	cg44914411	803	GGATCATGCTC ACTGCAGCCTCA A[T/C]CTCCTGGG CTCAAGTGATCC TCCTG	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment).	7.2E-59	22
5552	cg44914411	891	CCACCGTGTCT GCCTCTATTCTT G[T/C]AATTGAAT GAGATGCTATGA GGCCC	T	C				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment).	7.2E-59	22
5553	cg44914411	915	GTAATTGAATGA GATGCTATGAGG C[C/G]CTGAGCG ACCCACAGGAAA GTACTT	C	G				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment).	7.2E-59	22
5554	cg43859535	322	TGACTTTGAAG ACGTGGCTGTGA A[C/A]TTTCCCA GGAGGAATGGA GICTCC	C	A				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92987 ZINC FINGER PROTEIN ZFP6 - HOMO SAPIENS (HUMAN), 431 aa (fragment).	9.2E-59	19
5555	cg43924537	126	AGTGCTCGACTT TCTGGTGGCAG GG[C/gap]CCAGA GCTCACGGACAC CACTGACA	C	gap				SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa.	1.2E-58	

5556	cg43924537	128	TGCTCGACTTTC TGGTGGCAGGG CC[C/gap]AGAGC TCACGGACACCA CTGACAGT	C	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa.	1.2E-58	
5557	cg43924537	55	TTTTTTTTTTTT TTTTTTAGAAA T/A/AAACTCTTGT ATTGTAGCACAT TTC	T	A			SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:Q08726 CHROMOSOME XV READING FRAME ORF YOR262W - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 347 aa.	1.2E-58	
5558	cg43986278	2035	TCTAAATGAATTA CAGGTACAGATG [G/T]TATGCTAGG TGGAGTATGCTT GATA	G	T			SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SPTREMBL- ACC:O60395 PAC CLONE DJ0911H05 FROM 7Q21-Q22, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 133 aa (fragment).	1.9E-58	7
5559	cg44915744	710	ATACAGAGTTT ATTTGAGTTTT [C/T]TTTTTGTC ATTGTCTCATG CCTG	C	T			SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:O08765 GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2) - Homo sapiens (Human), and Rattus norvegicus (Rat), 117 aa.	1.9E-58	16
5560	cg42717343	615	AAATGCTGTGCC AGGCATCTCTAA G[C/gap]CTGCC CTTACTCTGTGT GGGTTTA	C	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:P15267 KIDNEY ANDROGEN- REGULATED PROTEIN PRECURSOR (KAP) - Homo sapiens (Human), and Mus musculus (Mouse), 121 aa.	1.9E-58	
5561	cg42346579	137	CTGCGATCACTC CAGCCGGTGTG GT[C/T]ACAGCCC CACTGGGCTCCT CCACCC	C	T			SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:P42128 MYOCYTE NUCLEAR FACTOR (MNF) - Mus musculus (Mouse), 617 aa.	2.2E-58	
5562	cg42346579	151	GCCGGTGTGGT CACAGCCCCACT GG[G/gap]CTCCT CCACCCGGGAC CTTTTGACC	G	gap			SILENT- NONCODING	UNCLASSIFIED	Human Gene Similar to SWISSPROT- ACC:P42128 MYOCYTE NUCLEAR FACTOR (MNF) - Mus musculus (Mouse), 617 aa.	2.2E-58	

5563	cg42346579	204	GGGCTCTCCAGT GGAAGAGGCGG AG[Gap]CAGAG GCGGTGGTGGC AGTGGCTGG	G	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P42128 MYOCYTE NUCLEAR FACTOR (MNF) - Mus musculus (Mouse), 617 aa.	2.2E-58	7
5564	cg43916632	144	ATTTTACTCAA CAGTCTGCTTT GATGTTTTTCT TCCATAAACAAA TAC	G	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15155 BET1P HOMOLOG - HOMO SAPIENS (HUMAN), 118 aa.	2.5E-58	
5565	cg43961591	1282	CAGAGTGGTCT GTCACCAAGCTG G[Gap]GACGCTG TCACCAACGTGC AGTCCAG	gap	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O35414 STATHMIN-LIKE PROTEIN B3 (RB3) - Rattus norvegicus (Rat), 189 aa.	3.1E-58	
5566	cg43997941	581	AGCTGGGTTAGA GAGAACTCAAAT TTTCJCTGATGGA AAACAAAACCGA ACAAA	T	C			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O08612 SRC3H3 BINDING PROTEIN - MUS MUSCULUS (MOUSE), 494 aa (fragment).	3.8E-58	8
5567	cg43930685	1505	TCTTGAGACAGA CATTAGCTTTCT GIC/GICTTCCCTA TTCTCATAAGCA GCTAC	C	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa.	4E-58	
5568	cg43930685	1506	CTTGAGACAGAC ATTAGCTTTCTG CIC/GITTCCTAT TCTCATAAGCAG CTACG	C	G			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa.	4E-58	
5569	cg42466209	111	AGAGCCACCGG CAAGACAGCGTG AC[Gap]CTGCT CACCTTCATCCT GCTGCTCA	G	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75827 DJ71L16.5 (KIAA0267 LIKE PUTATIVE NA(+)/H(+) EXCHANGER) - HOMO SAPIENS (HUMAN), 616 aa (fragment).	2.2E-57	

5570	cg43931116	257	ACAACAAGATG G GCCGTGATGAGT G[G/A]GTATAATA TATTATATATAT ATAT	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa.	2.8E-57	12
5571	cg43931116	532	TAACACACACTT G CTAAGCCACCTG T[G/A]ACCAACTT GGGAATTTCTGG CCCT	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa.	2.8E-57	12
5572	cg43931116	543	TCTAAGCCACCT G GTGACCAACTTG G[G/gap]AATTC TGGCCCTTGG GGACCACA	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa.	2.8E-57	12
5573	cg43931116	553	CTGTGACCAACT C TGGGAATTTCTG G[C/gap]CCCTTG GGACCCACATCT CAGCCCT	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15420 CAGH1 ALTERNATE OPEN READING FRAME - HOMO SAPIENS (HUMAN), 138 aa.	2.8E-57	12
5574	cg43924285	1009	TGGGGTGATTC G TGCCCTTTTTT [G/T]TTTGTAAG AAAGAGGTCCT TCAT	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H1.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5575	cg43924285	1172	AACTCTGTTTTT G TAAATAAAAAA[ G/A]CCTTACATG GTCAGGGATTGA TGA	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H1.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5576	cg43924285	219	ACAGCTCCTTAG A AAGGCCAATAAT A/A/CJAGTTGGAA AAAAGGGAGTTT CCACG	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H1.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15

5577	cg43924285	351	CAC TGGGTAACG TCCAGGCGAGG GC[C/gap]ACAGG CTGGACACAGG GAACACCTTT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5578	cg43924285	674	TAAGCATTGAGA CTTTAGAAATA GTATTTTCATT TCAACTTTTTATT ATAA	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5579	cg43924285	675	AAGCATTGAGAC TTTGAATAAGT TTATTTTCATT AACTTTTATTAT AAC	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5580	cg43924285	711	ACTTTTATTATA ACATGAGCTAAA C/gap]TTTAAGAA ACAACCCCTAGTC TTCTA	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD29804 F26H11.12 PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 323 aa.	4.2E-57	15
5581	cg43984035	270	AGGTACACAAGA GTTTGTGACACA A/A/gap]TAAAATA AGAATACCTCAC ACACGT	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa.	7.5E-57	5
5582	cg43984035	275	CACAAGAGTTTG TCAGACAAATAA A/A/gap]TAAGAAT ACTTCACACACG TATCAA	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa.	7.5E-57	5
5583	cg43984035	278	AAGAGTTTGTC GACAAATAAAAT A/A/gap]GAATAC TTACACACACGTA TCAACAC	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa.	7.5E-57	5

5584	cg43984035	281	AGTTGTGACGAC AAATAAAATAAG A[A]gap]TACTTCA CACACGTATCAA CACCAT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa.	7.5E-57	5
5585	cg43984035	310	TTACACACGTA TCAACACCATAC A[A]gap]GGCATT ATTCTTCACACA GTAACAT	A	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16568 COCAINE AND AMPHETAMINE REGULATED TRANSCRIPT PROTEIN PRECURSOR - Homo sapiens (Human), 116 aa.	7.5E-57	5
5586	cg44032150	279	CCTGAGGTCCTA AAACGATTGCAG A[G]gap]CCTTGG GGTGCCCGGTG CGGCTGCT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q18886 CODED FOR BY C. ELEGANS CDNA CEESM21F - CAENORHABDITIS ELEGANS, 221 aa.	7.5E-57	14
5587	cg44032150	713	TCTGTGTGTGAC AGAAGAGATTTT A[A]C]ACACAGTG TGGGAAGTTTCT ATTTT	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q18886 CODED FOR BY C. ELEGANS CDNA CEESM21F - CAENORHABDITIS ELEGANS, 221 aa.	7.5E-57	14
5588	cg44032150	714	CTGTGTGTGACA GAAGAGATTTTA A[A]C]ACACAGTG GGGAAGTTTCTA TTTTT	A	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q18886 CODED FOR BY C. ELEGANS CDNA CEESM21F - CAENORHABDITIS ELEGANS, 221 aa.	7.5E-57	14
5589	cg43982355	490	CATAGAAAACCT TGGA AAAA ACTT TTC/TTATAAAAC ACTGTTTCAATAT AATT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43290 HYPOTHETICAL 12.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 103 aa (fragment).	7.5E-57	
5590	cg43982355	500	TTTGGAAAAAAC TTTCTATAAAACA IC]gap]TGTTTCAA TATAATTTTATTA GCAG	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43290 HYPOTHETICAL 12.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 103 aa (fragment).	7.5E-57	



5591	cg43982355	703	TCAAGAACTAGA AATGAACCTGCAC G[C/T]GTAGTGTC ACTTAAAGCAAA GCCTC	C	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43290 HYPOTHETICAL 12.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 103 aa (fragment).	7.5E-57	
5592	cg43979919	118	CTCTATTTATATA TATATATATATA ap/TJAAAAGGTTTC TTTAGCAGTTAA ATAG	gap	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:Q18580 CODED FOR BY C. ELEGANS CDNA YK30B3.5 - CAENORHABDITIS ELEGANS, 755 aa.	1.2E-56	1
5593	cg43979919	122	TATTTATATATAT ATATATATAAA A[gap]GGTTCTTT AGCAGTTAAATA GATTC	A	gap			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:Q18580 CODED FOR BY C. ELEGANS CDNA YK30B3.5 - CAENORHABDITIS ELEGANS, 755 aa.	1.2E-56	1
5594	cg43919432	204	GTTTGGAAAGTT CACTCTAAAGAA T[G/A]AAGTCACC TGTTGTCACGTG CCTCC	G	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:O17088 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
5595	cg43919432	281	TACCATCCTGTG GCTCCTTAAGGA G[G/T]CTTCTCTC TTTAATTCTCCAT GAGG	G	T			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to SP TREMBL- ACC:O17088 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
5596	cg44926486	124	AACGTACATGGT TTAATACAACAA C[gap/A]AAAAAA ATTTAATCAAGT GAACGT	gap	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa.	1.5E-56	3
5597	cg44926486	131	ATGGTTTAATAC AACAAACAAAAA A[gap/A]TTTAATC AAGTGAACGTA ATAAAC	gap	A			SILENT- NONCODING NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa.	1.5E-56	3

5598	cg44926486	77	ATAATTGCTCAC AAAGATTCATAG A[gap]/TJTITTTT TTATTGTTAAGCT GCAAC	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa.	1.5E-56	3
5599	cg44926486	86	CACAAAGATTCA TAGATTTTTTTTTT gap/TJATTGTTAA GCTGCAACGTAC ATGGT	gap	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27785 PROTEIN TRANSLATION FACTOR SUI1 HOMOLOG - HOMO SAPIENS (HUMAN), 113 aa.	1.5E-56	3
5600	cg43991184	1164	AAACCATGTGGG TGCACAAAGCCA G[G/gap]CACTGC CAAGTGGAACAT GAGGTTA	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment).	2E-56	1
5601	cg43968980	232	CGTTGCCCCCTC AGCCTCTAGGAG G[C/gap]CTCAGG ATTATGGCGTCC ATCTTAT	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5602	cg43968980	262	GGATTATGGCGT CCATCTTATGAT AT/CTTGGCCAAA AGGAGACAGTCT TGGAG	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5603	cg43968980	268	TGGCGTCCATCT TATGATATTGGC C[A/G]AAAGGAG ACAGTCTTGGAG GIGCTG	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5604	cg43968980	360	GGGAAAGGAATC TTTAGGCAGACT G[C/gap]CATCCA GGGACTGCTATT CTGTTCA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5

5605	cg43968980	361	GGAAAGGAATCT TTAGGCAGACTG C[C/gap]ATCCAG GGACTGCTATTC TGTTTCAC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5606	cg43968980	45	TTTTTTTTTTTT TTTTTTTTTTTTA /TGTATTTAGGG ATGCATTTTGAA TAT	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5607	cg43968980	48	TTTTTTTTTTTT TTTTTTTTTAGTA /TJTTAGGGATG CATTTGAATATT TA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5608	cg43968980	49	TTTTTTTTTTTT TTTTTTTTTAGTAT /AJTTAGGGATGC ATTTTGAATATT AT	T	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5609	cg43968980	559	GGGAGCAGGAG CTGAGGTGGAG ACG[G/gap]CCAC TGCCTCTCTCAG CCTCTGTTTC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
5610	cg43308180	951	AGCCACCCACCT CCAAACACCTCCT G[A/T]GCGTCTGA TGCTCCACACCAG GCCAG	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD10847 CHEMOKINE - HOMO SAPIENS (HUMAN), 113 aa.	5.3E-56	
5611	cg43308180	959	ACCTCCAAACACC TCCTGAGCGTCT G[A/T]TGTCTCCA CCAGGCCAGCT CTCCTC	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD10847 CHEMOKINE - HOMO SAPIENS (HUMAN), 113 aa.	5.3E-56	

5612	cg43306180	960	CCTCCACACCT CCTGAGCGTCTG A/T/A/GCTCCAC CAGGCCAGCTCT CCTCC	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD10847 CHEMOKINE - HOMO SAPIENS (HUMAN), 113 aa.	5.3E-56	
5613	cg44001479	864	TTTCCGCACCAA CGCGCCCGCCA TG[G/gap]CTGTG CCGACACCAGAC CCCGAGTG	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39918 HSPC040 PROTEIN - HOMO SAPIENS (HUMAN), 109 aa.	1.4E-55	6
5614	cg44001479	295	CTGCAGATAAAA CCATCATCAGAA A/G/T/TATTAAAT TAATTGCATATTT TGAG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD39918 HSPC040 PROTEIN - HOMO SAPIENS (HUMAN), 109 aa.	1.4E-55	6
5615	cg43935092	599	CAGCCTGCTGTA CTGGCCATGCTG G[gap]/GCCAGCC CCACCTGGAGCT CAGTAA	gap	G				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD26992 VAMP5-LIKE PROTEIN HOMO SAPIENS (HUMAN), 116 aa.	1.8E-55	2
5616	cg44019498	366	AAAAGAAAGAAA GAAGAATGGAA A/G/A/JAAAAGAG AAAAAAACCACC ACAAA	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45970 HYPOTHETICAL 43.5 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 392 aa.	1.8E-55	15
5617	cg44019498	457	TGGTGAAGACTT TTGGTAGCAAAA T/C/T/TGCACGGT TCTTAAATGGG AGTCT	C	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45970 HYPOTHETICAL 43.5 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 392 aa.	1.8E-55	15
5618	cg43917388	313	AAGAAAAACTTT GTAATCAATATC C/T/C/GCTCATAA GTAAAAGTGGAA AAGAA	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q22453 SIMILARTO LDL RECEPTOR-RELATED PROTEIN. NCBI GI: 1055166 - CAENORHABDITIS ELEGANS, 1357 aa.	2.3E-55	1

5619	cg43917989	829	CGCCTTGCTGGT G TCTGAGCCCTGG G[G/A]CTCGGAC CACTGACCCTGG CGCTTG	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 ERECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.3E-55	11
5620	cg43928349	129	AAAAAGTGCTGC G TGC GGCCG CAG AC[G/gap]CCAGT GCTGGCCCTCA GGGGGCCCC	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5621	cg43928349	181	CAGCCGGCGAG C GGCGGGGACTT CCG[C/gap]CGCC AATCCCTGAGGG GGTAACATC	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5622	cg43928349	182	AGCCGGCGAGG C GGCGGGGACTT CGC[C/gap]GCCA ATCCCTGAGGG GGTAACATCG	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5623	cg43928349	238	CAATCCCTGAGC C TGGGCAGGGTG GG[C/gap]CCCCG TCACCCCTCTGG GCTGCCCCA	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5624	cg43928349	241	TCCCTGAGCTGG C GCAGGGTGGGC CC[C/gap]GCTCA CCCCCTGGGC TGCCCCACCC	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	

5625	cg43928349	247	AGCTGGGCAGG GTGGGCCCGC TCA[C/gap]CCCC CTGGGCTGCC ACCCCGGGGT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5626	cg43928349	252	GGCAGGTGGG CCCCGCTCACCC CC[C/gap]TGGC TGCCACACCCG GGGTGTTCC	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5627	cg43928349	293	GGGGTGTCCC GCCGACTTCTGG GC[G/gap]GGCC TCCCGGGCCAG GCCTGCCGG	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5628	cg43928349	307	GACTTCTGGCG GGCCTCCCG GC[C/gap]AGGCC TGCCGGGGGG GGCCCCGAG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5629	cg43928349	329	GGCAGGCCCTG CCGGGGCGGG GCC[C/gap]GAGC AGCCGGACTGG CCAGGTTACG	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5630	cg43928349	345	GGGGGGCGCG AGCAGCCGGAC TGG[C/gap]CAGG TTCAGCGCGCCT CAGTAGGGT	C	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	

5631	cg43928349	415	GGACACCTGGG AGATGCGCCGC GAG[G/gap]ACCG CCACAGCTTCCG CGCGAACTG	G	gap			SILENT- NONCODI- NG	UNCLAS- SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5632	cg43928349	450	GCTTCCGCGCG AACTGGCTGCTG CG[C/gap]ACCTC AGAGGGCTGCC CCGCGACCA	C	gap			SILENT- NONCODI- NG	UNCLAS- SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41633 LYSOSOMAL TRAFFICKING REGULATOR 2 - HOMO SAPIENS (HUMAN), 472 aa (fragment).	4.1E-55	
5633	cg42904952	109	CCTTGAAGTGAT CTCTAGGCCCCA G[C/gap]CCCCAA TCCGCCACCAT CCGTGCT	C	gap			SILENT- NONCODI- NG	UNCLAS- SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41781 CYTOPLASMIC PHOSPHOPROTEIN PACSIN2 - HOMO SAPIENS (HUMAN), 486 aa.	6E-55	
5634	cg43928664	28	TTTTTTTTTTTT TTTTTTTTTTAT /CJTTTACAAAGAT AATCTTTATTGAT A	T	C			SILENT- NONCODI- NG	UNCLAS- SIFIED	Human Gene Similar to SPTREMBL- ACC:O43805 NUCLEAR AUTOANTIGEN FO 14 KDA - HOMO SAPIENS (HUMAN), 119 aa.	9.8E-55	9
5635	cg43978709	487	GTAAGAATTTT ATTGTTCTATAG A/GCACCTCTGA AAAGAGATCTAA TTGA	A	G			SILENT- NONCODI- NG	UNCLAS- SIFIED	Human Gene Similar to SWISSNEW- ACC:O42204 INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16) - Gallus gallus (Chicken), 262 aa.	1.3E-54	
5636	cg43978709	582	TGAAGGCGTTAC AGCCCTCCTCTC C/A/GJAGGCTCA GGGCTGAGAAC GGTTAGC	A	G			SILENT- NONCODI- NG	UNCLAS- SIFIED	Human Gene Similar to SWISSNEW- ACC:O42204 INTEGRAL MEMBRANE PROTEIN 2B (TRANSMEMBRANE PROTEIN E3-16) - Gallus gallus (Chicken), 262 aa.	1.3E-54	
5637	cg43927929	216	GCCACAGCCTCCT CGAGTAGCTGG GAT/CJTACAGGT GCCCCGCCACCA CACCCAG	T	C			SILENT- NONCODI- NG	UNCLAS- SIFIED	Human Gene Similar to SWISSPROT- ACC:P35250 ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (A1 40 KD SUBUNIT) (RF- C 40 KD SUBUNIT) (RFC40) - Homo sapiens (Hutnah), 354 aa.	1.6E-54	7

5838	cg43927929	417	TAAAGGACAGTC ATGTTGGCTCCA G[C/gap]CTAAGG CGGCATTTTCCC CCATCAG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P35250 ACTIVATOR 1 40 KD SUBUNIT (REPLICATION FACTOR C 40 KD SUBUNIT) (A1 40 KD SUBUNIT) (RF- C 40 KD SUBUNIT) (RFC40) - Homo sapiens (Human), 354 aa.	1.6E-54	7
5839	cg41664708	437	TCACCTTACACG CTCATGGACTGA G[T/A]TTATACCTC ACCTTTTATGAA AGCAC	T	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1- ALPHA) - Homo sapiens (Human), 114 aa.	2E-54	1
5840	cg41664708	446	ACGCTCATGGAC TGAGTTTATACT C[A/G]CCTTTTAT GAAAGCACTGCA TGAAT	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P47992 LYMPHOTACTIN PRECURSOR (CYTOKINE SCM-1) (ATAC) (LYMPHOTAXIN) (SCM-1- ALPHA) - Homo sapiens (Human), 114 aa.	2E-54	1
5841	cg43135067	688	GCCCCGGAGCC CCATCCTGGGCC TG[C/gap]CCTGG CTGGCCAGGAC CCCAGCGGT	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83094 X11L2 - HOMO SAPIENS (HUMAN), 369 aa (fragment).	6.1E-54	19
5842	cg43983352	1027	GATTGCAGCTG GTTCTCCAGGG A[A/G]TTGGCCC CGAAGCTGGCTC AGTTCA	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD45832 WUGSC:H_DJ0747G18.5 PROTEIN - HOMO SAPIENS (HUMAN), 261 aa (fragment).	6.9E-54	11
5843	cg43983352	1039	GTTCTCCAGGG AATTGGCCCCGA A[G/gap]CTGGCT CAGTTCACCTCC AGGACCT	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD45832 WUGSC:H_DJ0747G18.5 PROTEIN - HOMO SAPIENS (HUMAN), 261 aa (fragment).	6.9E-54	11
5844	cg43123055	318	TAAGCCACGCTG TTGTGCTGCCCC C[gap]/TATTATTG GTGTCATTTCTG CAGTAT	gap	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P08949 NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN B] - Homo sapiens (Human), 121 aa.	8.8E-54	2



5645	cg43243118	170	GATATTATTGTC TTGACGCTGGTG [C/T]CAAAATAAA TATTAGAAAGTG TTTT	C	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q82599 MYELOBLAST KIAA0202 - HOMO SAPIENS (HUMAN), 508 aa (fragment).	9.9E-54	5
5646	cg43957121	174	TTAATGCTTTGG CAGATGAAGTAA C[G/A]TTTGAAAA CTGTTTGTGAAA ATAGT	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60067 HYPOTHETICAL 74.7 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 649 aa.	1.7E-53	4
5647	cg43957121	425	GCTTCCAGACA GTCAAGGCCGG AG[G/gap]TCGCT CCTGTCCTGTGG TCTGAGCC	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60067 HYPOTHETICAL 74.7 KD PROTEIN - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 649 aa.	1.7E-53	4
5648	cg43948151	80	CATAAAGTGCAT CTTATTAAAAAAT [G/A]TATAAAAC CACATAAATTCA GGGC	G	A			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62179 SEMAPHORIN C (SEM C) - MUS MUSCULUS (MOUSE), 782 aa (fragment).	2.3E-53	15
5649	cg43958224	284	TTGCTGTTTGT ACCGGGGCTCT GC[C/gap]CTGGT CCTGTCACCCCT GAGACGTC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment).	2.3E-53	19
5650	cg43958224	285	TGCTGTTTGT CCGGGGCTCTG CC[C/gap]TGGTC CTGTCACCCCTG AGACGTCC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment).	2.3E-53	19
5651	cg43958224	489	CAACACCCATTA GAAGCACCTGGA A[G/gap]GGGGGT TTTGGGAAACGG GCTCAGA	G	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43298 HYPOTHETICAL 13.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 118 aa (fragment).	2.3E-53	19

5652	cg43928097	224	TCTAACATTTATT TATTTACAGTTT G[gap]TTTTTTTT TGGCAACTATAA ATTA	G	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62739 RABIN3 - RATTUS NORVEGICUS (RAT), 460 aa.	4.3E-53	
5653	cg43969772	231	TAAATCATCATAA AAATGTTTAAAGT A[gap]AAAAAAA AAAAGAAAGAGA AAGAA	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
5654	cg43969772	243	AAAATGTTTAAAG TAAAAA A[gap]GAAAGA GAAAGAAAGAGA GGAGGTA	A	gap			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
5655	cg43969772	243	AAATGTTTAAAGT AAAAA A[gap]GAAAGA GAAAGAAAGAGA GGAGGTA	gap	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
5656	cg43969772	31	TTTTTTTTTT TTTTTTTTTTT TTTAACTAAAGG ACATTTATTTATT TT	A	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
5657	cg43934126	297	GCAATGGCCGCC ACGTGAGCTCAA AC[G/T]TCCGTT ATTCAAAGCAG TAATAA	G	T			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q60372 R33683_3 - HOMO SAPIENS (HUMAN), 103 aa (fragment).	4.9E-53	
5658	cg43983169	953	GTTTATTGTGCA GAACAGACAGTG AT/AJAATACACT AGAGAAATATTT TCAAC	T	A			SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P52926 HIGH MOBILITY GROUP PROTEIN HMGIC - Homo sapiens (Human), 109 aa.	7.7E-53	12

5659	cg43986294	1277	TGTGGTTTTGT GTTTTTTTTTTT T/gap CTTTTTCC ATAGGAAAGAAT ATATA	T	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O22730 UNKNOWN PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 240 aa.	5.9E-52	
5660	cg43986294	1333	GTAATCCTAAT TCAAAGATGGCT C A G T G T G A GGCATTGAGTT TGATT	A	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O22730 UNKNOWN PROTEIN - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 240 aa.	5.9E-52	
5661	cg43980016	384	TTTTTTTTTTT TTTTTTTTTTTT// G C T G C A T A A A TACTGTTATTT G	T	G			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62509 ZINC FINGER PROTEIN - MUS MUSCULUS (MOUSE), 354 aa (fragment).	7.1E-52	1
5662	cg42732394	160	GTAGAGTTAAGG GCTTGGCAAGTT G C /gap CCACTC CTATCCCTGGTC TAGCTGC	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60516 EUKARYOTIC INITIATION FACTOR 4E-BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 100 aa.	9.1E-52	5
5663	cg42732394	243	TCACTCCCTTCC AGATTAGATGAG G C /gap CCAGCT GGCCTTTGGATG CCCCAGG	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60516 EUKARYOTIC INITIATION FACTOR 4E-BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 100 aa.	9.1E-52	5
5664	cg42732394	245	ACTCCCTTCCAG ATTAGATGAGGC C C /gap AGCTGG CCTTTGGATGCC CCAGGAA	C	gap			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60516 EUKARYOTIC INITIATION FACTOR 4E-BINDING PROTEIN 3 - HOMO SAPIENS (HUMAN), 100 aa.	9.1E-52	5
5665	cg44923868	377	AAACAAGCTTGG TCTCTTCTCTGC C A T GGGTACCA CAGGGACACAC GCCAAG	A	T			SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD45963 ASPARTYL PROTEASE - HOMO SAPIENS (HUMAN), 518 aa.	1.2E-51	11

5666	cg43241808	1106	TTTCTCTCAAACA TCTGCCACCTGA G[G]gap]CTAAGC CTACACACGGCG TGGCTGA	G	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41781 CYTOPLASMIC PHOSPHOPROTEIN PACSIN2 - HOMO SAPIENS (HUMAN), 486 aa.	1.2E-51	
5667	cg43241808	137	ATTTTTCCTCA AATACTACACAT GTTTAAAGGAAC TGTTAAACTGAA AAAG	G	T				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD41781 CYTOPLASMIC PHOSPHOPROTEIN PACSIN2 - HOMO SAPIENS (HUMAN), 486 aa.	1.2E-51	
5668	cg43916927	392	AGCCATAAGTTA AAAAGAAGACAA G[C]gap]TGAAGC TACACACATGGC TGATGTC	C	gap				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60829 JM27 PROTEIN, COMPLETE CDS (CLONE IMAGE 145745 AND IMAGE 257878) - HOMO SAPIENS (HUMAN), 102 aa.	1.9E-51	
5669	cg43980942	553	ATTTCATTAACTT AAAAGGTGGACA TTTAAATGTTTAT TTTAAATCTAATT GAA	T	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P09132 SIGNAL RECOGNITION PARTICLE 19 KD PROTEIN (SRP19) - Homo sapiens (Human), 144 aa.	3.9E-51	5 (5q21)
5670	cg44014613	277	AATAGCAGCAAA CTGGGAAAAAAA A[gap/A]CCTCCT GTCCATAAATAG AAGTACC	gap	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P97443 ZINC-FINGER PROTEIN BOP - MUS MUSCULUS (MOUSE), 490 aa.	4.8E-51	1
5671	cg43994444	1045	GGACCTTGCACC ATCAGCTTTCT G[G/A]GTTTCCAG CCTCCTGCCTCA CACTC	G	A				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O75570 MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1) - Homo sapiens (Human), 445 aa.	5.8E-51	
5672	cg43994444	460	GAAGGCAAGCTA GCAGGATGCTCC CTT[C]GAAACCTC TTTTATTATGGG CCTTC	T	C				SILENT- NONCODI NG	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O75570 MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1) - Homo sapiens (Human), 445 aa.	5.8E-51	

5673	cg43894384	448	GTACAAATAGAA C ACCACAAAAGG TTC/TTGGATTG GGTTAAGGTGAA GAGAC	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15553 PYRIN - HOMO SAPIENS (HUMAN), 781 aa.	8E-51	
5674	cg43899706	83	GTTTATTCAACA C TTATGGCATGGC [C/gap]AGTGTA TTGTTCCAACAA AGGGAA	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42873 PLECKSTRIN 2 - MUS MUSCULUS (MOUSE), 353 aa.	8.2E-51	14
5675	cg43916704	1031	CGTGGCAGGGG G CAGCTATCTGGG AG[G/A]GCTAAAC AGCCTGGAGGC TGAGTCT	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa.	1.1E-50	20
5676	cg43916704	2091	TTGAAGCTGAGA T GGCTGTGGATCT A/T/C]AGGAGATT CCAGCAGCATCA TGCGT	T	C				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa.	1.1E-50	20
5677	cg43916704	386	CATCCAATTCCA G GCATGGTCAGCA C[G/A]GAGATATT CACAGAAAAGAA CCCAG	G	A				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa.	1.1E-50	20
5678	cg43916704	750	GAGCTTCCCAA C TCCTAGAGAATG A[C/T]TGACTTA GAAAGTTTGT TTGT	C	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O62265 F57C2.5 - CAENORHABDITIS ELEGANS, 387 aa.	1.1E-50	20
5679	cg41004313	161	GGACAAAAGACA A AAGAATGACACT TTA/TCTCCTCTT TTGACTTTGACA CCCAA	A	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62383 SUPPRESSOR OF TY 6 (S. CERVISIAE) HOMOLOG (SUPT6H) MUS MUSCULUS (MOUSE), 1726 aa.	2.5E-50	

5680	cg41004313	499	GTGGGGGAGAAG CTTGAGGCTGG GGC[C/gap]TCCT CACCATCATCCT CCTCTTCCA	C	gap		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREVISIAE) HOMOLOG (SUPT6H) MUS MUSCULUS (MOUSE), 1726 aa.	2.5E-50	
5681	cg42903672	129	AGGCGGGCGGG TGGGCGGGGGG AGC[C/gap]GAGC AGTCACGTATGG GGCATCTGC	C	gap		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34131 CGI-136 PROTEIN - HOMO SAPIENS (HUMAN), 125 aa.	3.5E-50	
5682	cg43258766	157	CCTGCGTGCCCTC CCTGCCAGTCTT C[C/T]CCGTCTAA CCCTCAGTCCCT CTATC	C	T		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa.	3.7E-50	7
5683	cg43258766	353	AGCAACAGTCC ATGCCATCCAGC C[T/C]GGGAGGC TGGGGGAGAGG AAGATGA	T	C		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa.	3.7E-50	7
5684	cg43258766	405	GGTGACTCCAGC ACAGCCAGCCTT G[C/gap]TGCGCA GGTGCCAGAGG CATAGGGA	C	gap		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa.	3.7E-50	7
5685	cg43258766	409	ACTCCAGCACAG CCAGCCTTGCTG C[G/A]CAGGTGC CAGAGGCATAG GGAGGAG	G	A		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19465 Y17G7B.18A PROTEIN CAENORHABDITIS ELEGANS, 378 aa.	3.7E-50	7
5686	cg41568177	62	GAGAAGACATTT TATTGTTCTGG G[gap/G]TCTCTG GAGGCCCATG GTGGGGCT	gap	G		SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P31151 S100 CALCIUM-BINDING PROTEIN A7 (PSORIASIN) - Homo sapiens (Human), 100 aa.	4.5E-50	1 (1q21)

5687	cg40357240	113	AGAGTGAATTTT TTCTTGGGGACT TC/GJTTTTCTC CAGGGAAGGCT AAAAAA	C	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45741 HYPOTHETICAL 112.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 1008 aa (fragment).	5.4E-50	
5688	cg44010855	1541	CATGTTCTTTC CCTCACCACAAC A/GTAAACATGCA GTACTAAAGCAA TATAT	G	T				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.8E-50	5
5689	cg44010855	1749	GCTATGTACATG TCAGAAACCAATT A/Ggap]CATTGC ATGCAGGTTTCA TATGCT	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.8E-50	5
5690	cg43916819	497	AAGGCATACAAC ATGAGCCTTG G/Ggap]CACTGC CTCACCAACCAC TGGTGGC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43182 DJ681N20.1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	6.1E-50	20
5691	cg43870748	328	ATAGGGGAAGAC AACAGGCCAAG GC/Cgap]ACTCT GTGTTACTTTTC CTGAAGTC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62418 DREBRIN-LIKE SH3 DOMAIN-CONTAINING PROTEIN SH3P7 - MUS MUSCULUS (MOUSE), 433 aa.	7.4E-50	7
5692	cg43970748	385	TTGAGGCACACA CTGGGGCCTGC AG/Ggap]CATCG AGTGAGCCGCG TGGAGGAAC	G	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62418 DREBRIN-LIKE SH3 DOMAIN-CONTAINING PROTEIN SH3P7 - MUS MUSCULUS (MOUSE), 433 aa.	7.4E-50	7
5693	cg43970748	773	TGGCAGTGGCC ACTCAGGGCTTG GC/Cgap]ACAGG CAGGGCTTGGCT CAGTATCC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62418 DREBRIN-LIKE SH3 DOMAIN-CONTAINING PROTEIN SH3P7 - MUS MUSCULUS (MOUSE), 433 aa.	7.4E-50	7

5694	cg43279836	464	TGAGATTTCATAT TAAAAAAGCCAC C[A/G]ACTGATCA TCTGAGAAACCA ACACA	A	G				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O77836 UDP-GLCNAC:A-1,3-D- MANNOSIDE B-1,4-N- ACETYLGLUCOSAMINYLTRANSFERAS E IV (EC 2.4.1.145) (ALPHA-1,3- MANNOSYL-GLYCOPROTEIN BETA-1,4- N- ACETYLGLUCOSAMINYLTRANSFERAS E) (N-GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E IV) - BOS TAURUS (BOVINE), 535 aa.	7.4E-50	
5695	cg43979181	139	TGGGAGCAGCT GGGATGATGGG GA[C/gap]CCCAC ATCCATAGGGCT GGGAGGTC	C	gap				SILENT- NONCODING	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P02818 OSTEOCALCIN PRECURSOR (GAMMA- CARBOXYGLUTAMIC ACID- CONTAINING PROTEIN) (BONE GLA- PROTEIN) (BGP) - Homo sapiens (Human), 100 aa.	7.4E-50	
5696	cg43298242	37	GGACAAGCCTTG CTTTATTGGGA A[G/T]GGATGGG ATCACAAATAAT CTCTGC	G	T				SILENT- NONCODING	water_ch annel	Human Gene SWISSPROT-ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	1.3E-163	
5697	cg42913771	348	CATGAGGTGTCG ACTTCCAGCCAC GT[C/J]AGATGCC GATTGCTTCCTG TGTC	T	C	Val	Ala (7868)		CONSERVATIVE	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.2E-116	
5698	cg43277632	1853	AACTACAGATGG TACACCTACATC TIG/CITGCAGGA AGTGGCTCCCCA CACTGG	G	C	Val	Leu (7869)		CONSERVATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3 )



5699	cg43931944	323	GCACTGGTAAAC CCCTCTCTGTAG AIGCJCTTGGTCC TGGCATTATGGG AGCCA	G	C	Glu	Asp (7870)	CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa.	0	
5700	cg43931944	324	CACCTGGTAAACC CCCTCTCTGTAGA GICGJTGGTCCCT GGCATTATGGGA GCCAT	C	G	Leu	Val (7871)	CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa.	0	
5701	cg43931944	688	TTCACCATGGTG CAAGTATGGCCT GTCJACGTCAAG TTCGACCTGTCA CTGAG	T	C	Val	Ala (7872)	CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P38606 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa.	0	
5702	cg43251803	2946	TAGCAGGACACT GCCATCTGAATC TIGCJCTCGGTAC GCACTCGTTTCA TGACT	G	C	Gln	Glu (7873)	CONSER VATIVE	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.1E-105	
5703	cg43251803	3000	CATCCCAGGCG GCCCCGGCTCC CCAIGJGCGGC CCCCGCCCCC ACGCCGCCG	G	C	Leu	Val (7874)	CONSER VATIVE	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.1E-105	
5704	cg43933735	444	TGGCATTATGCA GACTCCCTCAGG CIGAJTGCAGTC ATCCATCAGCAA TTGAC	G	A	Arg	His (7875)	CONSER VATIVE	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:Q12897 PROBABLE CALCIUM- TRANSPORTING ATPASE 9 (EC 3.6.1.38) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1472 aa.	1.7E-80	

5705	cg43988460	1624	CCAGCCTCCAAC TGGTATCTTCAT TATCTCAACCCC ATCTCGGGTCAG CTGTC	A	C	Ile	Leu (7876)	CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P19022 NEURAL-CADHERIN PRECURSOR (N- CADHERIN) - HOMO SAPIENS (HUMAN), 906 aa.	0	18 (18q11.2)
5706	cg43985533	328	AATAATTACCTG ATGGAAGTCACC C[G]A[CTTGCCG GATGTAACCAGC CACTTC	G	A	Ala	Val (7877)	CONSER VATIVE	cathepsin	Human Gene Similar to SWISSNEW- ID:P10619 LYOSOMAL PROTECTIVE PROTEIN PRECURSOR (EC 3.4.16.5) (CATHEPSIN A) (CARBOXYPEPTIDASE C) - HOMO SAPIENS (HUMAN), 480 aa.[pcls:SWISSPROT-ID:P10619 LYOSOMAL PROTECTIVE PROTEIN PRECURSOR (EC 3.4.16.5) (CATHEPSIN A) (CARBOXYPEPTIDASE C) - HOMO SAPIENS (HUMAN), 480 aa.	2E-52	7
5707	cg43980411	430	CTCTGCAATCAA TGCAATCCACAGG G[A/G]ATTATTTA CTGGAAAAGTGC AATAA	A	G	Asn	Asp (7878)	CONSER VATIVE	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG- SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222	18 (18q21.3)
5708	cg43970982	2132	GGACCTCGGGG AAGCGGAGGTG CCG[C/G]TGGTG CTCCTGGAGAAC GAGGCAGA	C	G	Ala	Gly (7879)	CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
5709	cg43970983	1219	GGGGGTCCTCA GTGGTGGGCCC ACA[G/C]AACAG CAGGAGCTGGG CCCTGGGCA	G	C	Glu	Gln (7880)	CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
5710	cg43970983	1668	CTGTAACAGACC TGCAAGCCACCG A[G/C]GTGCCCG GGCAGCGGGTG CGAGTGT	G	C	Glu	Asp (7881)	CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)

5711	cg43970983	1669	TGTAACAGACCT GCAAGCCACCG AG[G/C]TGCCCG GGCAGCGGGTG CGAGTGTC	G	C	Val	Leu (7882)	CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
5712	cg43991318	4971	CCGGGAGACCC CGAGGGAATACT CTA/TJCGCGTG GGCTGGGTCAC GGGGGCCG	A	T	Tyr	Phe (7883)	CONSER VATIVE	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
5713	cg43991318	5053	GTTGCGGATCTT CTTGATGGCAGA CT/GTCTTCATG AGGCTGAGTCG GTGGAT	T	G	Glu	Asp (7884)	CONSER VATIVE	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
5714	cg43933757	1606	TCCAGTGGGG GTGGGAGATCCT GC[A/G]TTGGAG AAACGACAGAAA GCACACA	A	G	Ile	Val (7885)	CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P10843 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0	5 (5p13)
5715	cg43084083	2416	TCTAACACCTG GGAAATTC AAG C[G/A]TTGGCATT TCAAACACTGGT ATA TG	G	A	Val	Ile (7886)	CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P01031 COMPLEMENT C5 PRECURSOR (CONTAINS: C5A ANAPHYLATOXIN) - HOMO SAPIENS (HUMAN), 1676 aa.	0	9 (9q34.1)
5716	cg43956185	955	AACATTTCATAA GGCTCCTACAT TTG/CJATAACGTA CTCTCTCACCAG A JGGA	G	C	Gln	Glu (7887)	CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
5717	cg43956185	1003	GGATATTACTC ATCTGTCTCGAC A/C/GJATATAAG CATTTGTACTG TGGGC	C	G	Val	Leu (7888)	CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1

5718	cg43956185	591	ATATCCACGTTT ACACACAAATTC A[G/A]CTGATTCA CCTGTTCTCAAA TAAAG	G	A	Ala	Val (7889)	CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
5719	cg42542496	440	CGTGACTCCCAT GTCCTTCACAGC A[G/A]ACTGAGC CAGTGCCCGAGA GGTTCAC	G	A	Arg	Lys (7890)	CONSER VATIVE	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.2E-189	3 (3q26.3)
5720	cg43957094	2211	AGCTTGCCCTGA TAAAAAAGCACC A[G/C]CCGGCGG AGCGGCCGCGG AGCGACC	G	C	Leu	Val (7891)	CONSER VATIVE	cyclin	Human Gene SWISSPROT-ID:P24863 G1/S-SPECIFIC CYCLIN C - HOMO SAPIENS (HUMAN), 303 aa.	7.9E-164	6
5721	cg43242733	635	GACTTGATGAGA ATGGAAAAGATT G[C/T]AATGGAGA AGGTGTGTTGGA AAGTC	C	T	Ala	Val (7892)	CONSER VATIVE	cyclin	Human Gene SWISSPROT-ID:P51959 G2/MITOTIC-SPECIFIC CYCLIN G1 - HOMO SAPIENS (HUMAN), 295 aa.	1.3E-154	5
5722	cg43996855	3915	AAGTTCTCCGGG TTAGGCCACTTC A[G/C]TGGGTCAT GATTCACAGACC ACTGG	G	C	Leu	Val (7893)	CONSER VATIVE	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.2E-293	2 (2p22)
5723	cg43966704	1275	CGGCCCTCAAA CCCGATGTCTTG ATT/CJCTCGCCCA GGATCCAGTCG GGCCCC	T	C	Ile	Val (7894)	CONSER VATIVE	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11

5724	cg4396704	596	GAGGTTGTCCCA GCCGCCCGTGA CA C A CCCCAG CATGCTTCTCAA TCAGTTC	C	A	Gly	Val (7895)	CONSER VATIVE	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11
5725	cg43962888	447	GCAGGCGACTG GGTTGGAGAGG GAG A G TCATG CTGGCTGCAAAG AAGGGACT	A	G	Ile	Val (7896)	CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
5726	cg43962888	463	GAGAGGGAGAT CATGCTGGCTGC AA A G GAAGG ACTGGACCCATA CAATGTA	A	G	Lys	Arg (7897)	CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
5727	cg43962888	517	GCCCCAAAGGG AGCTTCAGGCAC CA G A GGAAGA CCCTAATTTAGT CCCTCC	G	A	Arg	Lys (7898)	CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
5728	cg43962888	546	AGACCCCTAATT AGTCCCTCCAT CT A CCAACAAG AGAATAGTAGGC TGCA	T	A	Ser	Thr (7899)	CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
5729	cg43962888	621	CGTCTGGTTTG GCTGCACAAAGG C G C AGGCCCA GCGATGCCCCC GCTGTGG	G	C	Glu	Gln (7900)	CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
5730	cg4396112	3497	ACTTGCTTCCCA GCAAAACAGCG CA G C CTGCTC CAGGACCCCTCT GAACACC	G	C	Leu	Val (7901)	CONSER VATIVE	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)

5731	cg44033747	1337	TTGGCGAATATG GCTGCCATGTTT G/GCJAATCTACC ATGGTCCCATG GGCTG	G	C	Gly	Ala (7902)	CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0	9 (9p22)
5732	cg43057018	1597	TGACCTAATGAA CCAAGGAAAAAG C/A/GJTCCGAACA ATCCTCATCTTTT GAAG	A	G	Ile	Val (7903)	CONSER VATIVE	dehydrog enase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.lpcds:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.3E-209	4 (4q22)
5733	cg43973273	1476	CAGCCTTCTCTT GGACAGCGACAT A/C/GJATCCCTTT CTGGGGCATGA GTTTC	C	G	Val	Leu (7904)	CONSER VATIVE	dna_ma_ bind	Human Gene Homologous to SPTREMBL-ID:Q13097 DNA/RNA- BINDING PROTEIN - HOMO SAPIENS (HUMAN), 363 aa (fragment).	2E-112	
5734	cg43327854	1114	TCAAGTGGAGGA TGATGGGGATG GC/GJAATTACAT GTCTGAGCCTGA GGCTGT	G	A	Asp	Asn (7905)	CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.5E-57	1
5735	cg43958656	566	AACCGGCATGG CCAAAGCCGCG GCG/A/GJTCGGC ATCGACCTGGGC ACCACTA	A	G	Ile	Val (7906)	CONSER VATIVE	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0	6
5736	cg44017749	12288	GCGCCTCCTACC ACTTCCAACCGC C/G/AJCCGGCGA CAGATTGACCGG GGTGTC	G	A	Arg	His (7907)	CONSER VATIVE	eph	Human Gene SWISSPROT-ID:Q07854 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0	12

5737	cg43950268	2136	GCTCCCGGCTG AGGTTCAAGGG AATG/CJTCCTCA CTGTCCACCACA CCTCGGA	G	C	Asp	Glu (7908)	CONSER VATIVE	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16
5738	cg43982507	637	CATGGGCACGTC CGCGCTCTGGG CG/CJGTCTGGC TGCTGCTCGCGC TGTGCTG	C	G	Leu	Val (7909)	CONSER VATIVE	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0 9 (9p24)	
5739	cg43949555	1239	AATCTGATGGAT GACATAGAAAGG G/CJTAGTAGAC GATGGTGTAAAT ACTTTC	C	T	Ala	Val (7910)	CONSER VATIVE	eph	Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCOCCUS SP. (STRAIN SY), 545 aa. lpcis:SPTRMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa.	6.7E-80	21
5740	cg44011461	2430	GATGAGGGCATA GATGCTGCTGAA G/CJTGAGGTT GTCAGTCAAGTA GTATTT	G	C	Thr	Ser (7911)	CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0 (16q24.1)	16
5741	cg43942273	1775	CCTCAGGGGTC CAAGAGGCGGC TTG/CJCAAAAG GGATTCCCAGGA AAATGGC	G	C	Ala	Gly (7912)	CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P23141 LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE) - HOMO SAPIENS (HUMAN), 567 aa.	2.2e-310	16

5742	cg43942273	335	TACTTCTTTGTC CTTCAGCTTCTG G[G/C]CCGCCTG GGTGTGGCACC AATCTG	G	C	Ala	Gly (7913)	CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P23141 LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE) - HOMO SAPIENS (HUMAN), 567 aa.	2.2e-310	16
5743	cg43957743	1066	TGGCATACTGG ATATTTTAATCCA [G/C]TGGAGATAA AAGACAGCCAC TAGG	G	C	Thr	Ser (7914)	CONSER VATIVE	esterase	Human Gene SWISSNEW-ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment). pcis:SWISSPROT-ID:Q15166 SERUM PARAOXONASE/ARYLESTERASE 3 (EC 3.1.1.2) (EC 3.1.8.1) (PON 3) (SERUM ARYLDIAPHOSPHATASE 3) (A-ESTERASE 3) (AROMATIC ESTERASE 3) - HOMO SAPIENS (HUMAN), 341 aa (fragment).	1.9E-178	
5744	cg43286057	1921	GGACCCAGCAG GACGGGATATCT CC[A/C]TCGCCC CTCTCCTGGAGC ACTGTGA	A	C	Ile	Leu (7915)	CONSER VATIVE	gaba	Human Gene Homologous to SPTREMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa.	1.9E-121	9
5745	cg43286057	1925	CCAGCAGGACG GGATATCTCCAT CC[G/A]CCCTCTC CTGGAGCACTGT GAGAAC	G	A	Arg	His (7916)	CONSER VATIVE	gaba	Human Gene Homologous to SPTREMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa.	1.9E-121	9



5746	cg43989014	618	GTCTGCTGCGTA GGTGAGTTGGT C/C/C/CAAGGTC ACAGGCTGGGA GGGGTC	A	C	Val	Gly (7917)	CONSER VATIVE	glucuronidase	Human Gene Similar to SWISSPROT- ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	7.4E-80	5
5747	cg43943531	2148	TTTGAGCTTGAT GTCCTGGAGGAA G/C/G/ATATACCA CAGAACATTGGC TGGTC	C	G	Ala	Gly (7918)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0 (11q23.3)	11
5748	cg43943531	915	GTCCCTTTCATCA GAGCACATGGCA G/C/G/CTTTGGG GTCCTTGGTCTC TGCCAG	C	G	Ala	Gly (7919)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0 (11q23.3)	11
5749	cg43065548	1676	GGTCAGAGCAGT CAAGGAGGGGA CG/C/G/TGGGGC TGACCCAGCAG TGTCAGA	C	G	Leu	Val (7920)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 680 aa.	0 (15q15)	15
5750	cg44034764	282	CTCGGAGGTGT GGAGGGCTGTG AGT/G/TTCGTGA GAGTCCTGGGG GCTGGGCT	G	T	Asp	Glu (7921)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0 (Xp21.2)	7
5751	cg44004239	177	GACACCAGAGG GGCTTAGGCTTC TTG/C/ATCCACA GCAGAGTTTCT GGGATT	G	C	Gln	Glu (7922)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID:Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN-DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	
5752	cg43094362	292	AGACGTTGGACCA CTGGCTCACGAC A/C/T/GAGGCTG CCTCCTGGAATG GCTTGG	C	T	Arg	His (7923)	CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA-SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7

5753	cg43987514	964	TAGCGCAGAGA GTTCTGGCCG CTG/C/GTTCCG CTGGCCCCCAGT GCCCCAGG	C	G	Ser	Thr (7924)	CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-215	
5754	cg43958628	520	TATTACTTAATTG GTGAAAAAATTG C/TATATTGTGAA CTTAAAGGATCA GTA	C	T	Ala	Val (7925)	CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	8.6E-206	
5755	cg43059878	369	ACCACAGTGGCT TTTTTCACAGGT A/A/CJTTCACAAG ATGCTTTACAAC TTGGC	A	C	Leu	Val (7926)	CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa. Jpcls:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLIPOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa. Jpcls:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa.	6.6E-189 (17q23)	17 (17q23)
5756	cg42845511	1726	AAGATCTCGTAC GCTCAGTATGAG A/A/GJGTACCTGA AGTCAGACAACA TGATC	A	G	Lys	Arg (7927)	CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	2.9E-86 (20q12)	20 (20q12)
5757	cg43054905	1258	GTAGTCATAACC ATCCACATTAAAC CIG/AJCCGGCAT AACATAGAAATC CACAAG	G	A	Ala	Val (7928)	CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P55261 CARBOXYPEPTIDASE B PRECURSOR (EC 3.4.17.2) (47 KD ZYMOGEN GRANULE MEMBRANE ASSOCIATED PROTEIN) (ZAP47) - CANIS FAMILIARIS (DOG), 416 aa.	2.6E-85 (13q14.1 1)	13 (13q14.1 1)

5758	cg44021513	1357	TCTGGCCCTGCT GGTACGCGGGG GC[G]CTCTGCG CTCCTGCTGAAC TTCACCTC	G	C	Asp	Glu (7929)	CONSER VATIVE	glycoprotein	Human Gene Similar to SWISSPROT- ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)
5759	cg43985366	1819	TCITTTAAAGGA TTGGTAAACTGA A[C]TJTGTACAG TCATGTCAGAAC CAACT	C	T	Val	Ile (7930)	CONSER VATIVE	glycoprotein	Human Gene Similar to SWISSPROT- ID:P49222 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - MUS MUSCULUS (MOUSE), 690 aa.	8.9E-61	6 (6p25)
5760	cg42713500	1094	GAGGCCCGAGG CCGGGCCCTGC AGG[C]GJCGCCG TAGCCAAACGAC GAGTGCTG	C	G	Gly	Ala (7931)	CONSER VATIVE	homeobox	Human Gene SWISSPROT-ID:P78337 PITUITARY HOMEOBOX 1 (HINDLIMB EXPRESSED HOMEOBOX PROTEIN BACKFOOT) - HOMO SAPIENS (HUMAN), 314 aa. lpcis: SPTREMBL- ID:P78337 HINDLIMB EXPRESSED HOMEOBOX PROTEIN BACKFOOT - HOMO SAPIENS (HUMAN), 314 aa.	2.5E-174	
5761	cg43928699	378	GGTGAACGACTA CAGGCACGCCCT C[C]GJTCGGCCA CGACCCCTGG GCAAACC	C	G	Leu	Val (7932)	CONSER VATIVE	homeobox	Human Gene Homologous to SWISSPROT-ID:Q03014 HOMEOBOX PROTEIN PRH (HOMEOBOX PROTEIN HEX) - HOMO SAPIENS (HUMAN), 270 aa.	3.8E-148	10
5762	cg42908326	924	AGCAGCCGCCA AGACCACCCAGCA AG[A]GJACTCCA GCATCGCCGATC TCAGACT	A	G	Asn	Asp (7933)	CONSER VATIVE	homeobox	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEOBOX PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.8E-136	3
5763	cg43285385	434	TTCATTAAACAAA AACTCTGCTAAA T/AJAAAAATGCGG TTTTCACAGCAT TAGG	T	A	Tyr	Phe (7934)	CONSER VATIVE	hydrolase	Human Gene TREMBL-NEW- ID:G2951931 HUMAN GAMMA- GLUTAMYL HYDROLASE (EC 3.4.22.12) - HOMO SAPIENS (HUMAN), 318 aa.	4.8E-173	8

5764	cg43929210	956	ACTGGTTTGCA AAACGAGCCTTA A/C/T/TGCCTTGA ATCTTGACACAT CATT	C	T	Val	Ile (7935)	CONSER VATIVE	hydroxysteroid	Human Gene SWISSPROT-ID:P51659 ESTRADIOL 17 BETA- DEHYDROGENASE 4 (EC 1.1.1.62) (17- BETA-HSD 4) (17-BETA- HYDROXYSTEROID DEHYDROGENASE 4) - HOMO SAPIENS (HUMAN), 736 aa.	0	5
5765	cg44014662	1207	TCTCGAGCAAGA CGTTCAGTCCTG T/C/T/CATAATTA GTCCATGAGGAA TAAAC	C	T	Asp	Asn (7936)	CONSER VATIVE	hypoxanthine	Human Gene Homologous to SWISSPROT-ID:P00492 HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC 2.4.2.8) (HGPRT) (HGPRTASE) - HOMO SAPIENS (HUMAN), 217 aa.	9.1E-115	X (Xq26)
5766	cg43925670	312	TTTGAAGAAA AAGTCTGGTGAA G/T/A/TTCATAC TTGAATCAGGAT TGAGT	T	A	Thr	Ser (7937)	CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.   pcis: SPTREMBL-ID: Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
5767	cg42862121	1623	TCATGTGGGG CCAGACTGCAC GC/A/C/TCTGTGA GGCTCAGGCTTG GCAACA	A	C	Asp	Glu (7938)	CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:Q13568 INTERFERON REGULATORY FACTOR 5 (IRF-5) - HOMO SAPIENS (HUMAN), 504 aa.	4.2E-284	7
5768	cg43510640	257	GCCTGGACGAC CAACACTGGGAT GAT/C/GATGAG CAGAAATGGTCAT GAAGATG	T	C	Ile	Val (7939)	CONSER VATIVE	interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.2E-62	

5768	cg44339782	257	GCCTGGACGAC CAACACTGGGAT GATTCJGATGAG CAGAAATGGTCAT GAAGATG	T	C	Ile	Val (7940)	CONSER VATIVE	interferon	Human Gene Similar to SWISSPROT- ID:Q01628 INTERFERON-INDUCIBLE PROTEIN 1-8U - HOMO SAPIENS (HUMAN), 133 aa.	1.2E-62	
5770	cg43851261	4481	TTTTCAACCAGGC AAATCAAAAAGCC A[C/G]TCCAGAAA AATCTTTGCATG ACAAA	C	G	Thr	Ser (7941)	CONSER VATIVE	isomerase	Human Gene SWISSPROT-ID:Q02880 DNA TOPOISOMERASE II, BETA ISOZYME (EC 5.99.1.3) - HOMO SAPIENS (HUMAN), 1626 aa.	0	3 (3p)
5771	cg43989084	841	AATGCTTTGGTA TTTGATGGGTCT A[G/T]TTCAAGAG CCTCTAAACAAC TGTC A	G	T	Leu	Ile (7942)	CONSER VATIVE	isomerase	Human Gene SWISSPROT-ID:Q08752 40 KD PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PIPIASE) (ROTAMASE) (CYCLOPHILIN-40) (CYP- 40) (CYCLOPHILIN-RELATED PROTEIN) - HOMO SAPIENS (HUMAN), 370 aa.	1.3E-200	4
5772	cg44001328	901	GGGGTTGAAATA GCGCAGCAGCA CT[G/A]CGTTCCA AGTCTTGCTGTC CTGGCA	G	A	Ala	Val (7943)	CONSER VATIVE	isomerase	Human Gene SWISSPROT-ID:Q14376 UDP-GLUCOSE 4-EPIMERASE (EC 5.1.3.2) (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE) - HOMO SAPIENS (HUMAN), 348 aa.pcds:TREMBLNEW-ID:G2947219 UDP-GALACTOSE 4' EPIMERASE - HOMO SAPIENS (HUMAN), 348 aa.	9.9E-189	1
5773	cg43981450	1230	TCAGACTCAAGT CCAAGTCCTTTA A[G/T]CAGCAGT GCGTAGAACTGG GGTTCT	G	T	Leu	Ile (7944)	CONSER VATIVE	isomerase	Human Gene Homologous to SWISSPROT-ID:P70473 2- ARYLPROPIONYL-COA EPIMERASE (EC 5.-.-) - RATTUS NORVEGICUS (RAT), 361 aa.	1.8E-117	5

5774	cg43145505	314	AGAATGCCTCCG TGAGGCTACATT AAGTAAACCAT AAGCATGAACCT TTTAA	G	Ile	Val (7945)	CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P42336 PHOSPHATIDYLINOSITOL 3-KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.   pcids:SWISSPROT- ID:P42336 PHOSPHATIDYLINOSITOL 3- KINASE CATALYTIC SUBUNIT, ALPHA ISOFORM (EC 2.7.1.137) (PI3-KINASE P110 SUBUNIT ALPHA) (PTDINS-3- KINASE P110) (PI3K) - HOMO SAPIENS (HUMAN), 1068 aa.	0	3
5775	cg43018995	1904	CCCCAACTGCT CCCCCGAGCTTC TTTAA CCCCCATCA CCGTGCGCTGTT GCGAT	A	Phe	Tyr (7946)	CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P53667 LIM DOMAIN KINASE 1 (EC 2.7.1.-) (LIMK-1) - HOMO SAPIENS (HUMAN), 647 aa.	0	7 (7q11.23)
5776	cg43947829	1855	ACAAGCTTTTGT GCTTGCAAAAGGA A CT GCGCTGG GAAGAAATTTGAA GGACAC	T	Val	Ile (7947)	CONSER VATIVE	kinase	Human Gene TREMBL-NEW- ID:G2979628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa.	1.5E-217	
5777	cg43917871	1684	CCCAAGATATCA TTGAAACGTGGA TTC TTAAATTC TGTTGTAATTTGT CAATA	T	Asp	Asn (7948)	CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
5778	cg43981459	1050	ATTGTTTCCTGG TACAGACCATAT TIG ATCAGTTG AAGCTCATTTTA AGACT	A	Asp	Asn (7949)	CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:Q16539 MITOGEN-ACTIVATED PROTEIN KINASE P38 (EC 2.7.1.-) (MAP KINASE P38) (CYTOKINE SUPPRESSIVE ANTI- INFLAMMATORY DRUG BINDING PROTEIN) (CSAID BINDING PROTEIN) (CSBP) (MAX-INTERACTING PROTEIN 2) (MAP KINASE MXI2) - HOMO SAPIENS (HUMAN), 360 aa.	3.1E-194	6

5779	cg43987006	452	GGAGAACTTGAG GGGGCTGACGG GG[G]A]CCCGG GGCTACTGTTGA GGCGCCT	G	A	Ala (7950)	Val (7950)	CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P21425 RIBOSOMAL PROTEIN S8 KINASE I- (EC 2.7.1.-) (S8K) (P70-S8K) - RATTUS NORVEGICUS (RAT), AND ORYCTOLAGUS CUNICULUS (RABBIT), 502 aa.	3.1E-176	11
5780	cg44918533	870	GGACTGCAAGTA GGTGAGCACA CA[G]A]CCTTGA GACGTGGCTGG CTGAACC	G	A	Ala (7951)	Val (7951)	CONSER VATIVE	kinase	Human Gene Similar to SPTREMBL- ID:Q19632 SIMILAR TO SERINE/THREONINE PROTEIN KINASE. NCBI GI: 1086650 - CAENORHABDITIS ELEGANS, 821 aa.	1.2E-70	
5781	cg43981478	1274	CTTTTCAATAG CGCTTGCGAAA [A/G]CAGTAGT CCGACGGCCGG TGAGTC	A	G	Val (7952)	Ala (7952)	CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	
5782	cg43981478	1275	TTTTTCAATAGC GCTTGCGAAA [C/T]AGTAGGTC GACGGCCGGT AGTCC	C	T	Val (7953)	Ile (7953)	CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	
5783	cg43981478	1341	ACGTCAGCAAGA TTGTGGGCTGC A[G/C]CCGGGTG AGGTCACGCAG GATGGTG	G	C	Leu (7954)	Val (7954)	CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	
5784	cg43920644	1423	GTTCTGCAGCG CTGCCCCATGTCG ATT/G]CATCTTGA TGACATCATCAG CAGAG	T	G	Ile (7955)	Leu (7955)	CONSER VATIVE	kinesin	Human Gene SPTREMBL-ID:Q99661 MITOTIC CENTROMERE-ASSOCIATED KINESIN - HOMO SAPIENS (HUMAN), 725 aa.	0	1
5785	cg42918454	2315	CAGATGCAGCTG AGCCTGGCAGAA A[G/C]TGAAGCTT CCTGGGAACA CTAAC	G	C	Ser (7956)	Thr (7956)	CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:Q13753 LAMININ GAMMA-2 CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1193 aa.	0	1

5786	cg43983535	4190	TCAACAGCCTCC TTCTTTTCTCCA [CA]TGCAGTCAT GTTTTCTGATTT ACT	C	A	Val	Leu (7957)	CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
5787	cg42536982	7508	TCTGCATTGAGC GTTCTAATGCGT TIG[C]CAAGCGA AGCGGAATATAT CGTGCA	G	C	Gln	Glu (7958)	CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P25391 LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) - HOMO SAPIENS (HUMAN), 3075 aa.	0	
5788	cg42930646	1216	CGTCAATGTTAC TGATGCGGATAG C[G/C]TATGGATG GAAATGGACGAT GAGGA	G	C	Val	Leu (7959)	CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P07221 CALSEQUESTIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ-BINDING PROTEIN) - ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa.	1.8E-198	1
5789	cg43986144	718	AAGCTTGTCATG CCTCACAGCAGT G[C/T]GCACAAG ACTGCCACAGCCC AATGGA	C	T	Ala	Val (7960)	CONSER VATIVE	MHC	Human Gene Homologous to SWISSPROT-ID:P28068 CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 263 aa.	9.1E-147 (6p21.3)	6
5790	cg43111577	1089	GCTTATGAAGAA GAGAACAAAGCT G[G/T]GGAGAA ATGCCCAGAGAG CTGTCC	G	T	Gly	Val (7961)	CONSER VATIVE	misc_cha nnel	Human Gene TREMBL-NEW- ID:G1518639 CGMP-GATED CATION CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 1251 aa.	0 (16q13)	16
5791	cg44018843	483	GCCAGACCATCT CTGTGCACCCTG G[T/C]GCCCTCTG GGCCCTGAGTG CTTGCGC	T	C	Val	Ala (7962)	CONSER VATIVE	misc_cha nnel	Human Gene SPTREMBL-ID:Q15478 SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 1836 aa.	0 (17q23.1)	17
5792	cg40367355	1058	CGGATTCCTCTC AACCAGCCCACT G[C/T]CAAAATCC ACGTGGACTCCT CCTCT	C	T	Ala	Val (7963)	CONSER VATIVE	misc_cha nnel	Human Gene SPTREMBL-ID:O00564 INWARDLY RECTIFYING K+ CHANNEL HOMO SAPIENS (HUMAN), 375 aa.	4.1E-199	21



5793	cg44929972	1149	GTGACTTTTTTA TGAAGACATGGA [G/T]TCCTTGACG CAGATGCTTAGG GCCT	G	T	Glu	Asp (7964)	CONSER VATIVE	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
5794	cg43979114	287	CCTGCAGGACAC ACCATCCCCCAA GTC/CACACTGG ACTAAACTTCAG CATTCC	T	C	Val	Ala (7965)	CONSER VATIVE	ngf	Human Gene Homologous to TREMBLNEW-ID:G387171 NERVE GROWTH FACTOR - MUS MUSCULUS (MOUSE), 307 aa.	1.5E-130	1 (1p13.1)
5795	cg43924936	3009	CTCTTTACTTCA GCCTCCTCTTCT TTC/CACAATTCT TTTCGTTGCAA TGTC	G	C	Gln	Glu (7966)	CONSER VATIVE	nuc_rec pt	Human Gene TREMBLNEW- ID:G2655006 THYROID HORMONE RECEPTOR COACTIVATING PROTEIN - HOMO SAPIENS (HUMAN), 920 aa.	0	5
5796	cg30421838	2486	GCCAGCGCCTTT GCCCGCCGCG GA/CCTTCACCC TGTGCCTCGTCC ACCCCG	G	C	Glu	Asp (7967)	CONSER VATIVE	nuc_rec pt	Human Gene SWISSNEW-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa. [pcis:SWISSPROT-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa.	0	11 (11q22)
5797	cg43315956	2789	ACTTCCCTTCA CTCTGCCAGCTG G/C/CJTAAATACA CCACGAATTCCA GTGCT	G	C	Gly	Ala (7968)	CONSER VATIVE	nuc_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
5798	cg43315956	3542	CAGTGGGTCA GTCAGTCACCAC TC/CJTGCAATA AGACATTTCTA GCTACT	G	C	Val	Leu (7969)	CONSER VATIVE	nuc_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
5799	cg43972383	1195	ATCTCTCTAAAT AATGAACTTGA AC/AAATGAAAT AAAGCCTTGGAT AGCC	A	C	Glu	Asp (7970)	CONSER VATIVE	nuclease	Human Gene Homologous to SWISSPROT-ID:P12753 DNA REPAIR PROTEIN RAD50 (153 KD PROTEIN) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1312 aa.	1.8E-149	5

5800	cg43947341	270	CCAAGTCCTTGG GTTCTTTCCAG A[G/C]CTCTTACT TTCTGAGGGCCC AGCC	G	C	Ala	Gly (7971)	CONSER VATIVE	nuclease	Human Gene Homologous to SWISSPROT-ID:P07992 DNA EXCISION REPAIR PROTEIN ERCC-1 - HOMO SAPIENS (HUMAN), 297 aa.	1.1E-115	
5801	cg43951535	1535	GGTGAACCTACAG CGAGTAGCTTTT A[G/C]CCCTTTGC TTGGCAACCT GCTGA	G	C	Ser	Thr (7972)	CONSER VATIVE	nuclease nhib	Human Gene SPTREMBL-ID:Q13181 RNASE L INHIBITOR - HOMO SAPIENS (HUMAN), 599 aa.	2.5e-315	4 (4q31)
5802	cg44012756	2324	ACCTGCAAAGAC ATGACCAGTGGC T[A/T]CGTGTGCA CCTGCCGGGAG GGCTTC	A	T	Tyr	Phe (7973)	CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0	
5803	cg43297056	2389	CACTGCTTCCCC AGCCGGCCCTTC A[C/G]GCGCTTG GCAATCAGTGTC CACTGC	C	G	Val	Leu (7974)	CONSER VATIVE	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.9E-103	20 (20q13.1)
5804	cg42849556	1051	CCTCCTAGTTCC AAAGCCCTTGA A[G/A]ACCCAG CTGTCACCCAGGC CAGAAA	G	A	Arg	Lys (7975)	CONSER VATIVE	oxidase	Human Gene SWISSPROT-ID:P19878 NEUTROPHIL CYTOSOL FACTOR 2 (NCF-2) (NEUTROPHIL NADPH OXIDASE FACTOR 2) (P67-PHOX) - HOMO SAPIENS (HUMAN), 526 aa.	2.8E-287	1 (1q25)
5805	cg43999400	1238	GATGTGACATGG GCAACACAAGAA A[A/G]AATTTCTT TGCAGTGGCTCA GGAGG	A	G	Lys	Arg (7976)	CONSER VATIVE	peptidas e	Human Gene SWISSPROT-ID:P27487 DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN- 2) (ADABP) - HOMO SAPIENS (HUMAN), 766 aa.	0	2 (2q23)
5806	cg41626506	634	AGCCAGCGACAT GGAGATCCAAGT C[A/G]CCCGAGG GAGCCTCCCGG AGTCTAC	A	G	Val	Ala (7977)	CONSER VATIVE	peroxida se	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0	3 (3q26.3)

5807	cg42691989	825	CCGGGTGGTGTG GCCTCAGAGCG AA[G]C[C]CATT CTCAATCAGCAC GGCCCT	G	C	Ala	Gly (7978)	CONSER VATIVE	phosphatase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.9E-101	14 (14q24.1)
5808	cg43956369	5054	AGTTGAGCAAAA TTGGACACACCG G[T/A]ACCTCGTT CTGACTGAGTTA CACAG	T	A	Thr	Ser (7979)	CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R- PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa. [pcis:SWISSPROT- ID:Q15262 PROTEIN-TYROSINE PHOSPHATASE KAPPA PRECURSOR (EC 3.1.3.48) (R-PTP- KAPPA) - HOMO SAPIENS (HUMAN), 1439 aa.	0	6
5809	cg43321833	2339	CTCACGTTCCACC ATCAATCTCCTG G[G/T]GGTGATG CTCACCATCAAA AGGAGA	G	T	Gly	Val (7980)	CONSER VATIVE	phosphatase	Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0	20
5810	cg43956187	390	TACAGTAATAGA TTTTTGGAGGAT G[A/G]TATGGGA GTATAATGTTGT GATCAT	A	G	Ile	Val (7981)	CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q05209 PROTEIN-TYROSINE PHOSPHATASE G1 (EC 3.1.3.48) (PTPG1) - HOMO SAPIENS (HUMAN), 780 aa.	0	7 (7q11.23)
5811	cg38899343	3058	TGTTGGAAGCCCG CAAATCTGCATT T[G/A]ATTCCTG CAGCTGAAGGCT TTCCC	G	A	Asp	Asn (7982)	CONSER VATIVE	phosphatase	Human Gene SPTREMBL-ID:Q13187 INOSITOL POLYPHOSPHATE 4- PHOSPHATASE - HOMO SAPIENS (HUMAN), 938 aa.	0	

5812	cg43928335	3498	CAGCAAGAGCTA ATAGTACCTCAT CTTATCATCAT AATTGTATCTGT AAGAA	T	A	Glu (7983)	Asp (7983)	CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:P54613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS SCROFA (PIG), 602 aa (fragment).	3.2E-302	11 (11q22)
5813	cg43984117	823	GGTGACGTCAG GCCCAAACTGAC AG[G]CITCAGC CCCGCTTGCTGA TCGAGCG	G	C	Thr (7984)	Ser (7984)	CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:P53041 SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PP-T) (PPT) - HOMO SAPIENS (HUMAN), 499 aa.	2.1E-273	
5814	cg43988365	2812	ACAGTGCAAGGC CATGAAGTGCGG CIT/CITGTGTGTG TGCACGACCTGG TAAAA	T	C	Lys (7985)	Arg (7985)	CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q14642 TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 412 aa.   cds:SPTREMBL-ID:Q14642 INOSITOL 1,4,5-TRIPHOSPHATE 5- PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa.	2.6E-227	10
5815	cg42688448	1803	GGTGCAGGAC GAGCGCCCATG GTA[G]CITCTGAG GCTGGGCATGG GCATGGGC	G	C	Thr (7986)	Ser (7986)	CONSER VATIVE	polymerase	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIID - HOMO SAPIENS (HUMAN), 1083 aa.	0	20
5816	cg43988623	836	GGCACCATTGAA GTGTCAAAGGTG G[G]TTACGGGG ACTGTCTCTGGCT GTGTGG	G	T	Gly (7987)	Val (7987)	CONSER VATIVE	polymerase	Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.   cds:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.	7E-199	
5817	cg42937321	354	GGCGGTGGTCAT CAACATCTCCGG G[C]GTGCGCTT CGAGACGCAGC TGAAGAC	C	G	Leu (7988)	Val (7988)	CONSER VATIVE	potassium channel	Human Gene SWISSPROT-ID:P22001 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.3 (HPCN3) (HKG5) (HUKII) (HLK3) - HOMO SAPIENS (HUMAN), 523 aa.	5.4E-284	1 (1p21)

5818	cg43331104	330	GC GCGTGGTGA TCAACATCTCCG GG[GIC]TGGCT TCGAGACGCAG CTCAAGAC	G	C	Val	Leu (7989)	CONSER VATIVE	potassiu m_chann el	Human Gene SWISSPROT-ID:Q09470 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.1 (HUKI) (HUK1) - HOMO SAPIENS (HUMAN), 495 aa.	5.6E-266	12
5819	cg43262191	773	GGCTTTCGGTA CCTGCTGGGCTC T[G]ATCATGCTG CAGATCTTTGTG GACTA	G	A	Val	Ile (7990)	CONSER VATIVE	prostagla ndin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 843 aa.[pcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0	3
5820	cg43923853	1874	TGGAGTATGCAT ACAAGAAGTCGG C[C]ATCCACTGG TATTTATGACAC GCCA	C	A	Glu	Asp (7991)	CONSER VATIVE	protease	Human Gene Homologous to SWISSNEW-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA- 1) - HOMO SAPIENS (HUMAN), 277 aa.[pcis:SWISSPROT-ID:P42574 APOPAIN PRECURSOR (EC 3.4.22.-) (CYSTEINE PROTEASE CPP32) (YAMA PROTEIN) (CPP-32) (CASPASE-3) (CASP-3) (SREBP CLEAVAGE ACTIVITY 1) (SCA-1) - HOMO SAPIENS (HUMAN), 277 aa.	2E-149	4

5821	cg42918089	408	CCTATAACTGGA ATGTTAACTCC C[G]A[CG]TCATAG AAATAATGCAGA AGCCC	G	A	Arg	His (7992)	CONSER VATIVE	protease	Human Gene Homologous to SWISSNEW-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.   pcds:SWISSPROT-ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.4E-146	11 (11q21)
5822	cg43310246	1169	GCAAGACAGTG GATGGGCCCCCG GGA[G/C]GTCAC GCTGCAGGCCAT GGCCGATG	G	C	Glu	Asp (7993)	CONSER VATIVE	protease	Human Gene Homologous to SWISSPROT-ID:P21662 NEUROENDOCRINE CONVERTASE 1 PRECURSOR (EC 3.4.21.93) (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) (PROPROTEIN CONVERTASE 1) (PC3) (FURIN HOMOLOG) (PROPEPTIDE PROCESSING PROTEASE) - MUS MUSCULUS (MOUSE), AND MUS COCKII, 753 aa.	1.1E-141	20 (20p11.2)
5823	cg43310246	1170	CAAGACAGTGGG TGGGCCCCCGGG AG[G/C]TCACGC TGCAGGCCATG GCCGATGG	G	C	Val	Leu (7994)	CONSER VATIVE	protease	Human Gene Homologous to SWISSPROT-ID:P21662 NEUROENDOCRINE CONVERTASE 1 PRECURSOR (EC 3.4.21.93) (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) (PROPROTEIN CONVERTASE 1) (PC3) (FURIN HOMOLOG) (PROPEPTIDE PROCESSING PROTEASE) - MUS MUSCULUS (MOUSE), AND MUS COCKII, 753 aa.	1.1E-141	20 (20p11.2)

5824	cg43074055	536	CGACGCGGAGA ACAAACTGAACG AC[AG]TTCTCCT CATCCAGCTGAG CAGCCC	A	G	Ile	Val (7995)	CONSER VATIVE	protease	Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa.	5.7E-138	19 (19p13.3)
5825	cg42309989	317	GTTTAACGCCCTT ACTGACTGACTG A[G/A]CTATAGGC GAGGTGAAGGC TGGTCC	G	A	Ala	Val (7996)	CONSER VATIVE	protease	Human Gene Similar to SWISSNEW- ID:P31795 POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)] - RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN), 581 aa (fragment). pcis:SWISSPROT- ID:P31795 POL POLYPROTEIN (PROTEASE (EC 3.4.23.-); REVERSE TRANSCRIPTASE (EC 2.7.7.49); RIBONUCLEASE H (EC 3.1.26.4)) - RADIATION MURINE LEUKEMIA VIRUS (STRAIN KAPLAN), 581 aa (fragment).	8.3E-82	
5826	cg43979831	1345	GGCACCAGGCG TGCAGCAGCCAC CA[G/C]CTTCGC GATCAAATTCCT CTCTGCC	G	C	Ser	Thr (7997)	CONSER VATIVE	protease nhib	Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.1E-228	14
5827	cg43268468	1183	CGGTGAATGATG GATTCGTTCGC T[G/C]CTCCGCTC CCAGCGAGAGG GCCGAG	G	C	Gln	Glu (7998)	CONSER VATIVE	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188	17 (17p13.3)
5828	cg43268468	1184	GGTGAATGATGG ATTCTGTTGCT G[C/G]TCCGCTC CCAGCGAGAGG GCCGAGA	C	G	Glu	Asp (7999)	CONSER VATIVE	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188	17 (17p13.3)

5829	cg43268468	286	GCCCCTGTGTCT GTGTCCTCCTCAGT A[C/T]GAAGATGA AAGGCTGGTTAA GGTGA	C	T	Val	Ile (8000)	CONSER VATIVE	protease inhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188	17 (17p13.3 )
5830	cg43060292	907	AGGGAAGTTGT GGGTCTAATTC A[A/G]ACCTCAAG CCAAACACCATC ATGGT	A	G	Asn	Asp (8001)	CONSER VATIVE	protease inhib	Human Gene Similar to SWISSPROT- ID:P09008 CONTRAPSIN-LIKE PROTEASE INHIBITOR 6 PRECURSOR (CPI-26) (SERINE PROTEASE INHIBITOR 3) (SPI-3) (SPI-2.2) - RATTUS NORVEGICUS (RAT), 418 aa.	2.2E-83	X (Xq22.2)
5831	cg43938319	6705	CAACAAGTATGG GGTCAGCCTCAT C[G/A]ATCCCAA ACGAAGGATATC CTCAC	G	A	Asp	Asn (8002)	CONSER VATIVE	struct	Human Gene SPTREMBL-ID:Q13402 MYOSIN VIIA - HOMO SAPIENS (HUMAN), 2215 aa.	0	11 (11q13.5 )
5832	cg44033566	3186	GGACTCGCACC CTGAGCAGAAG GAG[A/G]ATATTG GTCAGCGGCAAA AACACTT	A	G	Asn	Asp (8003)	CONSER VATIVE	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa. Jpds:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0	14 (14q22)
5833	cg43957486	2089	ATCTGCGGGCC CGACTCGGCCCT TG[C/T]CCGCCA CATTGGCACCGA CTGTGAC	C	T	Ala	Val (8004)	CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P07204 THROMBOMODULIN PRECURSOR (FETOMODULIN) (TM) (CD141 ANTIGEN) - HOMO SAPIENS (HUMAN), 575 aa.	0	20 (20p11.2 )
5834	cg43916919	230	AAATTGCTTGAA GATGGGACTCTC A[C/T]GGCCCTG AGGCAGAATCTC CACCTG	C	T	Arg	His (8005)	CONSER VATIVE	struct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa. Jpds:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.	4.3E-188	2 (2cen)



5835	cg43918346	706	GTGGCACC GCC GGGATGGAAAGT GGC/GIAGAATG TTCATTTCATCG CTCGGG	C	G	Gln	Glu (8006)	CONSER VATIVE	struct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.4E-130	
5836	cg43973395	262	AGCAGCCGGA GAGGAGGCTGC GGA/GC/GAGGA GGAGGAAGCCC CCGAAGAGC	G	C	Glu	Asp (8007)	CONSER VATIVE	struct	Human Gene Homologous to SWISSNEW-ID:P13805 TROPONIN T, SLOW SKELETAL MUSCLE ISOFORMS - HOMO SAPIENS (HUMAN), 277 aa. lpcds:SWISSPROT-ID:P13805 TROPONIN T, SLOW SKELETAL MUSCLE ISOFORMS - HOMO SAPIENS (HUMAN), 277 aa.	2E-114 (19q13.4)	19
5837	cg43961212	2188	GATCTGGAAGCC GGACATCCTCTG A/GC/CAAGTCG ACTGATCCGCTG GC9AAC	G	C	Ala	Gly (8008)	CONSER VATIVE	struct	Human Gene Homologous to TREMBLNEW-ID:G1703715 PANTOPHYSIN=SYNAPTOPHYSIN HOMOLOG - MUS SP, 281 aa.	2.4E-114	7
5838	cg42522566	273	GGCCAGGTGCA CAGGTGTACAGA GA/GA/GTCTACA GGCCTTGCACTG GCAGCC	G	A	Arg	Lys (8009)	CONSER VATIVE	struct	Human Gene Similar to SWISSPROT- ID:P07313 MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (EC 2.7.1.117) (MLCK) - ORYCTOLAGUS CUNICULUS (RABBIT), 607 aa.	6E-55	
5839	cg43977322	1441	CTCGGGTCTCC AGCTGCAGGTT T/GC/CCTCTCCA GCTGTAATTGT GGTTC	G	C	Gln	Glu (8010)	CONSER VATIVE	struct	Human Gene Similar to SWISSPROT- ID:P37709 TRICHOHYALIN - ORYCTOLAGUS CUNICULUS (RABBIT), 1407 aa.	1.5E-52	16
5840	cg40386639	4912	ATTTTGGAGTC ACCTGCGAACG TA/TGGAAGTGA CCAACCGCCTTA GATCT	A	T	Tyr	Phe (8011)	CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0 (12q24.2)	12

5841	cg43987111	1818	GGAGTCTGAGAA CTTCGTGTATTT G[C/G]CCACAAG GGCAATAGAGCA GGTCTC	C	G	Gly	Ala (8012)	CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0	18 (1p34.1)
5842	cg43124627	1841	ATTTATTCAAGA GCTGCCAAAGAC TTAGTTCAGTGG GAAGACAAAAG AAATGA	A	G	Ile	Val (8013)	CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.   pcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.7E-79	16
5843	cg43124627	846	ATCATGGCCATA TTCTTTACCAGT G[C/C]AACAAAGT GGATATCCGAAA ATGACT	G	C	Gly	Ala (8014)	CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.   pcis:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.7E-79	16
5844	cg43933068	580	AGGTGGATGCC GAAGAAAAAGAA GAT/GIGTGAAT CTTGCTGCTGAGT GGGTGT	T	G	Asp	Glu (8015)	CONSER VATIVE	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.9E-75	12

5845	cg42711317	1131	TAAAGATGTGGG ATTGAAAAAAGA A[G/A]ATATTGCA ATGTGGGAAGTA AATGA	G	A	Asp (8016)	CONSER VATIVE	thiolase	Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa.	2.9E-221	11 (11q22.3)
5846	cg43278427	1120	CTTGATGTGTAA TGAGAGCAGTAT G[C/G]AGAGCTT GGCCAGAGAA AATCTGT	C	G	Glu (8017)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa.	0	14 (14q31)
5847	cg43278427	1124	ATGTGTAATGAG AGCAGTATGCAG A[G/C]CTTGCGC CAGAGAAAATCT GTGAAT	G	C	Thr (8018)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa.	0	14 (14q31)
5848	cg43306266	315	CCTACACAGGCA TGTGGCGGCC GA[G/C]CGTTCC GCCGAGGCGCG GGGCAACC	G	C	Glu (8019)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.8E-212	1 (1p31.2)
5849	cg42704646	311	CCTACACAGGCA TGTGGCGGCC GA[G/C]CGTTCC GCCGAGGCGCG GGGCAACC	G	C	Glu (8020)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.1E-194	1 (1p31.2)
5850	cg2514276	648	TACGTCACCATC TTCTACGCCCTG G[G/C]CTACCAC CACATCATGACG GCGAGG	G	C	Ala (8021)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P33032 MELANOCORTIN-5 RECEPTOR (MC5- R) (MC-2) - HOMO SAPIENS (HUMAN), 325 aa.	7E-172	

5851	cg40245117	1509	TGCTCTGTGTCATG GCTGCCTTTATC TTACJTCATCAAC TGCATCATCTAC TTTAA	A	C	Ile	Leu (8022)	CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P33765 ADENOSINE A3 RECEPTOR - HOMO SAPIENS (HUMAN), 318 aa.	1.5E-167	1 (1p21)
5852	cg32423505	737	CACATCAGAAGG AAGACTACCAT ATTGCGGCAAAAA CAAGCTTGAAAA GGCTA	T	C	Ile	Val (8023)	CONSER VATIVE	tm7	Human Gene Similar to SPTREMBL- ID:Q89609 G PROTEIN-COUPLED RECEPTOR - EQUINE HERPESVIRUS TYPE 2 (EHV-2), 383 aa.	1.2E-55	3 (3q21)
5853	cg43335562	339	CAAGACCTAGCT CCCCAGCAGAG AGTCJGGCCCC ACAACAAAAGAG GTCCAGC	T	C	Val	Ala (8024)	CONSER VATIVE	tm7 or	Human Gene Similar to TREMBLNEW- ID:G2853845 TNF RECEPTOR- RELATED RECEPTOR FOR TRAIL - HOMO SAPIENS (HUMAN), 386 aa.	2.3E-55	8
5854	cg43948839	798	TCCAGCGCGT GGCCCGCGGCT CCA[C/G]GTCCG CCACCGCGCCT CCTTTGCCA	C	G	Val	Leu (8025)	CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa. ipds:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.	0	17

5855	cg43948839	799	CCCAGCGCGTG GGCCGCGGCTC CAC[G/C]TCCGC CACCGCGCTC CTTTGCCAC	G	C	Asp	Glu (8026)	CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.lpcis:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.	0	17
5856	cg43936136	2321	TCTCCCAATTAT CTCGTTCACATC A/TATATAAAGTG ATGTCCGGCAGA CCAAAT	A	T	Phe	Tyr (8027)	CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q99840 TRANSCRIPTION FACTOR NFATX2 - HOMO SAPIENS (HUMAN), 1068 aa.	0	
5857	cg44130900	1488	AGAAACAATTTA GCACACTGGTCG A[G/T]TCAACAGC AACTGCTGGAAA AAAA	G	T	Glu	Asp (8028)	CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
5858	cg43920700	1055	GCCCCAAGTCCA TCGATGACAGTG A[G/T]ATGGAGA GCCCTGTTGATG ACGTGT	G	T	Glu	Asp (8029)	CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q14938 NUCLEAR FACTOR 1X (NFI-X) (NF-1X) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGCA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 441 aa.	2.1E-243 (19p13.3 )	19
5859	cg43255478	667	CGGCTGCAGGC GGCGCACCACG GGG[G/T]GGACG CGGGCATGGGT GACAGCCTC	G	T	Gly	Val (8030)	CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q92481 AP 2 BETA TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 449 aa.	5.4E-236	

5860	cg44012546	1960	ATCCGGAGGGC CGGGTGGTCGG GCG[C]GGGA TCCTCTCCAGC GGTTCCTC	C	T	Arg	His (8031)	CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:P70459 ETS-DOMAIN TRANSCRIPTION FACTOR ERF - MUS MUSCULUS (MOUSE), 551 aa.   pcsl:SPTREMBL- ID:P70459 ETS-DOMAIN TRANSCRIPTION FACTOR ERF (ERF) - MUS MUSCULUS (MOUSE), 551 aa.	8E-199	19
5861	cg43947189	2208	CTTGGTGCCCGA GGAAAGGATGAA A[C]GJATAAGTAT CTCGAGCATTG TCTCA	C	G	Val	Leu (8032)	CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.   pcsl:SWISSPROT-ID:P23193 TRANSCRIPTION ELONGATION FACTOR S-II (TRANSCRIPTION ELONGATION FACTOR A) - HOMO SAPIENS (HUMAN), 301 aa.	4.2E-158	8
5862	cg43982109	1818	CTCTGTCTCCAGA CCTTCCCAGGGC A[C]GJTCAGCAC GCCCCACATGCT TCGGAG	C	G	Ser	Thr (8033)	CONSER VATIVE	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00059 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1) - HOMO SAPIENS (HUMAN), 246 aa.	5.6E-131	10 (7p)
5863	cg43918185	141	AGAGCCCGGCC CGACGCCGCCA TGA[G/C]CGCCG CGCTCTTCAGCC TGGACGGC	G	C	Ser	Thr (8034)	CONSER VATIVE	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q03484 CCAAT/ENHANCER BINDING PROTEIN DELTA (C/EBP DELTA) (TRANSCRIPTION FACTOR CELF) - RATTUS NORVEGICUS (RAT), 268 aa.	2.1E-122	8
5864	cg43918209	1269	GTTGGGAAAGG CGCCCTCCGCTT GC[G/C]CCGGAG GGGGCTGCAGG CGATCGGC	G	C	Ala	Gly (8035)	CONSER VATIVE	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.7E-115	19

5865	cg44910788	258	TGATGCCTAGTG AGACTTTGGCCT G/C/TGGAAAATC TCTATCACATATA ATTA	C	T	Arg	His (8036)	CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.jpds:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.7E-89	
5866	cg42849540	1841	TCCAGAAAAGAGC TCTGCAGGCGG AG/C/GJAAAGGC AGGCAGCCCGG AAAGCAGA	C	G	Ala	Gly (8037)	CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.jpds:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	2E-88	20 (20q13)
5867	cg42532030	318	TATAAATGTGAT GAGTGTGGGAAA G/C/GJCTTCAGTC AGAGCTCAGATC TTATT	C	G	Ala	Gly (8038)	CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.jpds:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	1.9E-57	
5868	cg43984952	620	CTGCTGCAGGAC AGCGACTGCAAG G/C/TJGTCTCCG GAGGGCCCGCA GGCCAC	C	T	Ala	Val (8039)	CONSER VATIVE	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	9.6E-53	12 (12q23)
5869	cg43984952	662	GAGGCCCAACAA CACGGCCTGGC CG/C/TJCTCAGA AGCACGAGCCG CAACGAA	C	T	Ala	Val (8040)	CONSER VATIVE	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	9.6E-53	12 (12q23)

5870	cg43984952	733	CTCGTCCTTCAC CATTAAATCCCT G[C/G]AGAACCC ACCAGACGCCTT CAAGGC	C	G	Gln	Glu (8041)	CONSER VATIVE	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	9.6E-53	12 (12q23)
5871	cg43998978	4041	GCGCCCTGGCA AATCCAGGAGAC AG[C/G]TCCGCC CAGCAGCTGGC CCCAGGTG	C	G	Ala	Gly (8042)	CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
5872	cg43976701	2368	CTCCTTTCAAAA GTCAACCCCTCA C[G/A]CGTTCATA ATAATATGTATG CCTGG	G	A	Arg	His (8043)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa.	0	
5873	cg43976701	2370	CCTTTCAAAAGT CAACCCCTCACG C[G/A]TTCATAAT AATATGTATGCC TGGGG	G	A	Val	Ile (8044)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q15436 PROTEIN TRANSPORT PROTEIN SEC23 HOMOLOG ISOFORM A - HOMO SAPIENS (HUMAN), 765 aa.	0	
5874	cg44008864	1022	GGGATGATGGTC AGCTGAGAGCG CA[G/C]GTCATG GAGGCCGATGT CTGCCACA	G	C	Leu	Val (8045)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa.   pcis: SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0	



5875	cg44008864	3466	CACGTACACCCA GAGGGTGATCA GG[G/C]TCACCA GGAAGGGGCTG CACATCCA	G	C	Thr	Ser (8046)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa.   pcis:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0	
5876	cg43300853	418	CTGAGCAGCGC CTGGCGCAACAA CA[G/C]TGTCCTC GCTGCGGCTGC GGGACGGC	G	C	Ser	Thr (8047)	CONSER VATIVE	transport	Human Gene TREMBL-NEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.6E-261	5
5877	cg42876412	487	AGCATCGTGATG ACCACCTGCTCC A[G/C]CTTCTGTG CCTGGGCATGA TGCCT	G	C	Ser	Thr (8048)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q14973 SODIUM/BILE ACID COTRANSPORTER (NA(+)/BILE ACID COTRANSPORTER) (NA(+)/TAUROCHOLATE TRANSPORT PROTEIN) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE) - HOMO SAPIENS (HUMAN), 349 aa.	1.3E-184	14
5878	cg42876412	532	ATGCCCTCTCCTC CTATACATCTAC A[G/C]CAAAGG ATCTACGACGGA GACCTG	G	C	Ser	Thr (8049)	CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q14973 SODIUM/BILE ACID COTRANSPORTER (NA(+)/BILE ACID COTRANSPORTER) (NA(+)/TAUROCHOLATE TRANSPORT PROTEIN) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE) - HOMO SAPIENS (HUMAN), 349 aa.	1.3E-184	14

5879	cg43945806	591	GTAGGCCCAAT CCTTCCACAGGG A/C/TGGAATGAT GCTGCCAGTTCA CTGTC	C	T	Val	Ile (8050)	CONSER VATIVE	transport	Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, QDB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa.	2.2E-145	6
5880	cg43269525	4020	TCTCTTGACACC CATAATTCTCCG G/A/TJAAGAGTCT TCAAGAACAGTT GCTCG	A	T	Phe	Tyr (8051)	CONSER VATIVE	ubiquitin	Human Gene SWISSNEW-ID:Q92462 UBIQUITIN-PROTEIN LIGASE PUB1 (EC 6.3.2.-) - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 767 aa.	6.5E-163	15
5881	cg43120117	2272	TTCAAGGCTTTG CAAGGTTCTACA G/G/CJCGGGGCA GGCCCCCGCT GTTACCC	G	C	Gly	Ala (8052)	CONSER VATIVE	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa.	7E-121	
5882	cg43120117	2275	AAGGCTTTGCAA GGTTCTACAGGC G/G/CJGGCAGGG CCCCGGCTGTTT ACCATC	G	C	Gly	Ala (8053)	CONSER VATIVE	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa.	7E-121	
5883	cg43944666	606	TGTAATGAAGA AGGTATTCAGAA A/G/CJTAAAAAGA GACAACCCAGGA GCATCC	G	C	Val	Leu (8054)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O15228 DIHYDROXYACETONE PHOSPHATE ACYLTRANSFERASE (EC 2.3.1.42) (DAP-AT) (GLYCERONE-PHOSPHATE O-ACYLTRANSFERASE) - Homo sapiens (Human), 680 aa.	0	1
5884	cg43926985	1454	ACATGGATCCTC ATCCAGTTTGCA TTT/GTTAGGAGGA CTGACAAATGGT AGTGG	T	G	Leu	Val (8055)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment).	0	2
5885	cg43978862	901	GCACATACATCAT CCTCATAGCCTT C/T/GTTCATCAGT CTCCCCAGTGGT GGGAT	T	G	Glu	Asp (8056)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43020 COAT PROTEIN GAMMA-COP - HOMO SAPIENS (HUMAN), 874 aa.	0	3

5886	cg43935402	1689	AACTCTACAAAG TGCCCCCAGCA G/C/G/AGACCTC CTGGTCTCCACC TCCACC	C	G	Gln	Glu (8057)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4
5887	cg43984608	877	CTGGGCATCCCC TTCAGGATCCAG G/A/C/CCACGGT CTGGTAAGCCCT GAAGTC	A	C	Val	Gly (8058)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35443 THROMBOSPONDIN 4 PRECURSOR - Homo sapiens (Human), 961 aa.	0	5
5888	cg43971826	1014	GATCTTACATCG AAAAATGCCCTACA T/C/T/TTCAGTAG CTATGATATCAA ATGTA	C	T	Asp	Asn (8059)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13576 RASGAP-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 1575 aa.	0	5
5889	cg43924112	4787	ACTGGTTTTAAG GATTGAAGAATT C/A/C/CGCGTGA AGGGGAAAGTGT TCCAAA	A	C	Val	Gly (8060)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
5890	cg43988933	1077	TTACTGTCTCAT CTTGCTAGAATG A/G/A/AAATTCCTG AGACCCCTTGAAG AAGAT	G	A	Arg	Lys (8061)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46275 SEC63 PROTEIN - HOMO SAPIENS (HUMAN), 759 aa.	0	6
5891	cg43999667	3945	GTTTGTGCAGGA CTTTTTTTTCTA C/T/AAAGTTGTTT TCTGGGATCACT GCT	C	T	Val	Ile (8062)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60281 KIAA0530 PROTEIN - HOMO SAPIENS (HUMAN), 1563 aa (fragment).	0	6
5892	cg43986140	4121	TTGCTTTTGGAA CTTGATTTAAGT [C/T]GACACTGCC TACAGATCCCCC CTGT	C	T	Asp	Asn (8063)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14156 HYPOTHETICAL PROTEIN KIAA0143 - Homo sapiens (Human), 885 aa (fragment).	0	8

5893	cg43287069	1871	ACTACGGTTCTCA GAGTTGCTGAAT G[G/C]AATACACA ACAAAAGAGGG GACAGT	G	C	Gly	Ala (8064)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55197 AF-10 PROTEIN - Homo sapiens (Human), 1027 aa.	0	11
5894	cg43329920	1862	GTGGTCATCCTC TGATGACATCCG G[A/G]TCCTCCCA GCCCAGAGCCG GGCCCT	A	G	Ile	Val (8065)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16538 PROTEIN A-2 - HOMO SAPIENS (HUMAN), 588 aa.	0	12
5895	cg43916884	732	TTCTGCAGCTG CTGCTTTGTCTT T[G/C]CAGCCCC CTTGGCTTTCTT GGCTGG	G	C	Ala	Gly (8066)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
5896	cg43924701	403	AGTGGGTCCACA TAGGAGGCATCT A[T/G]TCTTTGT TACTGCTACTTT CATAA	T	G	Ile	Leu (8067)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13099 TG737 - HOMO SAPIENS (HUMAN), 824 aa.	0	13
5897	cg43924701	404	GTGGGTCCACAT AGGAGGCATCTA T[T/G]TCTTTGT ACTGCTACTTTC ATAAG	T	G	Glu	Asp (8068)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13099 TG737 - HOMO SAPIENS (HUMAN), 824 aa.	0	13
5898	cg43929104	1023	GCGAGGCAGGG CCAGCAGCAGG CGG[G/C]AGGGG ACGGCAAAACAG AACAGAAA	G	C	Gly	Ala (8069)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
5899	cg43055918	1732	CCCCTATAGGTA ATCCCGAGGGG TT[G/C]TCATCAA TGAAGCTATTCA GATGTG	G	C	Asp	Glu (8070)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17

5900	cg43984911	2446	GAACAGGCACA GGATGTAGGG GTA[G/C]TCAGG AGTGGCGGCAG CTGGACCCAG	G	C	Thr	Ser (8071)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12767 HYPOTHETICAL PROTEIN KIAA0195 - Homo sapiens (Human), 1358 aa.	0	17
5901	cg43927434	239	GGAGTCTTCATA GCATCTTCTCCA A[C/G]AGGTGCG AGGGTCTGGGG GCTCCGC	C	G	Val	Leu (8072)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92797 SYMPLEKIN - HOMO SAPIENS (HUMAN), 1142 aa.	0	19
5902	cg43074645	3991	CTGTGAGGCGCT CAGGAGAGAGA AG[G/C]AGCGAG AATTAGAACTGC AGCGTCA	G	C	Glu	Gln (8073)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43152 KIAA0402 - HOMO SAPIENS (HUMAN), 1735 aa (fragment).	0	21
5903	cg17663981	395	CAAAAACCCCTGC AGCTGCCCCAAA G[G/T]GGATGTC AACTACGCGTTT CTCCAT	G	T	Gly	Val (8074)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0	10 (10p11.2 3)
5904	cg43988854	6808	CTTGAAAGAGCT CTTCCAGACACC A[A/G]TATGCACT GACAAAGCCAC GACTCA	A	G	Ile	Val (8075)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
5905	cg43988854	9484	AATATCCCTGCG CTCCAGACGCCA A[A/G]ATAAGACT GAGGCAGAACA GCAAAT	A	G	Asn	Asp (8076)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
5906	cg43988854	9844	AAACCCATACCT AGAGACAAAAGTC A[G/C]TGAGAACA AAAGGTGCTTGA GGTCT	G	C	Ser	Thr (8077)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)

5907	cg44026807	1745	ATTCGGGCTGCT CCCATCTCCTGC CIA/GTGTCCAG GTTGCACATGAG AAGGAA	A	G	His	Arg (8078)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14397 GLUCOKINASE REGULATORY PROTEIN (GLUCOKINASE REGULATOR) - Homo sapiens (Human), 625 aa.	0	2 (2p23.3)
5908	cg43960198	1974	GAAGAACCACGC CAGGCAGGCGG GAIG/CJTTCGAG GTCTTGGACATC AAAGCTG	G	C	Val	Leu (8079)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
5909	cg43973129	1182	ATAAAGGGTTAT CCAGGCGTCCA GGIG/CJCCCTGA GGACCTGGAGT GGGAGCGC	G	C	Gly	Ala (8080)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P05060 SECRETOGNANIN I PRECURSOR (SGI) (CHROMOGNANIN B) - Homo sapiens (Human), 677 aa.	0	20 (20pter)
5910	cg44016815	1158	AAGTTTATCTTG AACAACAGGAAC [G/AT]GAAAAGCT TCAACAAAAAGA ATTA	G	A	Arg	His (8081)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75330 INTRACELLULAR HYALURONIC ACID BINDING PROTEIN - HOMO SAPIENS (HUMAN), 724 aa.	0	5 (5q33.2)
5911	cg44923983	299	CGCGGCACAG CGACGAGAACG ACGT/GJTGGGC AGCCTCACAAA GGAGAAAG	T	G	Val	Gly (8082)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q09161 80 KD NUCLEAR CAP BINDING PROTEIN (NCBP 80 KD SUBUNIT) (CBP80) - Homo sapiens (Human), 780 aa.	0	9 (9q22.3)
5912	cg43311566	932	CACGACCTGCTC ACCACTATGCC GTT/CJTACCCACC CACAGGTGTCCT ACTGC	T	C	Val	Ala (8083)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment).	0	X
5913	cg43277466	2078	TTCTCTCTCTTT TCCTCTCTCGCT G/CJGAGCTCTTC CAGCTCCTTTTG TTTC	G	C	Gln	Glu (8084)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q02040 PROTEIN XE7 - Homo sapiens (Human), 695 aa.	0	XY

5914	cg43139712	1736	AAGACCAGGAA AGGGGGAGCA GGGTTGACAA GAGGGCCGG GCAAGCAC	G	T	Gly	Val (8085)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60378 F23858_1 - HOMO SAPIENS (HUMAN), 608 aa (fragment).	0	
5915	cg43934688	1989	ATGGCTAAGAGA AAAAACCATAC AICGJAAATTGAA GAGTTTCTGAT GTAA	C	G	Gln	Glu (8086)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
5916	cg43972478	2072	ACTATGTTAGGC TGGCTTTCTATC A/CICGCGTGA AGGATGGGCA AGATGCC	A	C	Leu	Val (8087)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q43284 HZW10 - HOMO SAPIENS (HUMAN), 779 aa.	0	
5917	cg44003843	4744	CCAGCTGCCCC CTGCCCTTTGT GGCTTCCGGG CAGCTACAGCAG CATCGTC	C	T	Ala	Val (8088)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92545 MYELOBLAST KIAA0257 - HOMO SAPIENS (HUMAN), 1805 aa (fragment).	0	
5918	cg44015572	1259	GCATTTATGCTC CAATCTGCATCA AIGTTCAATAAT CTTCAAATACCT TCATT	G	T	Leu	Ile (8089)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16526 PHOTOLYASE-LIKE 1 (PHOTOLYASE HOMOLOG) - HOMO SAPIENS (HUMAN), 586 aa (fragment).	0	
5919	cg44024279	1802	CAAATAACAGAG GAACAACCTTGAG GICGJTGTCATTG CAGATTTCTCAG GCCTG	C	G	Ala	Gly (8090)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOGLOBULIN) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	
5920	cg43956210	1440	CCTGTAATCCTT TCTGCTCCCTGG TIA/TCTTAGATT TGATTAGCTATG GACAA	A	T	Tyr	Phe (8091)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)

5921	cg43949262	1762	GTCCGTTGGTGTAG GTCGTCCATGCA G/GC/CCTGGCAG CGCACAGTAAAT CTGGGA	G	Ala	Gly (8092)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	
5922	cg4395003	988	GCTGTAGAGAAA GTGAAGCGCACA A/A/GJAGATGAG CTAGAAGTCATT CATCTA	A	Lys	Arg (8093)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10155 60 KD RO PROTEIN (60 KD RIBONUCLEOPROTEIN RO) (RORNP) (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) - Homo sapiens (Human), 538 aa.	1.9E-289	1
5923	cg40918088	1908	AAAAGCCACAGA GGCCCGGATCA TTA/TTCAGTGGA GGATCACTACCC GCAAGG	A	Thr	Ser (8094)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51854 TRANSEKOLASE 2 (EC 2.2.1.1) (TK 2) (TRANSEKOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa.	1.8E-287	X (Xq28)
5924	cg43931056	1283	GAGAGACATGGA CTTGATCATCAA G/T/CJAATTTCTG TAACCTTCGAGA AAGCT	T	Val	Ala (8095)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTRMBL-ACC:Q15020 ORF - HOMO SAPIENS (HUMAN), 963 aa.	4.5E-286	12
5925	cg43949830	1073	AGAGTCAGTCGG TTTGGACAGCAC A/C/GTTTTTTCTG GATTCACCATTC AGACA	C	Ser	Thr (8096)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTRMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16
5926	cg43930921	535	TGGGAGTGAAGT GCAGACACCTGG A/G/TTCGATCCG CAGGAGCCGCTT GAGCA	G	Asp	Glu (8097)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
5927	cg43980328	717	TTGGTTGTCTTA GCCTGGATACCA G/A/TGGAGAAG ATGTCATCCATA TCATCA	A	Ser	Thr (8098)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10



5928	cg43254830	1270	TTTAACATTCCAAAG AGCTCTGACCCA [G/C]AACAGATG CGACAGAGTTTG CTGAC	C	Glu	Gln (8099)	CONSERVATIVE	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:BAA76821 KIAA0977 PROTEIN - HOMO SAPIENS (HUMAN), 1166 aa.	1.3E-251	2
5929	cg43982278	331	TTATGGCTTAGA C GAAGGGAACAG CTC/G/AAAGAAG CCCTTGAAGAGG GTGAGG	G	Glu	Gln (8100)	CONSERVATIVE	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAD01211 ASPARTYL AMINOPEPTIDASE - HOMO SAPIENS (HUMAN), 472 aa.	1.5E-250	2
5930	cg43973393	858	AAGGAATGTGCC A ATATATACAAAC A[A/G]AGCTCTCT GTTACTTGAAGC TGTGC	A	Lys	Arg (8101)	CONSERVATIVE	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q07617 INFERTILITY-RELATED SPERM PROTEIN - HOMO SAPIENS (HUMAN), 528 aa (fragment).	1.5E-241	
5931	cg43928134	1540	TTCAGATGGAGA C GTACTTCTGAAT T[C/T]TACTATCA GAAAATCCACAA AGATT	C	Arg	Lys (8102)	CONSERVATIVE	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:BAA77335 IDN3 PROTEIN - HOMO SAPIENS (HUMAN), 2265 aa.	5.8E-240	8
5932	cg44013460	1020	CACTGAGTTGAA C AAAGCTGGACTT C[C/G]CAGCTCC AATTGGACCCAG CAGCAG	C	Gly	Ala (8103)	CONSERVATIVE	UNCLASSIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.6E-237	1
5933	cg43982127	788	CGGCAAAAATCC C AACGTTGGGTGG A[C/T]AGAGGCG TCGATCATAAAG CACACA	C	Val	Ile (8104)	CONSERVATIVE	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAD34038 CGI-43 PROTEIN - HOMO SAPIENS (HUMAN), 483 aa.	1.1E-233	7
5934	cg43916785	3427	CATTCTCTCTT C CTTCTCTCTCTT C/TTTTCAGCTTC TTTCTCATATTCC CG	C	Arg	Lys (8105)	CONSERVATIVE	UNCLASSIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.5E-230	14

5935	cg43994204	1312	GAGGCTCTGCTG CAGCTGTGCGAG G[C]TJCCTAAGCC TGATGGAAACTG TCAAG	C	T	Ala	Val (8106)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.4E-221	19
5936	cg43994204	654	CTCCACCAAGGA GAGCTACCCGCA C[G]A]TCAAGACT GTCTGCGACGCA GCAGA	G	A	Val	Ile (8107)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.4E-221	19
5937	cg43989168	308	CACCTCATTAC TCGTTTAGCTTT G[G]C]CTTCAATC CTCTGGCCACTT CCAAT	G	C	Ala	Gly (8108)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P70541 TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP- GTP EXCHANGE FACTOR) - Rattus norvegicus (Rat), 452 aa.	2.2E-215	1
5938	cg43062448	1357	TTAAAGGAATCC ATAAAATGGTGA A[G]C]TCCCAGG AGTCCACAAAT GTAGCC	G	C	Leu	Val (8109)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213 (3q21.3)	3
5939	cg43049457	176	CTGAGCCGACAT CTTCACTCATCA A[T]C]GTCATTCT TGTCCTCTCTCC CCTCC	T	C	Ile	Val (8110)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10523 S-ARRESTIN (RETINAL S-ANTIGEN) (48 KD PROTEIN) (S-AG) (ROD PHOTORECEPTOR ARRESTIN) - Homo sapiens (Human), 405 aa.	5.5E-212	2
5940	cg44021565	1285	ACGCTGACCCAT GGAGGCTGCAA AGT/A]GATCACT GCCTTTGTGGTG TCCACT	T	A	Thr	Ser (8111)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
5941	cg44021565	388	CCAGAAATCCAAA GAGATTTCTAAA T[C]T]CCACTTTT TCCTTCTTTTCAG TTCT	C	T	Asp	Asn (8112)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92863 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1

5942	cg44128902	964	AAGATGGAGTCA GCAGATCAGGC CGT/CJTGCTGA GCTCAACGGGA CCCAGGTG	T	C	Val	Ala (8113)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201	1 (1p36.2)
5943	cg43967823	1057	GAGGACATGCTG GCTATGCCCAAG G/C/TJGGCGCTG CTCAACGACTGC GTGTGC	C	T	Ala	Val (8114)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P54826 GROWTH-ARREST-SPECIFIC PROTEIN 1 (GAS-1) - Homo sapiens (Human), 345 aa.	1.9E-193	9 (9q21.3)
5944	cg43944615	1568	AGCTCACACTCT TTTCGGGTTTGT TTC/TCTCTCTGG GCACTCCTAGTT TTAAT	C	T	Arg	Lys (8115)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14877 FRPHE - HOMO SAPIENS (HUMAN), 346 aa.	1.3E-192	
5945	cg43973314	1045	GCATTTGCAAAG CTTCCCCCAAT G/C/TJCTTGAGAA TTTCAAAAGAGG TAATC	C	T	Ala	Val (8116)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O75521 DBI-RELATED PROTEIN 1 (DRS-1) - Homo sapiens (Human), 364 aa.	3.6E-192	6
5946	cg43968431	492	ATTCACCACCCA CTTGGGTAAGGA G/C/GJCTTTGGG GTCCACCTGGG CCAGGTA	C	G	Gly	Ala (8117)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
5947	cg42374050	580	GGCTGGGTCAG AACCTGTTTAAAT GGT/CJGGCCAG CTTCTTGGACC TGTTGGT	T	C	His	Arg (8118)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15335 CHONDROADHERIN - HOMO SAPIENS (HUMAN), 359 aa.	4.1E-191	
5948	cg43119894	1986	ACGGTCAGGGT CCACATAATGCA TTTC/TJTTTCAT GTCACATTCTTC AGCAGT	C	T	Arg	Lys (8119)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAAT5235 LACTOSYLCEAMIDE ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.9) - MUS MUSCULUS (MOUSE), 387 aa.	2.3E-190	2

5949	cg43928652	1689	AGTTCGGGAGG CCATCTGGATGG CTC/TJTGATCCA CTCTGTGCGCTC CTTGGG	C	T	Arg	Lys (8120)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P08567 PLECKSTRIN (PLATELET P47 PROTEIN) - Homo sapiens (Human), 350 aa.	2.9E-190	2
5950	cg43996402	1313	TGCAAAACCCACT GTTTCTCATCTC C/G/CJCTATTAGC TCCGAGGGGTG CATCGA	G	C	Ala	Gly (8121)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
5951	cg43996402	653	TGCTTGTAAC T	C	G	Ser	Thr (8122)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
5952	cg43996402	854	CTTGGCTTTTC CCGGTTATGGTG A/C/GJTGCTAGAA AGTCTTCATGA AGCTT	C	G	Ser	Thr (8123)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
5953	cg43249389	1134	AGAAGTGGATCC ATTGCTTCGAGG A/C/AJGTCACGG CCATCATTTTCT GTGTCG	C	A	Asp	Glu (8124)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.4E-188	15
5954	cg43965001	785	AATGTGTCGCAG A TTGGCTATTGGG A/A/GJCGTCCTTC ACAAAATCCAC CTGAC	A	G	Val	Ala (8125)	CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD42861 NY-REN-2 ANTIGEN - HOMO SAPIENS (HUMAN), 570 aa.	1E-178	14
5955	cg43919917	1069	TGACTCAGAGCA C GGTGCCCCCAGG CA/C/AJTCGCC GGCTCCGCCCG CGCACCCCG	C	A	Leu	Ile (8126)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60808 BK833B7.1 - HOMO SAPIENS (HUMAN), 339 aa.	3.5E-178	22

5956	cg439889723	422	CGGGAGCTGCG GGGCGGAGCG AGG[C]TTGAGAT CCGGGTCTTCCT CCAGCAG	C	T	Ala	Val (8127)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
5957	cg439889723	595	GATAACAGGGCC ACTGGAAGAAGC C[G/C]TGGCAGT GGCTTTCTCGCA GGTGCT	G	C	Val	Leu (8128)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13486 PSE-BINDING FACTOR PTF DELTA SUBUNIT - HOMO SAPIENS (HUMAN), 334 aa.	1.5E-175	
5958	cg43928685	490	GTTCACTACAAT TCTAAATACAAG A[G/C]CTATGATA TAGCCCAAGATG CGCCG	G	C	Ser	Thr (8129)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168 (1p36.33 )	1
5959	cg43329803	854	GTGGTCATCCTC TGATGACATCCG G[A/G]TCCTCCCA GCCCAGAGCGG AGCCCT	A	G	Ile	Val (8130)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16664 PROTEIN A-1 - HOMO SAPIENS (HUMAN), 304 aa.	5.9E-167	12
5960	cg43315424	213	ATCATCAGGGAT GCTGGAGTCTG GC[C/G]CCCCC CACACCACCAGA GCTGAAG	C	G	Gly	Ala (8131)	CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60525 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA 5 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 538 aa.	8.8E-158	
5961	cg43990820	411	GGCCCCAGGCT TTCTTCCTTGTG CA[G/C]AACACTC TGCAAGGAGGC ATGCAGT	G	C	Leu	Val (8132)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment).	3.3E-150	3
5962	cg42928454	414	AAAGTCAGTGGT GTTCTTTTGA C[G/C]CCAAGGC TAGAACACATTT TAAGCC	G	C	Ala	Gly (8133)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P78345 RNASEP PROTEIN P38 - HOMO SAPIENS (HUMAN), 283 aa.	1.1E-144	10

5963	cg42706411	220	CATCAGGTGGAGC GAGATTAGAAAC AICGJTATTGATA AAATAACTCAAT ATGTT	G	Thr	Ser (8134)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P32856 EPIIMORPHIN (SYNTAXIN 2) - Homo sapiens (Human), 288 aa.	3.8E-140	7
5984	cg43260991	315	GGCCCCACAGG GAGCCAGGAGC CTGT/GJGCGCA GGCCCATGCGC AAGTCCTTC	G	Val	Gly (8135)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60949 TBC1 - MUS MUSCULUS (MOUSE), 1141 aa.	6.2E-140	
5965	cg43303845	863	AGAACAGCAACG GCAAAAGGAGCT G[C/G]AGCGGGA AAGGCTGGAGC GAGAAAG	G	Gln	Glu (8136)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q93263 AVENA - GALLUS GALLUS (CHICKEN), 550 aa.	1.9E-138	
5966	cg43952219	1065	TGCCACTCGCCA GTTTGCCAAAGA G[C/A]TCTACCAG ATTTTITGGAG GCATA	A	Glu	Asp (8137)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa.	2.5E-136	X
5967	cg43994220	226	GGGTCAGCGGG CACCAGGTTGCT CT[G/C]GAAGAG CTTGAGGATGTG GTTCTCG	C	Gln	Glu (8138)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
5968	cg43950180	577	TATGGAATCACA GTTATCTCCTTG C[C/T]TGATTCA ATTTTGGTTGAG AAGTG	T	Arg	Lys (8139)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q09996 PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS) - Caenorhabditis elegans, 1198 aa.	3E-131	5
5969	cg43918152	369	AACAGACAGTTA CGCAGCCATTTC A[G/C]AAGTGGAT CGATTGCAGTCA GAGCC	C	Glu	Gln (8140)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P09496 CLATHRIN LIGHT CHAIN A (BRAIN AND LYMPHOCYTE LCA) - Homo sapiens (Human), 248 aa.	5E-131	9 (12q23)

5970	cg43928955	175	GCCTAGTACTCT TATGTGAAGTCT AIC/GICAAAGCTTG TGCTCAAGGGAA CCAAG	C	G	Thr	Ser (8141)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14331 FRG1 - HOMO SAPIENS (HUMAN), 258 aa.	1.3E-128	
5971	cg43917824	646	CCAGTGCCCCAAC ATGACACCTTCA GIC/CJAGTCGGC CGGGAGAGGCA CTCGTGT	G	C	Gly	Ala (8142)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00236 KIAA0251 - HOMO SAPIENS (HUMAN), 820 aa (fragment).	1.3E-128	18
5972	cg43931286	511	GTGTTTGAAGAC CCAGTCATCAGT AIA/GIATTCACCA ACATGATGATGA TAGGA	A	G	Lys	Arg (8143)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD27775 30S RIBOSOMAL PROTEIN S7 HOMOLOG - HOMO SAPIENS (HUMAN), 242 aa.	1.4E-128	17
5973	cg43307840	438	TACATCCCCTGG AGATGGCCCCACC TTT/CJCTCTTTTG TCAGTTGGCAA CCAGC	T	C	Lys	Arg (8144)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P09861 U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A') - Homo sapiens (Human), 255 aa.	8.1E-125	15
5974	cg43067745	160	CACAGAAAGAGA TCACAGACTCCC TTAGJCCTTAGAA GAAGGGAGGTG GTAGAT	A	G	Val	Ala (8145)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
5975	cg43926002	380	CGGGCACAGAA ACACAGCAGCG GGA/GIC/CAGCA ACACCAGCACTG CCAACAGA	G	C	Ser	Thr (8146)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
5976	cg41045083	611	AGCTTCCACCAA GGTTGTACCAAT GIC/CJCTCCACG CGCCTGACGCC CCTGGCC	C	T	Ala	Val (8147)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P32970 CD27 LIGAND (CD27-L) (CD70 ANTIGEN) - Homo sapiens (Human), 193 aa.	3.3E-102	19 (19p13)

5977	cg43980312	2657	AACAGTATCTTT GGAAGTGGTCG AGATJTGTGTC AGCTCTGGACTC TCTACA	A	T	Ser	Thr (8148)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P34741 SYNDECAN- 2 PRECURSOR (FIBROGLYCAN) (HEPARAN SULFATE PROTEOGLYCAN CORE PROTEIN) (HSPG) (SYND2) - Homo sapiens (Human), 201 aa.	7.9E-101	8 (8q22)
5978	cg43252708	534	CCITGCCGAGAG ATTGACGTGTC CIGAJTTTGCATC CTGGGCTCCCT CGCTT	G	A	Val	Ile (8149)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75679 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa.	2.1E-100	
5979	cg43927693	713	GTATGGCGGGA CAACCATGGCTG GCIGAJTGGGG ACGGCGGCTGC CAGAGTGA	G	A	Arg	His (8150)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22
5980	cg42835634	532	TACTGTGACTTC TTCTACTTGAT GIGTJGACCAAA GGTAGGTCCTG GGATGAC	G	T	Gly	Val (8151)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43731 ER LUMEN PROTEIN RETAINING RECEPTOR - HOMO SAPIENS (HUMAN), 214 aa.	3E-92	22
5981	cg43921592	453	CCCCGGATGTG GATACCTATAAG GAGTJATTTCAT ATTTGTTGCGG AGTTCA	G	T	Glu	Asp (8152)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16548 BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC- SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) - Homo sapiens (Human), 175 aa.	4.9E-92	15
5982	cg43978148	536	GGAGAAATGCCA GACTTGTGGTAC CJAGJATTATATC ATCTCAGTCTTG AATT	A	G	Asn	Asp (8153)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4E-90	16



5983	cg43978148	690	GAAAAAGAGGTT GTTGCTGTAGCC C/A/GTGTCTGTTT ATCAAGCAATGC TCAGC	A	G	His	Arg (8154)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4E-90	16
5984	cg43059113	458	GCACTCAGCAGT GCGTGCTTTTTC TTT/CJTGGGAAA GGCAGGACAAC CAGCTT	T	C	Lys	Arg (8155)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa.	7.4E-89	3
5985	cg43960450	1409	CTTTTCCTGCAG ACGTTCAATAAT A/G/C/CAGCTAG ATTAGCCTCACG GTTTC	G	C	Ala	Gly (8156)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
5986	cg43960450	1544	TTCTCGCTCGTG TTCCCTCTTCTC T/G/A/JCCAATTGT TTCAGCACCTGG GCCTC	G	A	Ala	Val (8157)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
5987	cg43955851	519	GCCACACTCTCT GTGCATCGGCTT G/C/T/GCGTGTC CGGGTGGAAGG AGTIGAA	C	T	Arg	His (8158)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27745 CGI-36 PROTEIN - HOMO SAPIENS (HUMAN), 165 aa.	1.1E-87	2
5988	cg43922714	227	GAAGTAGGAGAA ACATTTAAATTA I/A/GJAGAAGCTGT TGTTTtagggag CAGC	A	G	Lys	Arg (8159)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34141 CGI-146 PROTEIN - HOMO SAPIENS (HUMAN), 193 aa.	9.8E-87	19
5989	cg43996941	481	TGAAGAAAACTC AGCTAAATTTCC T/G/A/JTAGGAAG GAGAGATTTTGA CATGCT	G	A	Val	Ile (8160)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16044 PREPRO-MELANIN- CONCENTRATING HORMONE - HOMO SAPIENS (HUMAN), 165 aa.	3.1E-83 (12q23)	12

5990	cg43920730	849	TTTTCTCTTTG TTTGTCCACTA C/GJAGCTCACT TCTCAGAGCTAA ACTC	G	Val	Leu (8161)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15182 CENTRIN - HOMO SAPIENS (HUMAN), 167 aa.	5E-83	
5991	cg43969140	528	TCGGCCCCACTC GCCAGTCACAAA G/GA/CATCATTA ACACTCAGACAG GCCAC	A	Ala	Val (8162)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
5992	cg43969140	595	GCCTTCAGAGCC TCAGCCTGCTCC A/C/AJAAACCCCTG GCAGGTGTGTCT TGGAA	A	Val	Leu (8163)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
5993	cg44936941	716	AAATACCAAC AGTTATTGCGTA C/C/TJTTGTAGCA TATGCTGGTTGT ACTTC	C	Arg	Lys (8164)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa.	7E-77	1
5994	cg44936941	755	TGGTTGTACTTC ATGAGGGTTGCG A/C/TJGGTCAGAC CAGAAAAACAGC AGTCT	C	Arg	His (8165)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa.	7E-77	1
5995	cg38622616	345	AGAAATCTTCAA TTTCACTTTTCATC [G/C]TCCATGGG TTCTTCTAAACTT GGAC	G	Asp	Glu (8166)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40849 SIRTUIN TYPE 1 - HOMO SAPIENS (HUMAN), 555 aa.	6.3E-76	
5996	cg43969639	959	CCAGACCCACTC TGCAGTAAGGTG TTT/ATCAAAACA GAAAATGCACAA ATGAA	T	Glu	Asp (8167)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C28A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3

5997	cg42696021	427	GCATGCTTCACA CAGTGGCTGTGC C/GA/JCCTTCACA ATGAAGTGAACC GGAG	G	A	Arg	His (8168)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.4E-69	
5998	cg42696021	481	GGCAAGCCTGAT TTTGACTGCTCA A/GA/JAGTTGATG AGCGATGGCGT GACGGC	G	A	Arg	Lys (8169)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.4E-69	
5999	cg43942822	344	GTCACCTCTGAG CCACATCTCAG G/C/TJCACTAGG GGAAGAAAAAT AGGTCC	C	T	Ala	Val (8170)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14678 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
6000	cg43955219	1361	GCCTCATGCTCT CTGGGATTGCAG A/C/GJCATCCAG GTCTGTCTTCGC CCCTGT	C	G	Asp	Glu (8171)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 IIII ALU SUBFAMILY SQ WARNING ENTRY IIII - Homo sapiens (Human), 593 aa.	6.4E-68	
6001	cg43927424	302	AGCGCAGTATT CAGAGAAAAGTA T/A/TJCTCTTCAG CTGAAGTACCCG CACCT	A	T	Thr	Ser (8172)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa.	1.9E-65	
6002	cg43927424	366	GTCGGGCAGGA ACAGAAACACAC CTA/TJCTTGCCA CTAGAACTCTGT AAJATT	A	T	Tyr	Phe (8173)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa.	1.9E-65	
6003	cg43082068	765	TTCTGGAGCTG CTGGTGAAAGAA A/C/GJCTCTGGA GGCCCCGGACTC CCCCGGAC	C	G	Thr	Ser (8174)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to REMTREMBL- ACC:G2352941 LEUKOCYTE- ASSOCIATED IG-LIKE RECEPTOR-1 - HOMO SAPIENS (HUMAN), 287 aa.	2.5E-65	

6004	cg42381630	271	TTGGCCTAGACC AAGGCGCTATGT ATC/GIAGCCTCCT GAAATGATTGGG CCTAT	C	G	Gln	Glu (8175)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.9E-64	
6005	cg43950549	466	TGACTGGATTAA AAGGTGTCAGA ATC/GJTTCAGAA GGTCAGAAATAG GAAGT	C	G	Leu	Val (8176)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.4E-62	
6006	cg43308257	839	TCAGAGCCGGC GGTGGTGCAGA AGA[G/A]AGCCA GTGCCAGTGA CCACACAGC	G	A	Arg	Lys (8177)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa.	2.9E-62	
6007	cg40968986	269	TGAGCTGGAGCA GGAGCAAGAGA GA[G/C]AGGGCT CCAGAATCATTG CCCAGAA	G	C	Glu	Gln (8178)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.1E-58 (11p15.2)	
6008	cg43052776	401	ACCAACAAAGAT TTCAGGGATTTT GT[C]CAGGGAG AAAAGTATCGG ACAGAA	T	C	Val	Ala (8179)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43247 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 323 aa (fragment).	3.6E-57	
6009	cg43942680	697	CTCGGAGGAGA GCGCCCTCAATC AC[G/C]TGCAGC ACCCGAGCGAC GAAGCCGA	G	C	Val	Leu (8180)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38498 T-CELL ACTIVATION PROTEIN - HOMO SAPIENS (HUMAN), 127 aa.	1.8E-55	10
6010	cg43511804	864	GGGCCTGATCTT CATACTCATCTT CT[C]TCATTGAG TACCATGACCCC TTCCA	T	C	Lys	Arg (8181)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa.	3.1E-51	4

6011	cg44341803	864	GGGCCTGATCTT CATACTCATCTT CTTCCTCATTGAG TACCATGACCCC TTCCA	T	C	Lys	Arg (8182)	CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa.	3.1E-51	4
6012	cg43291028	1907	CTCTAGGCCCTT GAGCTGATACTG AIGATGATGGTG GCATTCTTTATCT TCAC	G	A	Thr (8183)	Ile (8183)	NON- CONSER VATIVE	anglpoi etin	Human Gene SWISSNEW-ID:Q02763 ANGIOPOIETIN 1 RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR TIE-2) (TYROSINE- PROTEIN KINASE RECEPTOR TEK) (P140 TEK) (TUNICA INTERNA ENDOTHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 1124 aa. Jpls:SWISSPROT-ID:Q02763 ANGIOPOIETIN 1 RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR TIE-2) (TYROSINE- PROTEIN KINASE RECEPTOR TEK) (P140 TEK) (TUNICA INTERNA ENDOTHELIAL CELL KINASE) - HOMO SAPIENS (HUMAN), 1424 aa.	0	9
6013	cg43921977	2748	ATTATTCATCCAA T GTTCCATATTA T/CJCTCAAAAAA TTCAGGGGAGATC CTG	T	C	Asp (8184)	Gly (8184)	NON- CONSER VATIVE	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0	20
6014	cg43921977	2753	TCATCCAAGTTT A CCATATTATCTTC [A/C]AAAAAATTCA GGGAGATCCTGA AAGT	A	C	Phe (8185)	Leu (8185)	NON- CONSER VATIVE	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0	20
6015	cg43921977	2754	CATCCAAGTTT A CATATTATCTTCA [A/C]AAAAAATTCA GGGATCCTGAA AGTT	A	C	Phe (8186)	Cys (8186)	NON- CONSER VATIVE	apoptosis	Human Gene SWISSPROT-ID:P55060 CELLULAR APOPTOSIS SUSCEPTIBILITY PROTEIN - HOMO SAPIENS (HUMAN), 971 aa.	0	20

6016	cg43948568	2080	CCAGAGCCTGC CCGCTGGATGTC CTA/CJGATCATA TGGGGCCTGAA CAGCTCG	A	C	End	Glu (8187)	NON- CONSER VATIVE	apoptosis	Human Gene SWISSPROT-ID:P55211 CASPASE-9 PRECURSOR (EC 3.4.22.-) (CASP-9) (ICE-LIKE APOPTOTIC PROTEASE 6) (ICE-LAP6) (APOPTOTIC PROTEASE MCH-6) (APOPTOTIC PROTEASE ACTIVATING FACTOR 3) (APAF-3) - HOMO SAPIENS (HUMAN), 416 aa.	2E-222	1
6017	cg42913771	469	GCTTGTTCAAAG GAGACAAGTGTC A/GC/JAGCCTGG TTGGAAAACCCA AGATAT	G	C	Gln	His (8188)	NON- CONSER VATIVE	apoptosis	Human Gene Homologous to SWISSPROT-ID:P55212 CASPASE-6 PRECURSOR (EC 3.4.22.-) (APOPTOTIC PROTEASE MCH-2) - HOMO SAPIENS (HUMAN), 293 aa.	6.2E-116	
6018	cg43277632	1703	GACTGCAACAGT TCTTTATAATCCC [T/G]CTGTAATTA GCCCAGAAGAAG TCAG	T	G	Ser	Ala (8189)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0 (13q14.3 )	13
6019	cg43277632	774	AGCATGAAGGTT TCCCTGGAACAA G/GA/JCAGTGCC ACTGTGAAATAT GTGCCA	G	A	Gly	Asp (8190)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0 (13q14.3 )	13
6020	cg43252813	1307	CCAGAATCCCTG AGAAAAGCAATA G/A/TJGGCTGTAT CACCGGGGCTAT ATAGA	A	T	Glu	Val (8191)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSNEW-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.   pcids:SWISSPROT-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.	0 X (Xq12)	

6021	cg43252813	3832	CTCAAAATGCTCT TAATGCTCAGCA G[C/T]ATAAAGTC CTCATTGGTAAC CGGGA	C	T	His	Tyr (8192)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSNEW-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.[pcls:SWISSPROT-ID:Q04656 COPPER-TRANSPORTING ATPASE 1 (EC 3.6.1.36) (COPPER PUMP 1) (MENKES DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1500 aa.	0 X (Xq12)
6022	cg43931944	268	ACTATTCAGGTG TATGAAGAACT T[C/G]TGGTGTGT CTGTTGGAGATC CTGTA	C	G	Ser	Cys (8193)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P38806 VACUOLAR ATP SYNTHASE CATALYTIC SUBUNIT A, UBIQUITOUS ISOFORM (EC 3.6.1.34) (V-ATPASE 69 KD SUBUNIT) (ISOFORM VA68) - HOMO SAPIENS (HUMAN), 617 aa.	0
6023	cg43939527	1246	AGATGACCTCTC TGGTCTGACAT C[A/C]AGGCAATC TGTACAGAAAGCT GGTCT	A	C	Lys	Gln (8194)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SWISSPROT-ID:P49014 26S PROTEASE REGULATORY SUBUNIT 4 (P26S4) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 440 aa.	14 1.5E-233
6024	cg43958825	197	GTGGGTGAGCT CCGTGGCACCC CTG[C/G]GCAGT GCGATCATGCC GCCTCCAC	C	G	Arg	Pro (8195)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	11 7.8E-228
6025	cg43958825	198	TGGGTGAGCTCC GTGGCACCCCT GC[G/C]CAGTGC GATCATGCCCGC CTCCACA	G	C	Arg	Gly (8196)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SPTREMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	11 7.8E-228
6026	cg43933600	304	GCTCCAGGAGG AGGGCCGAGAA GGT[G/T]TTGACC TTGCTGCCCCCG CGCACCT	G	T	Ash	Lys (8197)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa.	19 4E-185

6027	cg44026571	415	GGAAATTATGGG TTTGATGCTTGG A/A/GJAAATTTGTT GATGATTATACC GTCAG	A	G	Lys	Glu (8198)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene SPTREMBL-ID:O00487 26S PROTEASOME-ASSOCIATED PAD1 HOMOLOG - HOMO SAPIENS (HUMAN), 310 aa.	3.8E-164	
6028	cg43284434	1995	ACTAACTTATATC GCAGAGTGGAAA [G/A]GGGGCCTC CTGGAGCACAAG ATGGG	G	A	Gly	Arg (8199)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q18788 C52E4.5 - CAENORHABDITIS ELEGANS, 590 aa.	4E-121	6
6029	cg43251803	2910	GGACCATCTGAG TCCACGTACTGC C[G/A]GCGTTTGA GGTAGCAGGAC ACTGCC	G	A	Arg	Trp (8200)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.1E-105	
6030	cg43251803	2961	ATCTGAATCTGC TCGGTACGCACT C[G/A]TTTCATGA CTGAACATCCCA GGCGG	G	A	Arg	End (8201)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene Homologous to TREMBLNEW-ID:G1732075 TBP- ASSOCIATED FACTOR - HOMO SAPIENS (HUMAN), 801 aa (fragment).	3.1E-105	
6031	cg43132502	357	GCTGGCCCCAG TGCAGTGGGTG GCA[C/T]CGCCG AGGCTGCTGTTA CGGCTCAT	C	T	Pro	Ser (8202)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.4E-58	11
6032	cg44000476	1164	AACGGTCTCAGA GGCTGGGTAATC T[A/C]CCTGAACA GCTCCCCCATGG GCACC	A	C	* End	Glu (8203)	NON- CONSER VATIVE	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:P78344 P97 - HOMO SAPIENS (HUMAN), 907 aa.	3.8E-53	3
6033	cg43966234	1864	TGGAACATGAG CATTACAGTTCTT T[G/G]TACAGTG ACAAGGTGAATA TCTT	T	G	Cys	Gly (8204)	NON- CONSER VATIVE	biotindep	Human Gene SWISSPROT-ID:P05165 PROPIONYL-COA CARBOXYLASE ALPHA CHAIN PRECURSOR (EC 6.4.1.3) (PCCASE) (PROPANOYL- COA:CARBON DIOXIDE LIGASE) - HOMO SAPIENS (HUMAN), 702 aa.	0	13 (13q32)



6034	cg43255401	810	GCTGGAAGTGG AGCCCGTGGGA ATG[A/C]CGGT GAAGGGGACCG CGTGGAAAT	A	C	Thr	Pro (8205)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P43121 CELL SURFACE GLYCOPROTEIN MUC18 PRECURSOR (MELANOMA- ASSOCIATED ANTIGEN MUC18) (MELANOMA-ASSOCIATED ANTIGEN A32) (S-ENDO 1 ENDOTHELIAL- ASSOCIATED ANTIGEN) (CD146 ANTIGEN) (MELANOMA ADHESION MOLECULE) - HOMO SAPIENS (HUMAN), 646 aa.	0	11
6035	cg44026834	1466	CTGCCCGATGGA GAGCGTAGAAC GT[C/A]ATCGCTG TACATAAGGAAG CTGTCG	C	A	Asp	Tyr (8206)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
6036	cg42558238	2115	TGACTGGAATAA CCAAAGCCTCCC CT[C/A]CCACAGC CAGAAGCTGAGA TTGGA	T	C	Tyr	His (8207)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.   cds:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
6037	cg43956560	1285	CTGGCAAGGAG ATTAAAAAAGG CA[AT]GAAATCC AAGAGAAGTATG AATGAC	A	T	Lys	Met (8208)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1E-218	1 (1q23)

6038	cg43956560	1287	GGCAAGGAGATT AAAAAAGGCAA GATTAATCCAAG AGAAGTATGAAT GACCC	A	T	Lys	End (8209)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P14151 L- SELECTIN PRECURSOR (LYMPH NODE HOMING RECEPTOR) (LEUKOCYTE ADHESION MOLECULE- 1) (LAM-1) (LEUKOCYTE SURFACE ANTIGEN LEU-8) (TQ1) (GP90-MEL) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 1) (LECAM1) (CD62L) - HOMO SAPIENS (HUMAN), 372 aa.	1E-218 1 (1q23)
6039	cg42388009	378	AAATGAAGGAGA AAACAATGAAGA A/C/TTCGACGAA GACGAAGACTCT GAGGC	C	T	Pro	Ser (8210)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P21815 BONE SIALOPROTEIN II PRECURSOR (BSP II) (CELL-BINDING SIALOPROTEIN) (INTEGRIN-BINDING SIALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa.	7E-172 4
6040	cg42388009	379	AATGAAGGAGAA AACAATGAAGAA C/C/TTCGACGAA GACGAAGACTCT GAGGCT	C	T	Pro	Leu (8211)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P21815 BONE SIALOPROTEIN II PRECURSOR (BSP II) (CELL-BINDING SIALOPROTEIN) (INTEGRIN-BINDING SIALOPROTEIN) - HOMO SAPIENS (HUMAN), 317 aa.	7E-172 4
6041	cg43303099	965	GAGACGGGAGG CCCGGGAGAAC TTG/C/A/C/GGTCT TTAGCTTCCTAG GACCCAT	C	A	Pro	Thr (8212)	NON- CONSER VATIVE	cadherin	Human Gene SWISSPROT-ID:P32942 INTERCELLULAR ADHESION MOLECULE-3 PRECURSOR (ICAM-3) (CDW50) (CD50 ANTIGEN) (ICAM-R) - HOMO SAPIENS (HUMAN), 547 aa.	8.7E-158 (19p13.3)
6042	cg42926989	269	GCTGGCAGCAC AAAGGCTTATCG CA/C/TTCAGGAAA GATGCAGCCACT CCTGCT	C	T	Val	Met (8213)	NON- CONSER VATIVE	cathepsin	Human Gene Homologous to SWISSPROT-ID:P08311 CATHEPSIN G PRECURSOR (EC 3.4.21.20) - HOMO SAPIENS (HUMAN), 255 aa.	1.7E-136 (14q11.2)
6043	cg43980411	1284	TTCTTATTATGCA TAAGATAACCAA C/G/TTCATTTTAT TTTTCGGCAGAT TTT	C	G	Asn	Lys (8214)	NON- CONSER VATIVE	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG- SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222 (18q21.3)

6044	cg43980411	1310	TGCATTTTATTTT TCGGCAGATTTT C/GCTCACCCCTA AAACTAAGCGTG CTGC	C	G	Ser	Cys (8215)	NON- CONSER VATIVE	cathepsin inhib	Human Gene SWISSPROT-ID:P05120 PLASMINOGEN ACTIVATOR INHIBITOR-2, PLACENTAL (PAI-2) (MONOCYTE ARG-SERPIN) (UROKINASE INHIBITOR) - HOMO SAPIENS (HUMAN), 415 aa.	3.2E-222 (18q21.3)	18
6045	cg43971453	2657	TGTCCAGCCATG AACTGTCCAAAG C/GC/JAGGGGG AAGGTCAGCGTG GAGATG	G	C	Arg	Gly (8216)	NON- CONSER VATIVE	chloride channel	Human Gene SWISSPROT-ID:P51788 CHLORIDE CHANNEL PROTEIN 2 (CLC 2) - HOMO SAPIENS (HUMAN), 898 aa.	0	3
6046	cg43970982	2131	TGGACCTCGGG GAAGCGGAGGT GCC[G/C]CTGGT GCTCCTGGAGAA CGAGGCAG	G	C	Ala	Pro (8217)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
6047	cg43970982	2222	GGACCAAAAGGA GGAATCGGCAAC C[G/C]GGGCCCT CGTGGGGAGAC GGGAGAT	G	C	Arg	Pro (8218)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
6048	cg43970982	4399	CAGCGCCAAACT CCACTGGGAGA GG[C/G]CTGAGC CCCCCGTCTT ATTTTAA	C	G	Pro	Ala (8219)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
6049	cg43131198	5672	GGCTCACACG GTGAAAGCAGAC TT[G/C]GAGTTT CCTCTGCTCCAG CACCAG	G	C	Leu	Phe (8220)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:P53420 COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1690 aa.	0 2 (2q36)	
6050	cg43970983	2792	CTGCGCTGGGA GCCGGTGCCCA GAG[C/A]GCAGG GCTTCCTCTGC ACTGGCAA	C	A	Ala	Glu (8221)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0 3 (3p21.3)	

6051	cg43970983	9090	ACGTCGGTTATT TCAGTGACTTGG TCAJCCGTGGG TCTAGCCTTCCC CCCTGT	C	A	Pro	Thr (8222)	NON- CONSER VATIVE	collagen	Human Gene SWISSPROT-ID:Q02388 COLLAGEN ALPHA 1(VII) CHAIN PRECURSOR (LONG-CHAIN COLLAGEN) (LC COLLAGEN) - HOMO SAPIENS (HUMAN), 2944 aa.	0	3 (3p21.3)
6052	cg41035069	1211	AATGGAGAAAT GGTTGAAAGGT GIAJCTTGGGTC CTCATGGTCCAC CTGGC	A	T	Asp	Val (8223)	NON- CONSER VATIVE	collagen	Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa.	0	6 (6q12)
6053	cg41035069	1438	AGGAATACACCA AACTCTGGTGG ATT/GJATTATAAC AAGGATAACAAG GGAAA	T	G	Tyr	Ser (8224)	NON- CONSER VATIVE	collagen	Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa.	0	6 (6q12)
6054	cg41035069	1441	AATACACCAAC TCTTGGTGGATA TT/GJATAACAAG GATAACAAGGGA AATGA	T	G	End	Ser (8225)	NON- CONSER VATIVE	collagen	Human Gene TREMBLNEW- ID:D1024188 TYPE XIX COLLAGEN A1 CHAIN - HOMO SAPIENS (HUMAN), 1143 aa.	0	6 (6q12)
6055	cg43991318	3625	TGGATGCCAGG GTCTCCCCTGGC TIG/CJGTACAGG ATCACCAGGCTC CCCTTT	G	C	Gly	Arg (8226)	NON- CONSER VATIVE	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
6056	cg44032748	1860	ACCTCAGAAATGG AGGGCCCTCGT GT/CJTCAGGGC GGAAAAGTACAGA CGCAGGC	C	T	Pro	Ser (8227)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P07357 COMPLEMENT COMPONENT C8 ALPHA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 584 aa.	0	1 (1p32)
6057	cg43281450	1987	TCAGCCTGGCAG GAATGCCCTGTCT TIC/TJCTGAAGCT CATAGCCTGGAC GGCAG	C	T	Glu	Lys (8228)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0	12 (12p13)

6058	cg43281450	2082	CTGGGGCTGGG GATCCTCCTCCC CTG/AJATTGCT CCGGAAGCAC ATTATC	G	A	Ser	Leu (8229)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P00736 COMPLEMENT C1R COMPONENT PRECURSOR (EC 3.4.21.41) - HOMO SAPIENS (HUMAN), 705 aa.	0	12 (12p13)
6059	cg43933757	1351	ATGGGCTCTTGA AGAGTATCTGGA T/A/G/AATTGAC CCCTGTGATTGC CGGCC	A	G	Lys	Glu (8230)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0	5 (5p13)
6060	cg43029278	607	TCTTCAGGATCA ATTACATGTTTG C/A/G/AAATGGAT GGTCAGCACAAAC CAATT	A	G	Gln	Arg (8231)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa.	7.5E-191	
6061	cg43029278	805	ACATGTAGTAAT GGAGAGTGGTC GG/A/CJACCACC TAGATGCATACA TCCATGT	A	C	Glu	Ala (8232)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q02985 COMPLEMENT FACTOR H-LIKE PROTEIN DOWN16 PRECURSOR - HOMO SAPIENS (HUMAN), 331 aa.	7.5E-191	
6062	cg43958185	1009	TACTCATCTGT CTCGACACTATA T/A/G/JAGCATTT GTACTGTGGGC GGATTC	A	G	Tyr	His (8233)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-180	1
6063	cg43958185	1286	TGGTGACCATCC TTCTTCTGTGCA T/G/T/TATGCGA GTCCAAAATGAT TTTGA	G	T	Thr	Lys (8234)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1
6064	cg43958185	609	AAATTCAGCTGA TTCACCTGTTCT C/A/G/AATAAAGC TTCTGTTGGCT GTCCA	A	G	Leu	Ser (8235)	NON- CONSER VATIVE	complem ent	Human Gene SWISSPROT-ID:Q03591 COMPLEMENT FACTOR H-LIKE PROTEIN 1 PRECURSOR (H36) - HOMO SAPIENS (HUMAN), 330 aa.	4.1E-190	1

6065	cg42542496	344	TTGCTCCTCGTG GTTCATGCTTCTC CTCJAACCTGCAA GGCTAACGCTGT CCAGC	T	C	Leu	Pro (8236)	NON- CONSER VATIVE	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.2E-169	3 (3q26.3)
6066	cg42542496	650	TCATCCCTCCTG GGGCAGCTTTCT G[G]A[ACAGGTC CGTCTCCTCCTT GGGGCC	G	A	Gly	Glu (8237)	NON- CONSER VATIVE	csf	Human Gene SWISSPROT-ID:P40225 THROMBOPOIETIN PRECURSOR (MEGAKARYOCYTE COLONY STIMULATING FACTOR) (C-MPL LIGAND) (ML) (MEGAKARYOCYTE GROWTH AND DEVELOPMENT FACTOR) (MGDF) - HOMO SAPIENS (HUMAN), 353 aa.	1.2E-169	3 (3q26.3)
6067	cg2752665	551	CCGGAAACCTCC TGTGCAACCCAG ATT[C]TATCACCT TTGAAAGTTTCA AAGAG	T	C	Ile	Thr (8238)	NON- CONSER VATIVE	csf	Human Gene Similar to SWISSPROT- ID:P04141 GRANULOCYTE- MACROPHAGE COLONY- STIMULATING FACTOR PRECURSOR (GM-CSF) (COLONY-STIMULATING FACTOR) (CSF) - HOMO SAPIENS (HUMAN), 144 aa.	5E-75	5 (5q31.1)
6068	cg34413286	435	GCGCTACGGGG ACGTCCTGCAGA TC[C]A[GCATTGG CTCCACGCCCGT GCTGGT	C	A	Arg	Ser (8239)	NON- CONSER VATIVE	cyto450	Human Gene SWISSNEW-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (CYP1A2) (P450-P3) (P(3)450) (P450 4) - HOMO SAPIENS (HUMAN), 515 aa.[pcis:SWISSPROT-ID:P05177 CYTOCHROME P450 1A2 (EC 1.14.14.1) (P450-P3) (P450-4) - HOMO SAPIENS (HUMAN), 515 aa.	4.6E-278	15 (15q22)

6069	cg40333008	607	GCTGGTGCCACT CCTTCTCATTGT G[C/A]TGCAGCG CCCACAGATTGA TGATAA	C	A	Gln	His (8240)	NON- CONSER VATIVE	cyto450	Human Gene SWISSNEW-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.lpcis:SWISSPROT-ID:P05093 CYTOCHROME P450 XVIIA1 (P450- C17) (EC 1.14.99.9) (STEROID 17- ALPHA-HYDROXYLASE/17,20 LYASE) - HOMO SAPIENS (HUMAN), 508 aa.	4.9E-274	10 (10q24.3)
6070	cg43063374	1580	TGATTGCTTCCT GATCAAAATGGA A[A/C]AGGAAAG CAAAACCAACAG TCTGA	A	C	Lys	Gln (8241)	NON- CONSER VATIVE	cyto450	Human Gene SWISSNEW-ID:P33259 CYTOCHROME P450 2C17 (EC 1.14.14.1) (CYP11C17) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa.lpcis:SWISSPROT-ID:P33259 CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa.	3.2E-254	10 (10q24.1)
6071	cg43063374	1591	TGATCAAAATGG AAAGGAAAGC A[A/C]AACCAACA GTCTGAATTCAC TATTG	A	C	Gln	His (8242)	NON- CONSER VATIVE	cyto450	Human Gene SWISSNEW-ID:P33259 CYTOCHROME P450 2C17 (EC 1.14.14.1) (CYP11C17) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa.lpcis:SWISSPROT-ID:P33259 CYTOCHROME P450 IIC17 (EC 1.14.14.1) (P450-254C) - HOMO SAPIENS (HUMAN), 468 aa.	3.2E-254	10 (10q24.1)
6072	cg43966704	576	CCGCCAGGGAT CACAGCAAGGA GGTT[A]GTCCCA GCCGCCCGTGA CACCCCCA	T	A	Asn	Tyr (8243)	NON- CONSER VATIVE	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.8.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11
6073	cg43966704	597	AGGTTGTCACAG CCGCCCGTGAC AC[C/A]CCCAGC ATGCTTCTCAAT CAGTTCT	C	A	Gly	Cys (8244)	NON- CONSER VATIVE	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.8.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11

6074	cg43962888	453	GACTGGGTTGGA GAGGGAGATCAT G[C]A]TGGCTGC AAAGAAGGGACT GGACCC	C	A	Leu	Met (8245)	NON- CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
6075	cg43923204	1812	GGTGACCCGACAT CATGCAGTAGCC G[C]T]CCCCGGA GTAGTCTTCACG GAGGCC	C	T	Gly	Asp (8246)	NON- CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.7E-52	17
6076	cg43923204	1924	GCGCCAGGATC GAGGCTGCCCCG TGG[C]T]CGCTGT CCAGCCCATGAC AGCGGGG	C	T	Ala	Thr (8247)	NON- CONSER VATIVE	cytochrome	Human Gene Similar to SWISSPROT- ID:P21592 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX10 PRECURSOR - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 462 aa.	1.7E-52	17
6077	cg43967318	1615	TATTTTCTTTCT GGCCCTTTGTGC [C/A]AAAGAGCA GGATGCCTTTGA AACCG	C	A	Gly	Cys (8248)	NON- CONSER VATIVE	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
6078	cg34396112	1048	CACCCCATAGCT GAAGTAGTGGAA G[G]C]GGTTCCC TGAGTTAGTCTC AAAGCT	G	C	Pro	Arg (8249)	NON- CONSER VATIVE	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6079	cg34396112	2946	TCTGAAGGACTG TCAGGTAGAACT T[G/C]AAGAAGAA GCTGAGGGTGA GGTGCC	G	C	Phe	Leu (8250)	NON- CONSER VATIVE	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6080	cg34396112	2949	GAAGGACTGTCA GGTAGAACTTGA A[G/C]AAGAAGCT GAGGGTGAGGG TGCACC	G	C	Phe	Leu (8251)	NON- CONSER VATIVE	dehydrogenase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)



6081	cg34398112	2952	GGACTGTCAGGT AGAACTTGAAGA A[G/C]AAGCTGA GGGTGAGGGTG CACCGGA	G	C	Phe	Leu (8252)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6082	cg34398112	3012	TGCCACACAGGG GCATGGGAGG CAG[A/C]TGCAG CTCCTCTGCCAG TCCTGCAC	A	C	His	Gln (8253)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6083	cg34398112	3498	CTTGCTTCCCAG CAAACACAGCGCA G[C/G]TGCTCCA GGACCCCTCTGA ACAGCT	C	G	Gln	His (8254)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6084	cg34398112	3721	CTCAATGCCAAT CTCCGTGTTCCTCC C[A/T]CGACCAG CTTGGCGTCAGG GTGCTG	A	T	Val	Glu (8255)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6085	cg34398112	3806	GCCTGTATCCAC GTCACACGCTCC C[C/T]TCAAATC GCAGCTGCTTCC GAGGA	C	T	Gly	Arg (8256)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6086	cg34398112	3925	CTCTGGTTTGAA TAAAGATGGCGA G[A/T]GGCTGACT GAGTGGTCTTTC TTCIG	A	T	Leu	His (8257)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)
6087	cg34398112	3983	CAGCAATTTGGA TTATCCCATCT C[C/T]TCCACAGC ATCCACCATCCC TGGCA	C	T	Gly	Arg (8258)	NON- CONSER VATIVE	dehydrog enase	Human Gene SPTREMBL-ID:Q16712 XANTHINE DEHYDROGENASE/OXIDASE (EC 1.1.1.204) - HOMO SAPIENS (HUMAN), 1333 aa.	0	2 (2p23)

6088	cg44033747	1336	CTTGGCGGAATAT GGCTGCCATGTT T[G/C]GAATCTAC CATGGTTCCCAT GGGCT	G	C	Gly	Arg (8259)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:P23378 GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (EC 1.4.4.2) (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN) - HOMO SAPIENS (HUMAN), 1020 aa.	0 9 (9p22)
6089	cg43314766	1220	TAGAAATACCCCA TGGTGTGCAAAAT TT[C]AACAGCAT TGTCCTAAGTCGG CATCA	T	C	Lys	Glu (8260)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:P00352 ALDEHYDE DEHYDROGENASE, CYTOSOLIC (EC 1.2.1.3) (CLASS 1) (ALDHII) (ALDH-E1) - HOMO SAPIENS (HUMAN), 500 aa.	7.2E-273 9 (9q21)
6090	cg43996714	1790	ACAGGCCCGGG ATAAGATGGTCC AG[C/A]TGTGGC CTGTAGGGGGCG AAGGTGCT	C	A	Ala	Ser (8261)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.6E-266 11
6091	cg43996714	2474	CCCTTCACCAGC CCTACGCTTCGG C[G/A]GCCAGGG AAGCCCAACAAGA TAACGC	G	A	Arg	Cys (8262)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2979625 PYRUVATE DEHYDROGENASE COMPLEX PROTEIN X SUBUNIT PRECURSOR - HOMO SAPIENS (HUMAN), 501 aa.	1.6E-266 11
6092	cg43330439	729	GCCTAGCAGCTG TCCAAAGTACAC CT[C]GGTGGTC AGCAGGATGCA GGCCCGAG	T	C	Gln	Arg (8263)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2677802 PROLINE DEHYDROGENASE/PROLINE OXIDASE - HOMO SAPIENS (HUMAN), 516 aa.	2.1E-257
6093	cg43057018	1639	CTTTGAAGATG CCAGGAGCAATT C[G/A]GAATACTA TCTGATTGAATG TGAAC	G	A	Gly	Arg (8264)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSNEW-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.   pcds:SWISSPROT-ID:P08319 ALCOHOL DEHYDROGENASE CLASS II PI CHAIN (EC 1.1.1.1) - HOMO SAPIENS (HUMAN), 391 aa.	1.3E-209 4 (4q22)

6094	cg44986087	939	CGCCAGCTTGAA GGCATACTCGGC ATTATGGCGAG GGACTTGGCCTT GGTGAT	T	A	Asn	Ile (8265)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:P51553 ISOCITRATE DEHYDROGENASE (NAD), MITOCHONDRIAL SUBUNIT GAMMA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+ SPECIFIC ICDH) - HOMO SAPIENS (HUMAN), 393 aa.	9.6E-207	X
6095	cg44917703	1242	GGCTACAGCACCT ACAACCGACTTC ATTGCAAGTCTG TCATCGGTCACC TGCAG	T	C	Ile	Thr (8266)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.8E-205	13
6096	cg44917703	1247	CAGCACCAAC CGACTTCATCAA GTTGCTGTCATC GGTCACCTGCAG ACTAA	T	G	Ser	Ala (8267)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.8E-205	13
6097	cg44917703	1266	ATCAAGTCTGTC ATCGGTCACCTG CTAGCTAAAG GGAGCTAGAGC CCTTA	A	C	Gln	Pro (8268)	NON- CONSER VATIVE	dehydrog enase	Human Gene TREMBLNEW- ID:G2737886 NAD+-SPECIFIC ISOCITRATE DEHYDROGENASE BETA PRECURSOR - HOMO SAPIENS (HUMAN), 385 aa.	8.8E-205	13
6098	cg43923979	864	AAAATCTTTGA CTGAGCTTCCGG ATGATGAAATTC AAAGGAACCCCA TACAT	G	A	Pro	Leu (8269)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:P11177 PYRUVATE DEHYDROGENASE E1 COMPONENT, BETA SUBUNIT PRECURSOR (EC 1.2.4.1) (PDHE1-B) - HOMO SAPIENS (HUMAN), 359 aa.	4E-192 3 (3p13)	
6099	cg43960596	296	CCTGGGCTGTAG CGGGTTCGGGG GTGTTTCGAGCA GTCAGGGCATG CTCCAGG	G	T	His	Asn (8270)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSPROT-ID:Q92781 11 CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa. lpdts:SWISSPROT-ID:Q92781 11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.	4.4E-170	12

6100	cg43960596	857	TCCACCCACCTTG GCTGCCTGCTG GA[A/C]GCTCTG GGGATCAGTGAT ATCCAAC	A	C	Phe	Val (8271)	NON- CONSER VATIVE	dehydrog enase	Human Gene SWISSNEW-ID:Q92781 11 CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.lpcis:SWISSPROT-ID:Q92781 11-CIS RETINOL DEHYDROGENASE (EC 1.1.1.105) (11-CIS RDH) - HOMO SAPIENS (HUMAN), 318 aa.	4.4E-170	12
6101	cg43969759	919	AGAAATCTGCTCC GTGAAGGCTCCT G[C/T]GATGGCA GCAACACCTATG ATGGCT	C	T	Ala	Thr (8272)	NON- CONSER VATIVE	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.8E-109	11
6102	cg43969759	1199	CAACACGCTGAT TGGAAAGCTTGT T[G/C]TTGGTGAT TCGCAGAGCAG CCAAGA	G	C	Asn	Lys (8273)	NON- CONSER VATIVE	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.8E-109	11
6103	cg43969759	431	GTGTAAAGGAGT CATAGTCTGGAG T[G/T]TAGACCAG GGATCTTACAAA AGCCT	G	T	Tyr	End (8274)	NON- CONSER VATIVE	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.8E-109	11

6104	cg43248620	1748	AGGCCCCCTTCC TGCCGCCCCCGG GG[AT]TCGGGA CCCCCGTTTGAA GACCACT	A	T	Ile	Asn (8275)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SPTREMBL-ID:Q14550 ZINC-FINGER DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 1482 aa.	0	1
6105	cg40993080	3300	TGGCGTGCCG CTCTCTCTCCC CTT[G]CAGCGT TTTTCTGCCAT TTCTTG	T	G	Lys	Gln (8276)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0	6
6106	cg40993080	3302	GGCGTGCCCT CTCTCTCTCCC TC[AT]CGCGTT TTCCTGCCATT CTTGTA	A	T	Val	Glu (8277)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0	6
6107	cg40993080	3306	TGCCCCCTCTC CTCCCTTCACG C[G/AT]TTTCT GCCATTCTTGT ACTCA	G	T	Arg	Ser (8278)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0	6
6108	cg40993080	3307	GCCCCCTCTC TGCCCTTCACG G[AT]TTTCTC CCATTCTTGTA CTCAT	T	G	Lys	Asn (8279)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSPROT-ID:P21580 TUMOR NECROSIS FACTOR, ALPHA- INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20) - HOMO SAPIENS (HUMAN), 790 aa.	0	6
6109	cg42913756	366	GGCAGCCAGCT CCAATCCCAAAG GG[G/AT]CCCAGA TGCAGCCGATCT CCCTCCC	G	T	Ala	Ser (8280)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSPROT-ID:P48378 DNA BINDING PROTEIN RFX2 - HOMO SAPIENS (HUMAN), 723 aa.	0	19 (19p13.3 )

6110	cg43988954	670	CCGGTTTCGAAG ACCATCCAGGCG G[G/A]AGCCAC ACCAATGGAGAA GTGGTC	G	A	Ser	Phe (8281)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene SWISSNEW-ID:Q15633 TAR RNA BINDING PROTEIN (TRANS- ACTIVATION RESPONSIVE RNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 366 aa. pcis:SWISSPROT- ID:Q15633 TAR RNA BINDING PROTEIN (TRANS-ACTIVATION RESPONSIVE RNA BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 366 aa. pcis:SPTREMBL-ID:Q12878 TAR RNA BINDING PROTEIN 2 - HOMO SAPIENS (HUMAN), 366 aa.	6.4E-194	12
6111	cg43955901	755	CTGCAAAAGCATT GTGAGCTGCATC A[C/T]TTTGTGCA TTGCCACAGGAG ATACC	C	T	Ser	Asn (8282)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SWISSNEW- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SWISSPROT- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.	9.4E-97	2
6112	cg43955901	770	AGCTGCATCACT TTGTGCATTGCC A[C/A]AGGAGATA CCGGAGCCATG ACAGAC	C	A	Cys	Phe (8283)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SWISSNEW- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A (XLRBPA) - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SWISSPROT- ID:Q91836 DOUBLE STRANDED RNA BINDING PROTEIN A - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa. pcis:SPTREMBL-ID:Q91836 RNA BINDING PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 298 aa.	9.4E-97	2

6113	cg43130017	338	TGAAGCGATGCGT AGATACCTGAAG GT/CJTTCAC ACTGCTTGCAAT CATA	C	Thr	Ala (8284)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	2.9E-95	
6114	cg43918693	4135	AGCTTCTTGTCG TTCATCAGCTGC A/GTTCAGGTAAT CTGGGGTGGGC TTCGGC	T	Leu	Met (8285)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:O01367 KH RNA BINDING PROTEIN (WHO) - DROSOPHILA MELANOGASTER (FRUIT FLY), 405 aa.	3.6E-74	6
6115	cg43327854	1115	CAAGTGGAGGAT GATGGGGATGG CG/A/GTTACATG TCTGAGCCTGAG GCTGTG	G	Asp	Gly (8286)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.5E-57	1
6116	cg43327854	1434	GCATGAACCGCT CGGAACAGGTCT T/C/AJACGTGCTC TGTGTGCCAGGA GACAT	A	Phe	Leu (8287)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.5E-57	1
6117	cg43327854	1435	CATGAACCGCTC GGAACAGGTCTT C/A/CJCGTGCTCT GTGTGCCAGGA GACAT	C	Thr	Pro (8288)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	5.5E-57	1
6118	cg43946971	1232	TCACCGAGTACT CGAGCTTGATA A/G/CJGACACG TGGTGACACACAG ACTGCA	C	Lys	Asn (8289)	NON- CONSER VATIVE	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	4.9E-52	6 (6p21.3)
6119	cg43269465	324	AGGAGCTGGTC GAACACAGCTGC GGT/C/AJCTCCTC ATTACACAGTCG GTCCCGG	C	Asp	Tyr (8290)	NON- CONSER VATIVE	dynein	Human Gene Homologous to SPTREMBL-ID:Q27810 DYNEN HEAVY CHAIN ISOTYPE 6 (EC 3.6.1.3) (ADENOSINETRIPHOSPHATASE) (ADENYLPHOSPHATASE) (ATP MONOPHOSPHATASE) (TRIPHOSPHATASE) (ATPASE) - TRIPNEUSTES GRATILLA (HAWAIIAN SEA URCHIN), 1125 aa (fragment).	9.7E-111	

6120	cg43950268	2402	TAGAACTCCTCA TGTTGCCACTCA C[G/C]GACATCCT TGGGGTCCATCA TCCAG	G	C	Arg	Gly (8291)	NON- CONSER VATIVE	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16
6121	cg43982507	2645	GCCAATAAATTC ACTGGATCAGAG C[T/A]AGCCACTC TAGTCAACAACG TGAAT	T	A	Leu	Gln (8292)	NON- CONSER VATIVE	eph	Human Gene SWISSPROT-ID:P98155 VERY LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR (VLDL RECEPTOR) - HOMO SAPIENS (HUMAN), 873 aa.	0	9 (9p24)
6122	cg43945212	1793	GTTGCGCGCGG AGCCCTATCCCA CG[T/C]CGCGCT TCGGCAGCCAAT GCATGCA	T	C	Ser	Pro (8293)	NON- CONSER VATIVE	eph	Human Gene SWISSPROT-ID:P43135 APOLIPOPROTEIN A1 REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa.	5.8E-232	7
6123	cg41554010	1092	GGTGCAGCAGAT GGAACAGCTCAG G[C/A]AGAAACTG GGCCCCCATGC GGGGGA	C	A	Gln	Lys (8294)	NON- CONSER VATIVE	eph	Human Gene SWISSNEW-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.   pcds:SWISSPROT-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.	1.8E-203	11 (11q23)
6124	cg41554010	1093	GTGCAGCAGATG GAACAGCTCAGG C[A/C]GAAACTG GGCCCCCATGC GGGGGAC	A	C	Gln	Pro (8295)	NON- CONSER VATIVE	eph	Human Gene SWISSNEW-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.   pcds:SWISSPROT-ID:P06727 APOLIPOPROTEIN A-IV PRECURSOR (APO-AIV) - HOMO SAPIENS (HUMAN), 396 aa.	1.8E-203	11 (11q23)
6125	cg43985169	958	ACTGCTAAAATT AGTTTACGAGAG G[C/A]ATTGTGTG GCTGCTCAATTA ATGTA	C	A	Ala	Glu (8296)	NON- CONSER VATIVE	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	



6126	cg43949555	217	CCACTCGTACAG CATATGGACCAA ATTATGGAATGAA CAAAATGGTTAT CAACC	T	A	Asn	Lys (8297)	NON- CONSER VATIVE	eph	Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCUS SP. (STRAIN SY), 545 aa. Jcds:SPTRMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa.	6.7E-80	21
6127	cg43949555	858	ACAGTGTGATA AAGAAATGCTGAA ATTATGATGATGA ATTTAGTAAGG GAGAA	T	A	Ile	Lys (8298)	NON- CONSER VATIVE	eph	Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCUS SP. (STRAIN SY), 545 aa. Jcds:SPTRMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa.	6.7E-80	21
6128	cg43984905	1866	GGGCCAGAGAT GGACGTGTACCA GG[A/G]CCGCTT CCAGGACAACG GGCCCTGT	A	G	Asp	Gly (8299)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0	3
6129	cg43984905	2088	ACAGTGGAGATC CATGGCGTGAG CC[G/A]GGACGT GGCCAGCCGCC AGACTGCT	G	A	Arg	Gln (8300)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0	3

6130	cg43984905	2262	TTCATTGGCCAG AGTACCATCCCC TTTGGGAACAGCC TCAAGCAAGGAT ACCGC	T	G	Leu	Trp (8301)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0	3
6131	cg43984905	884	TGAGCGCTACGA GCCCAGCGAGA CTG/AJCCAAGG CGCAGCGGCAG ATGACCAA	G	A	Ala	Thr (8302)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P51178 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC- III) - HOMO SAPIENS (HUMAN), 756 aa.	0	3
6132	cg44011461	2013	GTAGAGGGAGTT TATATCTCTTCC [A/G]TATTGTAGC GCTCCAGGAGCT CGGG	A	G	Met	Thr (8303)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0 (16q24.1 )	16
6133	cg44011461	2420	GGTAGTGCTGGA TGAGGGCATAGA TIG/CJCTGCTGAA GGTGAGGTTGTC AGTCA	G	C	Ser	Arg (8304)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0 (16q24.1 )	16

6134	cg44011461	2423	AGTCTGGATGA GGGCATAGATGC TTCGCTGAAGGT GAGGTTGTCAGT CAAGT	G	C	Ser	Arg (8305)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0	16 (16q24.1)
6135	cg44011461	963	AACCGTCGCTT GAACCTGTTGTT GTCATCACTCG GCTCCACAGATC TCCAC	C	T	Gly	Asp (8306)	NON- CONSER VATIVE	esterase	Human Gene SWISSPROT-ID:P16885 1- PHOSPHATIDYLINOSITOL-4,5- BISPHOSPHATE PHOSPHODIESTERASE GAMMA 2 (EC 3.1.4.11) (PLC-GAMMA-2) (PHOSPHOLIPASE C-GAMMA-2) (PLC- IV) - HOMO SAPIENS (HUMAN), 1252 aa.	0	16 (16q24.1)
6136	cg42031001	362	CCCGCTGCCACT GATAGGAACCCT ATGTTAGGCTCCA GCAGCAGACAG AGCAGC	G	T	Arg	Ile (8307)	NON- CONSER VATIVE	tgf	Human Gene Homologous to SWISSPROT-ID:P12034 FIBROBLAST GROWTH FACTOR-5 PRECURSOR (FGF-5) (HBGF-5) - HOMO SAPIENS (HUMAN), 268 aa.	6.1E-141	4
6137	cg43320667	824	TTGCTGGTGGAG CTGCCCGCCTG GGGTCCTGCTC AGGACCATTCCTC TGGGCGA	G	C	Pro	Ala (8308)	NON- CONSER VATIVE	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0 3 (3p25)	
6138	cg43320667	825	TGCTGGTGGAG CTGCCCGCCTG GGGTCCTGCTC AGGACCATTCCTC TGGGCGAA	C	G	Gln	His (8309)	NON- CONSER VATIVE	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0 3 (3p25)	
6139	cg43320667	853	CTCAGGACCAT CTCTGGCGGAAC GATGTTGCTTCG CTGGGCTGGAC CATGAC	A	G	Ile	Thr (8310)	NON- CONSER VATIVE	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0 3 (3p25)	

6140	cg43286057	1828	GGGGGGCATGC TGCTAATCGACC TGTT/GTGATCCT GATCTACTGGCA GGGTGT	T	G	Cys	Gly (8311)	NON- CONSER VATIVE	gaba	Human Gene Homologous to SPTRMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa.	1.9E-121	9
6141	cg43286057	1841	CTAATCGACCTG TGATCCTCTGATC TTAGTCTGGCAG GGTGTGGAACC CCTGCCGA	A	G	Tyr	Cys (8312)	NON- CONSER VATIVE	gaba	Human Gene Homologous to SPTRMBL-ID:O08621 GABA-BR1B RECEPTOR - RATTUS NORVEGICUS (RAT), 844 aa.	1.9E-121	9
6142	cg43969076	1020	ACACATCTGCAT CACTTCCTCTGC ATG/TAGGGGTA GTGGCTGGTAC GGAAAGC	G	T	Ser	Tyr (8313)	NON- CONSER VATIVE	glucuronidase	Human Gene SWISSPROT-ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	0	7 (7q21.11)
6143	cg43969076	237	TGGTATCAGTCT TGCTCAAGTAAA C[G/A]GGCTGTTT TCCAAACATTGT GACTT	G	A	Pro	Leu (8314)	NON- CONSER VATIVE	glucuronidase	Human Gene SWISSPROT-ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	0	7 (7q21.11)
6144	cg43969014	688	ATCACCATCCTC CCACGAGTACAG GT/GJAGGCGGG GTGTTCTGTGCAT CAGGTA	T	G	Tyr	Ser (8315)	NON- CONSER VATIVE	glucuronidase	Human Gene Similar to SWISSPROT- ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	7.4E-80	5
6145	cg43285373	12871	TCTGCCCTGGATG AATGGAGAGGAC C[G/C]CAACATCC TGGTTTTCGAGG ACCTT	G	C	Arg	Pro (8316)	NON- CONSER VATIVE	glycoprotein	Human Gene SWISSPROT-ID:P08164 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 2 (MEGALIN) (GLYCOPROTEIN 330) - HOMO SAPIENS (HUMAN), 1751 aa (fragment).	0	2

6146	cg43286488	1356	CTCCAGGTAAGT A ATGAGTGACCCAC A[A]GJTGCCCG AGAGATCAGGGT TCCACT	G	Leu	Pro (8317)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20/MME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.lcds:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0	12
6147	cg43943531	1467	CAGGATTCCACC A TACCCTATTAA A[A]TTGAAGTGG CAAGTGGGATGA TACTG	T	Asn	Ile (8318)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3 )
6148	cg43943531	504	TCCTTCACGCC A ATCGTCACGTAC C[A]TCCCTTACCA AAGAGCTCAAGG ATGCA	T	His	Leu (8319)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3 )
6149	cg43943531	881	TACTGCCTGGGC T ACTATACTTTCTA [T]G/CAGATCTC C[TT]GTGGGTT CCAG	G	Met	Arg (8320)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P46978 OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG (B5) (INTEGRAL MEMBRANE PROTEIN 1) - MUS MUSCULUS (MOUSE), 705 aa.	0	11 (11q23.3 )
6150	cg43065490	1172	ACTATAATGAGG G AGGGACTTCAGA A[G/C]GGAGAAG GCCAGAGAGGC AGAATCT	C	Lys	Ash (8321)	NON- CONSER VATIVE 1096	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)

6151	cg43065549	1598	GGGTTATGATGG ATGGCAGATTCT C[G/C]ACCCAAG TGCTCCTAATGG AGGTGG	G	C	Asp	His (8322)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
6152	cg43065549	1738	CCATAAATGCCT CATGTGTGGTCT G[G/A]AAGTGCT GTGAGGATGGG ACACTGG	G	A	Trp	End (8323)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
6153	cg44034764	1079	GTGCTCGGGCC AAAGCCTCAGG AA[A/C]AAACAAA GCCGCCAGCGT GGGCTCG	A	C	Phe	Val (8324)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0	7 (Xp21.2)
6154	cg44034764	266	CTGAGGGGCC GTGGACTCGGA GGT[G/T]TGGAG GGCTGTGAGTGT CGTGAGAG	G	T	His	Asn (8325)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0	7 (Xp21.2)
6155	cg43997653	1941	CAAGCGCCATGT ATTCCACTTCGG C[A/G]CCGTGAG CCCCCAGAGCTC CCAGGC	A	G	Thr	Ala (8326)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P50895 LUTHERAN BLOOD GROUP GLYCOPROTEIN PRECURSOR (B-CAM CELL SURFACE GLYCOPROTEIN) (AUBERGER B ANTIGEN) (F8/G253 ANTIGEN) - HOMO SAPIENS (HUMAN), 628 aa.	0	
6156	cg44004239	391	GAAGACCCAAGT TACCCATCCTGG G[G/C]TGAGTGC CCACCTCAGAAG TCAAAAT	G	C	His	Gln (8327)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:Q12889 OVIDUCT-SPECIFIC GLYCOPROTEIN PRECURSOR (OVIDUCTAL GLYCOPROTEIN) (OVIDUCTIN) (ESTROGEN-DEPENDENT OVIDUCT PROTEIN) - HOMO SAPIENS (HUMAN), 678 aa.	0	

6157	cg43010733	1380	GAGCCCTTCGGC TTCCACATGCGC A/C]GTGCTCT ACGGCTTCTCT GGAAG	C	Lys	Thr (8328)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:Q09327 BETA-1,4-MANNOSYL-GLYCOPROTEIN BETA-1,4-N-ACETYLGLUCOSAMINYL- TRANSFERASE (EC 2.4.1.144) (N- GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E III) (N- ACETYLGLUCOSAMINYLTRANSFERAS E III) (GNT-III) (GLCNAC-T III) - HOMO SAPIENS (HUMAN), 531 aa.	5E-304	
6158	cg43094362	191	CCCACTGCTCTA CTTCATGGTCAC C/A/C]CTCCTGTC CAGGAAGATCAG TGGCC	C	Ser	Arg (8329)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6159	cg43094362	271	ATGCCTGCGGTT ACGGGAAGCAG AC]G/C]TGGACC ACTGGCTCACGA CAGGAGG	C	Thr	Arg (8330)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6160	cg43094362	287	GAGCAGACGT GGACCACTGGCT CA/C]TGACACGA GGCTGCCTCCTG GAATGG	T	Val	Met (8331)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6161	cg43987514	963	CTAGCGCAGAGA GTTCGTGGCCG CT]G/C]CTCCGC TGGCCCCCAGT GCCCCAG	C	Ser	Arg (8332)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-215	

6162	cg43301245	866	GGCATAGGGA CCTGCTGGCCG AGG[A/G]TTCTAT GGACTGTGGCTC CGCGGAG	A	G	Ile	Thr (8333)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	3E-210	1
6163	cg43074195	2209	GACCCCAAGCA GCACCACCACAA CT[C/A]AAATTAC CAAGACTGTAAA AGGTGG	C	A	Gln	Lys (8334)	NON- CONSER VATIVE	glycoprot ein	Human Gene SPTREMBL-ID:Q14245 ERYTHROID MEMBRANE PROTEIN 4.1 - HOMO SAPIENS (HUMAN), 641 aa.	1.4E-197	1
6164	cg43988092	2155	AGCGGGGAAAT GTGGAAAGAAA TTT[C/A]ACAAA TAATGTAGCACC AGAAGA	T	C	Lys	Glu (8335)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSPROT-ID:Q01885 TRAM PROTEIN (TRANSLCATING CHAIN-ASSOCIATING MEMBRANE PROTEIN) - CANIS FAMILIARIS (DOG), 373 aa.	4E-192	8
6165	cg42671047	1163	ATCATCCTCTAC TGGGGACACCA CTTT/CJTTCATG AATTGGATTGCC TTGGTA	T	C	Phe	Ser (8336)	NON- CONSER VATIVE	glycoprot ein	Human Gene SWISSNEW-ID:P29017 T- CELL SURFACE GLYCOPROTEIN CD1C PRECURSOR (CD1C ANTIGEN) - HOMO SAPIENS (HUMAN), 333 aa.lpcis:SWISSPROT-ID:P29017 T-CELL SURFACE GLYCOPROTEIN CD1C PRECURSOR (CD1C ANTIGEN) - HOMO SAPIENS (HUMAN), 333 aa.	2.8E-184	1 (1q21)
6166	cg43991224	193	AGGCAGGTGATC AGGATGCCCTTC T[C/G]TCATCTGT CTACCTACAGCC TGGTT	C	G	Ser	Cys (8337)	NON- CONSER VATIVE	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa (fragment).	1.5E-139	



6167	cg43981224	297	GGATGAAAGAGAC GCAGCTGTACAC A[C/A]CTGCTTCC TTAAAATGCTCT CTGCA	A	Pro	Thr (8338)	NON- CONSER VATIVE	glycoprot ein	Human Gene Homologous to SWISSPROT-ID:P41217 OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 274 aa (fragment).	1.5E-139	
6168	cg43076975	1728	TAACAATGCATT A TCAGCTCGTCAG C[A/T]TTGGGAAG CTGTCCATTGAA AAGGC	T	Ile	Phe (8339)	NON- CONSER VATIVE	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa.lpcis:SWISSPROT-ID:P15144 AMINOPEPTIDASE N (EC 3.4.11.2) (MICROSOMAL AMINOPEPTIDASE) (GP150) (MYELOID PLASMA MEMBRANE GLYCOPROTEIN CD13) - HOMO SAPIENS (HUMAN), 966 aa	3.4E-120	5
6169	cg43924574	470	TAGGGAACCTGC G TGATCCTGGAGC C[G/A]CGTGATCT TGGCTCCTTTCA GGAAC	A	Arg	Trp (8340)	NON- CONSER VATIVE	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP- 39) (39 KD SYNOVIAL PROTEIN) (YKL- 40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcis:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa	1E-108	1

6170	cg44929742	869	CAGGGTCAGCC GGTACATCTGGG CC[T/G]GGGCAT TGGGCTCCAGC CGAAGCAG	T	G	Gln	Pro (8341)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSNEW- ID:P17426 ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2AP2 ADAPTIN ALPHA A SUBUNIT) MUS MUSCULUS (MOUSE), 977 aa.lpcis:SWISSPROT-ID:P17426 ALPHA ADAPTIN (A) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2AP2 ADAPTIN ALPHA A SUBUNIT) - MUS MUSCULUS (MOUSE), 977 aa.	5.4E-94	19
6171	cg44021513	1356	TTCTGGCCCTGC TGGTACGCGGG GG[C/G]GTCTGC GCTCCTGCTGAA CTTCACT	C	G	Ala	Pro (8342)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P20963 T-CELL SURFACE GLYCOPROTEIN CD3 ZETA CHAIN PRECURSOR (T-CELL RECEPTOR T3 ZETA CHAIN) - HOMO SAPIENS (HUMAN), 163 aa.	8E-84	1 (1q22)
6172	cg43983795	1531	TACGGCCCTCG GGCCCGTAGAAT TTC/TGCGGCCTT TGGTCACATCGA ACACC	C	T	Glu	Lys (8343)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.2E-74	X
6173	cg41568631	1756	GCACCCAGAAG GCTCAGACGCA GAG[C/G]GGAAG GCAGTAGAGACA GCAGCAGC	C	G	Arg	Gly (8344)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.9E-70	14 (14q11.2 )

6174	cg41588631	1757	CACCCAGAAAGG CTCAGACGCAGA GC/GC/GAAGGC AGTAGAGACAGC AGCAGCC	G	C	Arg	Pro (8345)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	9.9E-70	14 (14q11.2)
6175	cg42659724	773	ACTTTACTAAAA GCTTATTCTGT C/TATATATCATA TTTGAGAAATC ATCCA	A	T	Gln	Leu (8346)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SWISSNEW- ID:P26717 NKG2-C TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 231 aa. Jcds:SWISSPROT-ID:P26717 NKG2- C TYPE II INTEGRAL MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 231 aa.	1.8E-69	
6176	cg43918233	1027	TCTTCAGAGCCT ACTGAGGATGTG G/G/GGCCCAA GAGGCTGAAGAT GATGAT	A	G	Glu	Gly (8347)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
6177	cg43918233	534	CAGCCCCAACAG GTCGGGTGCGG AG/GC/GCAAAGA CCCCAAAAGACA GCCCTAG	G	C	Ala	Pro (8348)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to SPTREMBL- ID:Q63575 TRANS GOLGI NETWORK (TGN) SPECIFIC INTEGRAL MEMBRANE PROTEIN TGN38 PRECURSOR - RATTUS NORVEGICUS (RAT), 380 aa.	7.6E-67	2
6178	cg43078615	248	CTGTCCGGCGCT GCCTGCCCTCT G/GC/GGCCCTAA CACTGGAAGCAG CTCTCA	G	C	Trp	Cys (8349)	NON- CONSER VATIVE	glycoprot ein	Human Gene Similar to TREMBLNEW- ID:G2809819 ERYTHROCYTE MEMBRANE GLYCOPROTEIN RH50 - HOMO SAPIENS (HUMAN), 409 aa.	7.1E-60 (1p36.2)	1
6179	cg44913214	2075	AAGCTGTTGAAT TTGGAGGGCTTT C/C/TATCAGGGA GCCAGTCACGAT TGTC	C	T	Pro	Leu (8350)	NON- CONSER VATIVE	helicase	Human Gene TREMBLNEW- ID:G2801555 PUTATIVE ATP- DEPENDENT MITOCHONDRIAL RNA HELICASE - HOMO SAPIENS (HUMAN), 786 aa.	0	10

6180	cg43956596	3949	CCGGAAGAGC AAGGGAGCCC ATG[A/G]CCCCTC GCCGCACGCCA GCCCGCTT	A	G	Thr	Ala (8351)	NON- CONSER VATIVE	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.lpcis:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0	16
6181	cg43916626	2284	CTCTCTGTGAAT CTGGCTGGCAA GTATJGTCTGT TGGTGATATAAT CAGGGC	A	T	Leu	Gln (8352)	NON- CONSER VATIVE	helicase	Human Gene Homologous to SWISSPROT-ID:P45818 ATP- DEPENDENT RNA HELICASE ROK1 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 564 aa.	4.8E-103	17
6182	cg43971940	930	GATTGTGTAGCC ACCTCCTCCAAG CTTATTCAGTAAT GGTAAGTTAAAA GTTT	T	A	Lys	Met (8353)	NON- CONSER VATIVE	histone	Human Gene SWISSPROT-ID:Q92769 HISTONE DEACETYLASE 2 (HD2) - HOMO SAPIENS (HUMAN), 488 aa.	2.5E-176	6
6183	cg42341753	1486	GGCGAGAAGCC ATCAGGTGGAGC CC[C/T]GGCTGC GGATGGCGAGC AGGACGAG	C	T	Pro	Leu (8354)	NON- CONSER VATIVE	homeobo x	Human Gene SWISSPROT-ID:Q14774 HOMEBOX PROTEIN HLX1 (HOMEBOX PROTEIN HB24) - HOMO SAPIENS (HUMAN), 488 aa.	5.2E-263	1
6184	cg43332152	982	CCTGGGCGCCA AGCGGCGGGA CCG[C/G]GCACC ACCATCAAAGCC AAGCAGCT	C	G	Arg	Gly (8355)	NON- CONSER VATIVE	homeobo x	Human Gene SWISSPROT-ID:P36199 HOMEBOX PROTEIN LIM-1 (HOMEBOX PROTEIN LMX-2) - MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND MESOCRICETUS, 406 aa.	3.4E-227	17
6185	cg41637704	1202	GGAGCTGCTGG GGCCGCCAGCG CCG[C/G]GAGAC AAGGGCAGCGG ACCGCCTGC	C	G	Arg	Gly (8356)	NON- CONSER VATIVE	homeobo x	Human Gene SWISSPROT-ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.2E-224	7

6186	cg43143467	630	CTTGCCAACGTA CCAGCTGTCGGA G[A/C]CCTCTTAC CAGCCACATCT ATTCC	A	C	Thr	Pro (8357)	NON- CONSER VATIVE	homeo x	Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment).	2.1E-179	2 (2q35)
6187	cg43143467	631	TTGCCAACGTAC CAGCTGTCGGA GA[C/A]CTCTTAC CAGCCACATCT ATTCCA	C	A	Thr	Asn (8358)	NON- CONSER VATIVE	homeo x	Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment).	2.1E-179	2 (2q35)
6188	cg42721526	769	GGTCTCTTGCC CATCTCTCCGGC C[G/A]CCCCGCC AGGAAACGACGA GAAGGC	G	A	Ala	Thr (8359)	NON- CONSER VATIVE	homeo x	Human Gene Homologous to TREMBLNEW-ID:G282175 HXA1_HUMAN HOMEOBOX PROTEIN HOX-A1 - HOMO SAPIENS (HUMAN), 335 aa.	6.9E-144	7
6189	cg42359655	4927	CCTATTTCAAG AATGGAGATTAC A[G/A]TGAGGTG ATGAAGACGCG GATCCGT	G	A	Ser	Asn (8360)	NON- CONSER VATIVE	hydrolas e	Human Gene SWISSPROT-ID:P09848 LACTASE-PHLORIZIN HYDROLASE PRECURSOR (EC 3.2.1.108) (EC 3.2.1.62) (LACTASE- GLYCOSYLKERAMIDASE) - HOMO SAPIENS (HUMAN), 1927 aa.	0	2 (2q21)
6190	cg43296921	553	AGCCGCCTGGC TCATTCCCTCTC CTT[G/T]CAGGTT AACAGAGAGGTT GATGTC	T	G	Lys	Thr (8361)	NON- CONSER VATIVE	hydrolas e	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.3E-238	15 (15q23)
6191	cg43927025	192	GTTGGTGGTCTG TTTGGTTCTCTG G[A/C]CCCTGCAT TCTGAGGGGTCT GGAGG	A	C	Thr	Pro (8362)	NON- CONSER VATIVE	hydrolas e	Human Gene SWISSPROT-ID:P38571 LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTERYL ESTERASE) - HOMO SAPIENS (HUMAN), 399 aa.	5.1E-224	10 (10q24)

6192	cg43927025	213	CTGGACCCCTGCA TTCTGAGGGGTC T[G/A]GAGGGAA ACTGACAGCTGT GGATCC	G	A	Gly	Arg (8363)	NON- CONSER VATIVE	hydrolas e	Human Gene SWISSPROT-ID:P38571 LYSOSOMAL ACID LIPASE/CHOLESTERYL ESTER HYDROLASE PRECURSOR (EC 3.1.1.13) (LAL) (ACID CHOLESTERYL ESTER HYDROLASE) (STEROL ESTERASE) (LIPASE A) (CHOLESTERYL ESTERASE) - HOMO SAPIENS (HUMAN), 399 aa.	5.1E-224	10 (10q24)
6193	cg43285385	621	ACATTGAAAAAC TTCITTAACITTT IC/TAATTCATTGT AAAATTCTTCAC GGAG	C	T	Glu	Lys (8364)	NON- CONSER VATIVE	hydrolas e	Human Gene TREMBLNEW- ID:G2951931 HUMAN GAMMA- GLUTAMYL HYDROLASE (EC 3.4.22.12) - HOMO SAPIENS (HUMAN), 318 aa.	4.8E-173	8
6194	cg43925670	1254	GCCTCTGAAGGA TATGGAAGCTGA CT/GCTGTTCTCCT GGGTAGCTTCA TGCTC	T	G	Ser	Arg (8365)	NON- CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa. [pcls:SPTRMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)]	0	1

6195	cg43925670	438	CCACTTTTCGGT GCCAATTCAAAG C[AT]GGTGAGTT TCAGTTTATCTC CTTCC	A	T	Cys	Ser (8366)	NON- CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.  cds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
6196	cg43925670	479	ATCTCCTTCCTC ACAGTTGATTGT G[G/T]TCAGTCGT CCATGCACCACC ACTTC	G	T	Thr	Asn (8367)	NON- CONSER VATIVE	interferon	Human Gene SWISSPROT-ID:Q16666 GAMMA-INTERFERON-INDUCIBLE PROTEIN IFI-16 (INTERFERON- INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR) - HOMO SAPIENS (HUMAN), 729 aa.  cds:SPTREMBL-ID:Q16666 IFI16=INTERFERON-INDUCIBLE MYELOID DIFFERENTIATION TRANSCRIPTIONAL ACTIVATOR - HOMO SAPIENS (HUMAN), 729 aa (fragment)	0	1
6197	cg43082514	349	AAAAGATGCACC ACTCTTTAGAAA C[T/C]GGGCAAT CCATACAGGAAA GCATCA	T	C	Trp	Arg (8368)	NON- CONSER VATIVE	Interferon	Human Gene SWISSPROT-ID:P14316 INTERFERON REGULATORY FACTOR 2 (IRF-2) - HOMO SAPIENS (HUMAN), 349 aa. (fragment)	5.5E-188 (4q35.1)	4
6198	cg43926568	578	TGAAATTCCTGA AACCGACCATAG T[G/A]GAAATGTA TGTCCTGCATTG TTTCT	G	A	His	Tyr (8369)	NON- CONSER VATIVE	interferon	Human Gene Homologous to SPTREMBL-ID:Q13325 RETINOIC ACID- AND INTERFERON-INDUCIBLE 58K PROTEIN RI58 - HOMO SAPIENS (HUMAN), 482 aa.	4.8E-141 (10q23)	10

6199	cg43972852	849	TTACACATCTCAC TAACAAAGTTTGA G[G/T]ACAAGACT GTGGCATATACA GAGCA	G	T	Asp	Tyr (8370)	NON- CONSER VATIVE	isomerase	Human Gene SWISSPROT-ID:P30101 PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (EC 5.3.4.1) (ERP60) (58 KD MICROSOMAL PROTEIN) (P58) (GRP58) (ERP57) - HOMO SAPIENS (HUMAN), 505 aa.	3.8E-274	
6200	cg44929725	2694	ATTGAGAAAGAG AGATTCTATGAA A[A/G]CCGGTGC AGCCAGTGACA CCATCA	A	G	Asn	Ser (8371)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6201	cg42859664	747	GGTCCACTTCAC GGGACTTGCT G[A/G]GCCCCC TGAGGCTGCATA GACCCC	A	G	Leu	Pro (8372)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P07332 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES) - HOMO SAPIENS (HUMAN), 822 aa.	0	15 (15q26.1)
6202	cg42859664	748	GTCCACTTCACG GGGACTTGCTG A[G/A]GCCCCCT GAGGCTGCATAG ACCCCA	G	A	Leu	Phe (8373)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P07332 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FES/FPS (EC 2.7.1.112) (C-FES) - HOMO SAPIENS (HUMAN), 822 aa.	0	15 (15q26.1)
6203	cg43917392	3326	ATTGTCTCACT GGGTACTAACAG A[C/T]TAAAGGAT AGAGCGTAGTGA CTAAT	C	T	Ser	Asn (8374)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P34925 TYROSINE-PROTEIN KINASE RYK PRECURSOR (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 604 aa.	4.0e-315	
6204	cg43957153	329	TGAGGAGGGGG AGCTGAGAGATC AC[C/T]GCATGGA GATCACAAATAAG GAACCTC	C	T	Arg	Cys (8375)	NON- CONSER VATIVE	kinase	Human Gene SPTREMBL-ID:Q61399 CYCLIN-DEPENDENT PROTEIN KINASE - MUS MUSCULUS (MOUSE), 783 aa.	1.2E-304	4 (1p36)
6205	cg43952792	1126	CCGCGAGAGTG AAACCACCAAAG GT[G/T]CCTATTC ACTTCTATCCG TGATTG	G	T	Ala	Ser (8376)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P08241 PROTO-ONCOGENE TYROSINE- PROTEIN KINASE FYN (EC 2.7.1.112) (P58-FYN) (SYN) (SLK) - HOMO SAPIENS (HUMAN), 536 aa.	4.3E-300	6 (6q21)



6206	cg43965549	1355	GCCCAGAGAGG ATCAGCCACGCT GT[C/A]GAGTCT GGACTCTGCCCT CTTGA	C	A	Gln	Lys (8377)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE - SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)
6207	cg43965549	1356	CCCAGAGAGGAT CAGCCACGCTGT C[A/C]GAGTCTG GACTCTGCCCTC TTGGAG	A	C	Gln	Pro (8378)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P41279 COT PROTO-ONCOGENE - SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (C-COT) (CANCER OSAKA THYROID ONCOGENE) - HOMO SAPIENS (HUMAN), 467 aa.	2.3E-253	10 (10p11.2)
6208	cg43967889	1158	GAATTACGGGAC CCAAATGTCAAA CTT[A/C]ACCAATG GGCGAGACACA CCTGCA	T	A	Leu	Gln (8379)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P49841 GLYCOGEN SYNTHASE KINASE-3 BETA (EC 2.7.1.37) (GSK-3 BETA) - HOMO SAPIENS (HUMAN), 420 aa.	1.9E-226	3
6209	cg43967889	663	ATCTGCCATCGG GATATTAAACCG C[A/G]GAACCTCT TGTTGGATCCTG ATACT	A	G	Gln	Arg (8380)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P49841 GLYCOGEN SYNTHASE KINASE-3 BETA (EC 2.7.1.37) (GSK-3 BETA) - HOMO SAPIENS (HUMAN), 420 aa.	1.9E-226	3
6210	cg43963232	2187	AGTACTGTCCCC GCGAGCATCGA GG[G/C]ATTCTA CTGCACCATCTCT CTTCCA	G	C	Ile	Met (8381)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P31323 CAMP-DEPENDENT PROTEIN KINASE TYPE II-BETA REGULATORY CHAIN - HOMO SAPIENS (HUMAN), 417 aa.	4.6E-223	7 (7q22)
6211	cg43947829	1933	ACAGGTAATGGA TTCTGACAAGGA A[T/A]TTGCTGAG TCACGAGAACAC GTTT	T	A	Ile	Phe (8382)	NON- CONSER VATIVE	kinase	Human Gene TREMBLNEW- ID:G2979628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa.	1.5E-217	

6212	cg38438124	850	ATGGGATCACCC TTCAACCCAGT T[G/C]GTGGCA TGTACCGGCTTA ATGTTG	G	C	Leu	Phe (8383)	NON- CONSER VATIVE	Kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII-ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P-5- KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.8E-216	10
6213	cg43917871	1966	TCAGCCAAACCC CAGTCTATTAGT C[G/A]TAGCTTTC TGTGCTCATGAT CAATC	G	A	Arg	End (8384)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
6214	cg43933472	2482	TTTCATTGCTC GATGGTTGGTGC T[C/T]GAATAATG TCATTGATTCCA ATGAT	C	T	Arg	Gln (8385)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P28482 EXTRACELLULAR SIGNAL- REGULATED KINASE 2 (EC 2.7.1.-) (ERK2) (MITOGEN- ACTIVATED PROTEIN KINASE 2) (MAP KINASE 2) (MAPK 2) (P42-MAPK) (ERT1) - HOMO SAPIENS (HUMAN), 360 aa.	5.4E-197	22
6215	cg38309035	487	TGCAGGGACTC GAAGTAGGGATG GG[C/A]CAGCGC CTGCGCTGCCGT CACCCGC	C	A	Ala	Ser (8386)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P53778 EXTRACELLULAR SIGNAL- REGULATED KINASE 6 (EC 2.7.1.-) (ERK6) (ERK5) (STRESS-ACTIVATED PROTEIN KINASE-3) (MITOGEN- ACTIVATED PROTEIN KINASE P38 GAMMA) (MAP KINASE P38 GAMMA) - HOMO SAPIENS (HUMAN), 367 aa. lpcis: SPTREMBL-ID:Q99588 STRESS-ACTIVATED PROTEIN KINASE-3 - HOMO SAPIENS (HUMAN), 367 aa.	2.9E-195	

6216	cg43928089	347	AGTAATCTTTGGT GCTGGATCATAC [T/C]CCAACATTT TCTGAATGAGGT CAAA	C	Glu	Gly (8387)	NON- CONSER VATIVE	kinase	Human Gene SWISSNEW-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa.   pcds:SWISSPROT-ID:P49759 PROTEIN KINASE CLK1 (EC 2.7.1.-) (CLK) - HOMO SAPIENS (HUMAN), 484 aa.	1.6E-192	
6217	cg43007055	693	CGGAGCGGGG CGGCGTCGCCC TCC[G/T]CGGCC GAGAAAGGTGA GCCGGCCGC	T	Ala	Ser (8388)	NON- CONSER VATIVE	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
6218	cg43007055	798	AGCGAGGCTG CCGAGCCCGGC TCG[C/G]CCACG GCCGCGGAGG AGAGGCCGC	G	Pro	Ala (8389)	NON- CONSER VATIVE	kinase	Human Gene TREMBLNEW-ID:G260237 MYRISTOYLATED ALANINE-RICH C KINASE SUBSTRATE PROTEIN, MARCKS, 80K-L PROTEIN=MACS GENE PRODUCT - HOMO SAPIENS, 332 aa.	1.7E-168	6 (6q22.2)
6219	cg43982923	912	AGTTGCAATGGT GACCTCGATCCT G[A/T]GATTGTAA AGTCATTCTCT TCCAG	T	Glu	Val (8390)	NON- CONSER VATIVE	kinase	Human Gene SWISSPROT-ID:P49615 CELL DIVISION PROTEIN KINASE 5 (EC 2.7.1.-) (TAU PROTEIN KINASE II CATALYTIC SUBUNIT) (TPKII CATALYTIC SUBUNIT) (KINASE PSSALRE) (CRK6) - MUS MUSCULUS (MOUSE), 292 aa.	3.6E-159	19
6220	cg43969473	2576	GCCTCCAGCAT TGGCAAATCGAA C[G/A]TGGACAG ACGTCAGGCAGA AATGG	G	Val	Met (8391)	NON- CONSER VATIVE	kinase	Human Gene SPTREMBL-ID:Q27467 SIMILARITY TO TYROSINE-PROTEIN KINASE - CAENORHABDITIS ELEGANS, 1280 aa.	2.1E-154	11
6221	cg44018530	539	ATGCTGAACATG CTTCGTGGGGCT A[T/A]CTTTTGT TTCTCTGTAGTC TCITT	T	Asp	Val (8392)	NON- CONSER VATIVE	kinase	Human Gene Homologous to SPTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment).	1.7E-129	12

6222	cg43266014	257	GAGCGAGGGCG TGACGCTCGTCG TGTT/GJACAGATA AGCTTGTTCTGG TGTTGGC	T	G	Tyr	Asp (8393)	NON- CONSER VATIVE	kinase	Human Gene Similar to SWISSPROT- ID:P23919 THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE) - HOMO SAPIENS (HUMAN), 212 aa.	1E-87	
6223	cg43984445	308	TTACCTCTCTCA TGAGGCTCTCTT GT/AJTTGGTTAC TTCCTCAGAAAA ATCAT	T	A	Lys	Asn (8394)	NON- CONSER VATIVE	kinase	Human Gene Similar to SWISSPROT- ID:Q16854 DEOXYGUANOSINE KINASE PRECURSOR (EC 2.7.1.113) (DGUOK) - HOMO SAPIENS (HUMAN), 277 aa   pcds:SPREMBL-ID:Q16854 DEOXYGUANOSINE KINASE (EC 2.7.1.113) - HOMO SAPIENS (HUMAN), 277 aa.	8.7E-73	2
6224	cg43985883	186	AGTCACAAGCGG AAGAGGAGATCT C[G/A]AAGGAGC ACACAAGAGAAC AGGAAT	G	A	Arg	Gln (8395)	NON- CONSER VATIVE	kinase	Human Gene Similar to SWISSNEW- ID:O35493 PROTEIN KINASE CLK4 (EC 2.7.1.-) - MUS MUSCULUS (MOUSE), 481 aa.	1.2E-64	
6225	cg43985883	226	AGAACAGGAATT GTATACCATC A[G/C]GTGTTAA ACAATCTGATTG TGCTC	G	C	Gln	His (8396)	NON- CONSER VATIVE	kinase	Human Gene Similar to SWISSNEW- ID:O35493 PROTEIN KINASE CLK4 (EC 2.7.1.-) - MUS MUSCULUS (MOUSE), 481 aa.	1.2E-64	
6226	cg43982810	2277	GGACCCAAACAT CATCCATCTATT A[G/T]CTGTGTGT ATCACTGATGAC CCTCT	G	T	Ala	Ser (8397)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:Q16832 RECEPTOR PROTEIN-TYROSINE KINASE TKT PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE TYRO 10) (NEUROTROPHIC TYROSINE KINASE, RECEPTOR- RELATED 3) - HOMO SAPIENS (HUMAN), 855 aa.	0	1

6227	cg14396889	1094	CAATCAGCTTTG GTTACCATCGTA G[A/G]AAAGGGA TTTATAAATGCTA CCAAT	A	G	Glu	Gly (8398)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P36888 FL CYTOKINE RECEPTOR PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR FLT3) (STEM CELL TYROSINE KINASE 1) (STK-1) (CD135 ANTIGEN) - HOMO SAPIENS (HUMAN), 993 aa.	0	13
6228	cg44021449	2713	GAAGATCTACAG TGGGGACTACTA TTC/TGTCAAGGC TGTGCCTCCAA CTGCC	C	T	Arg	Cys (8399)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:Q08418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0	15
6228	cg43322545	1212	GGAGGGAGTGC CCCTGGGCCCC CCT[G/A]AGAACA TTAGTGCTACGC GGAATGG	G	A	Glu	Lys (8400)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa. lpcis:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)
6230	cg43991478	1301	AGTAGGTCGGAC GGCCGGTGAGT CC[G/C]GGTTCA CAGTCAAGACGT CAGCAAG	G	C	Pro	Arg (8401)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	
6231	cg43991478	1895	GTGCTCCACGTA CTCTGTCAACCAT G[A/C]TATTTTCA GGGCCGCGCAC ACAGAC	A	C	Ile	Ser (8402)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	

6232	cg43991478	894	GCGGCTAGGTCT CGGTGGATGTAG TTCGCTGCGCG TGCAGATAGGCC ATGCC	G	C	His	Asp (8403)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	0
6233	cg43991478	895	CGGCTAGGTCTC GGTGGATGTAGT GTC/GTGGCGGT GCAGATAGGCCA TGCCCT	C	G	Gln	His (8404)	NON- CONSER VATIVE	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	0
6234	cg43920644	2056	TGACATTCCAAA GTAGCCCGAAAT TTCGCTTTAATCA TTCGGGGCAAAT CCGAG	T	C	Lys	Glu (8405)	NON- CONSER VATIVE	kinesin	Human Gene SPTREMBL-ID:Q99661 MITOTIC CENTROMERE-ASSOCIATED KINESIN - HOMO SAPIENS (HUMAN), 725 aa.	0	1
6235	cg43942537	1165	CACTGTCTCTTC CAAAACCTTCAC GTC/TCTGTCTT GCTTGTTCTCGT CTATC	C	T	Gly	Asp (8406)	NON- CONSER VATIVE	kinesin	Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.   pcis:SWISSPROT-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.	0	10
6236	cg43942537	1250	TTTTCTGATCT GTGGCTTTCAAC TTC/TCTCATGTT CTACTCTTAGAC GTCC	C	T	Glu	Lys (8407)	NON- CONSER VATIVE	kinesin	Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.   pcis:SWISSPROT-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.	0	10
6237	cg43964874	3378	ACCAGTGCCACT GTGATCCCAAGCA GTC/TGGGCAGT GCCCATGCTCTCC CCAATG	G	T	Arg	Ser (8408)	NON- CONSER VATIVE	laminin	Human Gene SWISSNEW-ID:P55268 LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) - HOMO SAPIENS (HUMAN), 1798 aa.   pcis:SWISSPROT- ID:P55268 LAMININ BETA-2 CHAIN PRECURSOR (S-LAMININ) - HOMO SAPIENS (HUMAN), 1798 aa.	0	3 (3p21)

6238	cg43983535	2722	TTTGTGTGCAAA GTATGTTTCTCC G[C/A]TGCAGCC AGTGAATGTAAT CACACG	C	A	Arg	Met (8409)	NON- CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
6239	cg42536982	7509	CTGCATTGAGCG TTCTAATGCGTT G[C/G]AAGCGAA GGCGAATATATC GTGCAG	C	G	Leu	Phe (8410)	NON- CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P25391 LAMININ ALPHA-1 CHAIN PRECURSOR (LAMININ A CHAIN) - HOMO SAPIENS (HUMAN), 3075 aa.	0	
6240	cg44009224	84	GGTCAGCTGCA GCATGGGATGG CTG[A/T]GGATCT TTGGGGCAGCC CTGGGGCA	A	T	Arg	Trp (8411)	NON- CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:Q16787 LAMININ ALPHA-3 CHAIN PRECURSOR (EPILIGRIN 170 KD SUBUNIT) (E170) - HOMO SAPIENS (HUMAN), 1713 aa.	0	
6241	cg42930646	1215	TCGTCAATGTTA CTGATGCGGATA G[C/G]GTATGGA TGGAAATGGACG ATGAGG	C	G	Ser	Arg (8412)	NON- CONSER VATIVE	laminin	Human Gene SWISSPROT-ID:P07221 CALSEQUESTIN, SKELETAL MUSCLE ISOFORM PRECURSOR (ASPARTACTIN) (LAMININ-BINDING PROTEIN) - ORYCTOLAGUS CUNICULUS (RABBIT), 395 aa.	1.8E-198	1

6242	cg43958558	451	TGAAGTGGTCAGT GTTCAACCCAGTA CTATGTGATTTT GAATGGTTTCCC ACTTT	A	Gln	His (8413)	NON- CONSER VATIVE	laminin	Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.lpcis:SWISSPROT-ID:P17931 GALECTIN-3 (GALECTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE- BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.	3.9E-139	14 (14q21)
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6243	cg43958558	762	GGGCCAGTGGC AGGGTAGGCTC CGG[G/T]GGCAC TTGGCTGTCCAG AAGATGGG	G	T	Pro	Thr (8414)	NON- CONSER VATIVE	laminin	Human Gene Homologous to SWISSNEW-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa.lpcis:SWISSPROT-ID:P17931 GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE- BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-31) (GALACTOSIDE-BINDING PROTEIN) (GALBP) - HOMO SAPIENS (HUMAN), 249 aa	3.9E-139	14 (14q21)
6244	cg43931460	732	AGGTCAGGATTT TGCAGGTCCACT G[A/C]CAGGTGA AGGCGAGTCCG GCCATT	A	C	Ser	Ala (8415)	NON- CONSER VATIVE	MHC	Human Gene Similar to SWISSPROT- ID:P25963 MAJOR HISTOCOMPATIBILITY COMPLEX ENHANCER-BINDING PROTEIN MAD3 - HOMO SAPIENS (HUMAN), 317 aa.	7.6E-69	14
6245	cg43111577	1062	AGCCACACAGGG TACAGAGGTGGT TC[G/C]AGCTTAT GAAGAAGAGAAC AAAGCT	G	C	Arg	Pro (8416)	NON- CONSER VATIVE	misc_cha nnel	Human Gene TREMBLNEW- ID:G1518639 CGMP-GATED CATION CHANNEL BETA SUBUNIT - HOMO SAPIENS (HUMAN), 1251 aa.	0	16 (16q13)
6246	cg40367355	647	TTTATTCATGGG GACTTAGAACCC G[G/A]TGAGCCC ATTCAATCAT CCCCC	G	A	Gly	Asp (8417)	NON- CONSER VATIVE	misc_cha nnel	Human Gene SPTREMBL-ID:O00584 INWARDLY RECTIFYING K+ CHANNEL HOMO SAPIENS (HUMAN), 375 aa.	4.1E-199	21

6247	cg44929972	1119	TTCTCTTTGAATT GGCCAGAGGAA TTA/GGAGAGTG ACTTTTTATGA AGACA	A	G	Ile	Met (8418)	NON- CONSER VATIVE	ngf	Human Gene TREMBLNEW- ID:E1216872 NERVE GROWTH FACTOR-INDUCIBLE PC4 HOMOLOGUE - HOMO SAPIENS (HUMAN), 453 aa.	4.7E-214	7
6248	cg39307062	350	GCAAGATCGACA AGACGCAGCGC AA/G/CJCGCTGT CCCTTCTGCCGC TTCCAGA	G	C	Lys	Asn (8419)	NON- CONSER VATIVE	nucl_rec pt	Human Gene SWISSPROT-ID:Q13285 STEROID HORMONE RECEPTOR AD4BP (STEROIDGENIC FACTOR 1) (STF-1) (SF-1) (FUSHI TARAZU FACTOR HOMOLOG 1) - HOMO SAPIENS (HUMAN), 461 aa.	7.2E-257	
6249	cg43315956	3132	GTGTTACACCTT GCCAACCCAGCTC CTTA/GCCCTTTGG AAATGGATGACA CAGAA	T	A	Leu	Gln (8420)	NON- CONSER VATIVE	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
6250	cg43315956	3422	AATGCCACCTCT CATTCAAGAAAT GIC/AJTGAGAAAT TCTGAAGGACAT GAACC	C	A	Leu	Met (8421)	NON- CONSER VATIVE	nucl_rec pt	Human Gene SWISSPROT-ID:P10826 RETINOIC ACID RECEPTOR BETA-2 (RAR-BETA-2) (RAR-EPSILON) - HOMO SAPIENS (HUMAN), 448 aa.	2.3E-244	3
6251	cg43935583	1345	TCAGTATGGCTC TTTTCCAGGTGG CT/CJTTCCTGGG GGAATGCCTGGT AATT	T	C	Phe	Leu (8422)	NON- CONSER VATIVE	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
6252	cg43935583	1383	TGCCCTGGTAAT TCCCCGGAGGAA TIG/AJCCCTGGAAT GGGAGGGGGCA TGCCTG	G	A	Met	Ile (8423)	NON- CONSER VATIVE	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
6253	cg43935583	1411	TGGAATGGGAG GGGGCATGCCCT GGA/AJGTGGCT GGAATGCCCTGGA CTCAATGA	A	G	Met	Val (8424)	NON- CONSER VATIVE	nucl_rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22

6254	cg43935583	1527	ATGTGGCTCAGAG ACCCAGCAAATA T[G/A]TCAAAATA CCAGAGCAACCC AAAGG	A	Met	Ile (8425)	NON- CONSER VATIVE	nuc <sub>l</sub> _rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
6255	cg43935583	1577	GTTATGAATCTC ATCAGTAAATTG TTC/GJAGCCAAAT TTGGAGGTCAAG CGTAA	G	Ser	End (8426)	NON- CONSER VATIVE	nuc <sub>l</sub> _rec pt	Human Gene SWISSPROT-ID:P50502 HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR- ASSOCIATED P48 PROTEIN) - HOMO SAPIENS (HUMAN), 369 aa.	1.3E-195	22
6256	cg43949686	1320	CCGCGCCACC CACCATCTCCAA CC[A/C]GCCTCA CCTCATCTCCTC TGCCAAG	C	Gln	Pro (8427)	NON- CONSER VATIVE	nuc <sub>l</sub> _rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.4E-167	
6257	cg44926804	811	TCAGTGGGCGC TCAGCTCACAGC T[G/T]CTCAAATG GGAACAGATGG GAAGCT	T	Gln	Lys (8428)	NON- CONSER VATIVE	nuclease	Human Gene SWISSPROT-ID:Q01831 DNA-REPAIR PROTEIN COMPLEMENTING XP-C CELLS (XERODERMA PIGMENTOSUM GROUP C COMPLEMENTING PROTEIN) (P125) HOMO SAPIENS (HUMAN), 939 aa.	0	3
6258	cg43952559	268	AGCCAGGATTGCG CTTCTCCTGCTA T[G/A]ATTCCAAA AAATTGGCCTTT AATAG	A	Met	Ile (8429)	NON- CONSER VATIVE	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.   pcis:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.8E-156	

6259	cg43952559	765	CAAAAATTACTA GGGGACATTAAAT TJA/GIGATATGAC CTGCTCTAGGCA TTCCT	A	G	End	Tyr (8430)	NON- CONSER VATIVE	nuclease	Human Gene SWISSNEW-ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - HOMO SAPIENS (HUMAN), 874 aa.[pcds:SWISSPROT- ID:P10266 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - HOMO SAPIENS (HUMAN), 874 aa.	7.8E-156	
6260	cg44130572	604	TAATGAGAACAA AGTTACAAACATA C/T/C/JAGAGCCTG TGGACATAGCTA AGACA	T	C	End	Gln (8431)	NON- CONSER VATIVE	nuclease	Human Gene Similar to SWISSNEW- ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE] - MUS MUSCULUS (MOUSE), 1300 aa.[pcds:SWISSPROT-ID:P11369 RETROVIRUS-RELATED POL POLYPROTEIN (REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE) - MUS MUSCULUS (MOUSE), 1300 aa.	2.4E-53	
6261	cg43951535	1536	GTGAACCTACAGC GAGTAGCTTTTA G/C/GJCCTTTGCT TGGGCAAAACCTG CTGAT	C	G	Ser	Arg. (8432)	NON- CONSER VATIVE	nuclease nhib	Human Gene SPTREMBL-ID:Q13181 RNASE L INHIBITOR - HOMO SAPIENS (HUMAN), 599 aa.	2.5e-315	4 (4q31)

8262	cg43988571	2468	GCCTCTTGACCTA CACTTGCAGCAC C[AT]AGGTGAAG ACCTTGCTGCTA AATGC	T	Lys	End (8433)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSNEW-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT- 10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa.jpcls:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa.	0	10 (10q24)
6263	cg43988571	2469	CCTCTTGACCTC A ACTTGCAGCACCC A[AT]GGTGAAGA CCTTGCTGCTAA ATGCT	T	Lys	Met (8434)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSNEW-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (H2TF1) (ONCOGENE LYT- 10) (LYT10) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT] - HOMO SAPIENS (HUMAN), 898 aa.jpcls:SWISSPROT-ID:Q00653 NUCLEAR FACTOR NF-KAPPA-B P100 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P52 SUBUNIT) (H2TF1) (ONCOGENE LYT-10) (LYT10) - HOMO SAPIENS (HUMAN), 898 aa.	0	10 (10q24)
6264	cg38524555	192	AAGAGCTCTGGG G GCCGGGGGCGG CA[G/C]GGGCTC CGGGGGCTCGG GTTCGGGT	C	Arg	Thr (8435)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P22681 PROTO-ONCOGENE C-CBL - HOMO SAPIENS (HUMAN), 906 aa.	0	11 (11q23.3)
6265	cg38524555	600	GAGAAATTCAG C CCTAGGCGAAAC C[C/T]AACCAAAC TGTCCTCATCT TCAGC	T	Pro	Leu (8436)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P22681 PROTO-ONCOGENE C-CBL - HOMO SAPIENS (HUMAN), 906 aa.	0	11 (11q23.3)

6266	cg36524555	663	GAACATAAAGGA ATCTTTCCAAGT GA/GJACTCTTTC AGGAGACACAT TTCGG	A	G	Glu	Gly (8437)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P22681 PROTO-ONCOGENE C-CBL - HOMO SAPIENS (HUMAN), 906 aa.	0	11 (11q23.3 )
6267	cg44012756	2030	GGCTACACAGG GAGCATGTGTAA CAT/GJCAACATC GATGAGTGTGCG GGCAAC	T	G	Ile	Ser (8438)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0	
6268	cg44012756	2323	CACCTGCAAAGA CATGACCAGTGG CT/AJACGTGTGC ACCTGCCCGGA GGGCTT	T	A	Tyr	Asn (8439)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0	
6269	cg44012756	559	TGTCAACGAGTG TGGCCAGAAGC CC/GJAGGCTTT GCCGCCACGGA GGCACCTG	G	A	Gly	Arg (8440)	NON- CONSER VATIVE	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0	
6270	cg43966629	5250	AACCTCGGGATC CTGCAGAGGTTT G/GJTTCTCTGTG ATCGTTGTGGA GGTGG	G	T	Thr	Asn (8441)	NON- CONSER VATIVE	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q81210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.3E-123	1
6271	cg43966629	5251	ACTTCGGGATCC TGCAGAGGTTTG G/TGJTCCTGTGA TGC GTTGTGGAG GTGGT	T	G	Thr	Pro (8442)	NON- CONSER VATIVE	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q81210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	1.3E-123	1
6272	cg43297056	944	GGCAGTGTGGA CATCATCAGCTT CA/CJATCCTCA TCCACAATGTCA AGAGCC	C	T	Val	Met (8443)	NON- CONSER VATIVE	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.9E-103	20 (20q13.1 )

6273	cg42804626	196	GTGCCTTGACGA TACAGCTAATTC A/GCJAATCATTT TGTGGACGAATA TGATC	G	C	Gln	His (8444)	NON- CONSER VATIVE	oncogen e	Human Gene Similar to SWISSPROT- ID:P01118 TRANSFORMING PROTEIN P21/K-RAS 2B - HOMO SAPIENS (HUMAN), 188 aa.	1.1E-97	12
6274	cg44028217	428	AACGCTCAAAG ACCACGGGCGG GTTG/CJCCAGGG GTCGTTCTGGTG GTAGATG	G	C	His	Asp (8445)	NON- CONSER VATIVE	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0 7 (7q31)	
6275	cg44028217	569	GGCAGCACCTG GTCGGCCATGG AGT/A/GIGATCTG CAGGCGGTACT GCGCTTGT	A	G	Tyr	His (8446)	NON- CONSER VATIVE	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0 7 (7q31)	
6276	cg44028217	691	GCCTGGCGCTC CCAGGAGTACTG CGT/CJCTGCTCC AGAGTTGGCTGG ACCACG	T	C	Thr	Ala (8447)	NON- CONSER VATIVE	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0 7 (7q31)	
6277	cg43972840	945	GAGGGCAGCAG CTGTCCCTTCCG AA/C/AJAGCTATG GCTGTGCTGAG GAAGCCC	C	A	Thr	Lys (8448)	NON- CONSER VATIVE	oxygenas e	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168 (16p13.3 )	16

6278	cg43948682	1212	AAGGTCCTATTC GTCTCAGGGACT G/GGCGCGTAG TGAATGATGGCG CCGTTG	A	G	Ser	Pro (8449)	NON- CONSER VATIVE	peptidase	Human Gene Similar to TREMBLNEW- ID:G2887937 PEPTIDASE, PUTATIVE - BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE), 592 aa.	5E-75	10
6279	cg42347730	1427	TAGTCCCTAAAG GTGATAATCTGC A/C/TGGAAGGCTC CCAGGATTTTCC GGGCT	C	T	Val	Met (8450)	NON- CONSER VATIVE	peroxidase	Human Gene SP TREMBL-ID:Q13408 SALIVARY PEROXIDASE - HOMO SAPIENS (HUMAN), 712 aa.	0	17
6280	cg41626506	1001	CTCCAGGCCTCC AGGTTCAATGCCA G/T/GGATGCTGT CACAAAGACTCAA AGTCT	T	G	Thr	Pro (8451)	NON- CONSER VATIVE	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0 (3q26.3)	3
6281	cg41626506	2405	TTCTCACAAAGTC ATCTGGCAGTCA G/C/AJCCCTCCC CCGAAGGCAGC TTTGCTG	C	A	Ala	Ser (8452)	NON- CONSER VATIVE	peroxidase	Human Gene SWISSPROT-ID:P07202 THYROID PEROXIDASE PRECURSOR (EC 1.11.1.8) (TPO) - HOMO SAPIENS (HUMAN), 933 aa.	0 (3q26.3)	3
6282	cg42691989	826	CGGGTGGTTGT GCCTCAGAGCG AAG/C/GJACACATT CTCAATCAGCAC GGCCCTG	C	G	Ala	Pro (8453)	NON- CONSER VATIVE	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSH-PX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.9E-101 (14q24.1)	14
6283	cg42535091	1803	GCAGGATTGAAG AAGAGCAGAAAA G/C/GJAAGAGGA AAGGGCAGCAAT ATACAA	C	G	Ser	Arg (8454)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q06124 PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (PTP-1D) (SH PTP3) (SH-PTP2) - HOMO SAPIENS (HUMAN), 593 aa.	0	12
6284	cg42535091	1840	GCACGAATATAC AAATATTAAGTAT T/C/CTCTAGCGG ACCAGACGAGTG GAGA	T	C	Ser	Pro (8455)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q06124 PROTEIN-TYROSINE PHOSPHATASE 2C (EC 3.1.3.48) (PTP-2C) (PTP-1D) (SH PTP3) (SH-PTP2) - HOMO SAPIENS (HUMAN), 593 aa.	0	12



6285	cg43920534	4593	GGCTGTTTGGCC CACTTTGTTGAC C[G/A]TCTCCATA TCACACAGATTG TCCAC	A	Thr	Met (8456)	NON- CONSER- VATIVE	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0	12
6286	cg43920534	4727	TCACACAGATTG TCCACTAAATC C[A/G]ACATGCTT CTTCTTTACCCC AGTGA	G	Trp	Arg (8457)	NON- CONSER- VATIVE	phosphatase	Human Gene SPTREMBL-ID:Q10728 SERINE/THREONINE PROTEIN PHOSPHATASE PP1 SMOOTH MUSCLE REGULATORY M110 SUBUNIT (110 KDA SUBUNIT) - RATTUS NORVEGICUS (RAT), 976 aa.	0	12
6287	cg43321833	2318	ACTGACGTGATC GCTGGCCTCCTC A[C/T]GTTACCA TCAATCTCCTGG GGGIG	T	Thr	Met (8458)	NON- CONSER- VATIVE	phosphatase	Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0	20
6288	cg43321833	2324	GTGATCGCTGGC CTCCTCACGTTT A[C/T]CATCAATC TCCTGGGGGTG ATGCTC	T	Thr	Ile (8459)	NON- CONSER- VATIVE	phosphatase	Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0	20
6289	cg43321833	2330	GCTGGCCTCCTCA ACGTTACCCATC A[A/T]TCTCCTGG GGGTGATGCTCA CCATC	T	Asn	Ile (8460)	NON- CONSER- VATIVE	phosphatase	Human Gene TREMBLNEW- ID:G2828708 RECEPTOR PROTEIN TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 1461 aa (fragment).	0	20
6290	cg42460457	1437	GGTCACGCTAG TGTCAGCTGTGG G[G/A]GCCGTCA CCAGTCTCCTAT TGACAT	A	Gly	Ser (8461)	NON- CONSER- VATIVE	phosphatase	Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa.	0	3 (3p14.2)
6291	cg42460457	1473	GTCTCCTATTGA CATTTTAGACCA G[T/C]ATGCGCG TGTGGGGAAGA ATACCA	C	Tyr	His (8462)	NON- CONSER- VATIVE	phosphatase	Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa.	0	3 (3p14.2)

6292	cg42460457	3466	ACCTTCGTGTGC CTCATCCTTCTC ATTCGTGTGTGC TCGTTACTGGA GAGGG	T	C	Ile	Thr (8463)	NON- CONSER VATIVE	phosphat ase	Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa.	0	3 (3p14.2)
6293	cg42460457	5419	CAATACCAAGTTC ATCTATAAGCA AIGTGTCTTAGCT TGGTCAGCACTA AAGAA	G	T	Arg	Met (8464)	NON- CONSER VATIVE	phosphat ase	Human Gene SWISSPROT-ID:P23470 PROTEIN-TYROSINE PHOSPHATASE GAMMA PRECURSOR (EC 3.1.3.48) (R- PTP- GAMMA) - HOMO SAPIENS (HUMAN), 1445 aa.	0	3 (3p14.2)
6294	cg43928335	3499	AGCAAGAGCTAA TAGTACCTCATC TTTATCATCATAA ATTGTATCTGTA AGAAA	T	A	Glu	Val (8465)	NON- CONSER VATIVE	phosphat ase	Human Gene SWISSPROT-ID:P54613 PROTEIN PHOSPHATASE PP2A, 65 KD REGULATORY SUBUNIT, BETA ISOFORM (PROTEIN PHOSPHATASE PP2A SUBUNIT A, BETA ISOFORM) (P65-BETA) - SUS SCROFA (PIG), 602 aa (fragment).	3.2E-302	11 (11q22)
6295	cg43988365	2003	AACGAGATGTCC AGTTCATACAGT CIC/TGTCCCTTAA AGACAGACAACCT CCTTG	C	T	Gly	Arg (8466)	NON- CONSER VATIVE	phosphat ase	Human Gene SWISSPROT-ID:Q14642 TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 412 aa. Jcds:SPTREMBL-ID:Q14642 INOSITOL 1,4,5-TRIPHOSPHATE 5- PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa.	2.6E-227	10
6296	cg43307302	1279	TTGGTTGGCGCT TTTGTGGCTGG AIC/GIACGTGTTT TTCAGCAAAATG CGCTA	C	G	Thr	Arg (8467)	NON- CONSER VATIVE	phosphat ase	Human Gene SWISSPROT-ID:P17706 T- CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) (TCPTP) - HOMO SAPIENS (HUMAN), 415 aa.	8.7E-218	18 (18p11.3)
6297	cg44004203	3233	TCCATTGTTGCT GATCTGGAACCT CT/CICCTTTTGT AGTTGCCGAAAC TTCAC	T	C	Glu	Gly (8468)	NON- CONSER VATIVE	phosphat ase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	9E-211	

6298	cg43269274	1136	TCCTCCATCCCA GTTTTCAGCAGGA TGTGGGCGGT TGCCACAGGGCT TCTGCT	G	T	Pro	Gln (8469)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
6299	cg43269274	1137	CCTCCATCCAG TTTTAGCAGGAT G[G]TGGCCGTT GCCACAGGGCTT CTGCTG	G	T	Pro	Thr (8470)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
6300	cg43269274	1984	AGCGAGTAGCG AGGTGAGGACG ACA[C/A]GCGG GGCTCTCCTCTC GCAGCTTC	C	A	Arg	Leu (8471)	NON- CONSER VATIVE	phosphatase	Human Gene SWISSPROT-ID:Q16690 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
6301	cg43301213	527	CAGAAATGCATCC CTAAAACTCAGG A[G/A]AGAGGCA GTAAGGAACCCA GCACAA	G	A	Glu	Lys (8472)	NON- CONSER VATIVE	phosphatase inhib	Human Gene Similar to SWISSPROT-ID:Q13522 PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (I-1) - HOMO SAPIENS (HUMAN), 171 aa.	7.8E-70	12
6302	cg44021995	2419	TAAAGTAGTGA CAGCCTGGCCC CA[T/C]CCATTAG TAATGTTTTAGT GCAGGG	T	C	Ser	Pro (8473)	NON- CONSER VATIVE	phosphorylase	Human Gene SWISSNEW-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa. ipclis:SWISSPROT-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa.	0	16

6303	cg44021995	2429	GACAGCCTGGC CCCATCCATTAC TA[AC]TGTTTA GTGCAGGGCAA ACAGGTA	A	C	Asn	Thr (8474)	NON- CONSER VATIVE	phosphor ylase	Human Gene SWISSNEW-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa.[pcls:SWISSPROT-ID:Q93100 PHOSPHORYLASE B KINASE BETA REGULATORY CHAIN (PHOSPHORYLASE KINASE BETA SUBUNIT) - HOMO SAPIENS (HUMAN), 1092 aa.	0	16
6304	cg43996195	1215	TGTCACCTTCCA GAGTGGGTACC CTT[C]CATACAT GTGGAACCTGCC CTGCAT	T	C	Glu	Gly (8475)	NON- CONSER VATIVE	phosphor ylase	Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.4E-155	
6305	cg43996195	1216	GTCACCTTCCAG AGTGGGTACCCT TIC/TATACATGT GGAACCTGCCCT GCATC	C	T	Glu	Lys (8476)	NON- CONSER VATIVE	phosphor ylase	Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.4E-155	
6306	cg42688448	1817	CGCCCATGGTA GTCTGAGGCTG GGC[AC]TGGGC ATGGGCCTGCAT CTGGGCCA	A	C	His	Gln (8477)	NON- CONSER VATIVE	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0	20
6307	cg42688448	1823	TGGTAGTCTGAG GCTGGGCATGG GC[AC]TGGGCC TGCATCTGGGCC AAGGCCT	A	C	His	Gln (8478)	NON- CONSER VATIVE	polymera se	Human Gene SPTREMBL-ID:O00268 SUBUNIT OF RNA POLYMERASE II TRANSCRIPTION FACTOR TFIIID - HOMO SAPIENS (HUMAN), 1083 aa.	0	20
6308	cg44022214	2014	TGGAAGCTCAG GCATTGAGCGTG TIA[G]GGAGCGG AGCTTGACTCC CGCAGC	A	G	Tyr	His (8479)	NON- CONSER VATIVE	polymera se	Human Gene SWISSNEW-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.[pcls:SWISSPROT- ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.	0	19 (19q13.3)

6309	cg43958858	2406	CACAGAAATCCAT CAACCGGGACA GC[G]AAGAGC CCTTCTCTCAG TTGAGAT	G	A	Glu	Lys (8480)	NON- CONSER VATIVE	polymera se	Human Gene SWISSNEW-ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME-ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.   pcis:SWISSPROT- ID:P25205 DNA REPLICATION LICENSING FACTOR MCM3 (DNA POLYMERASE ALPHA HOLOENZYME- ASSOCIATED PROTEIN P1) (RLF BETA SUBUNIT) (P102 PROTEIN) - HOMO SAPIENS (HUMAN), 808 aa.	0	6 (6p12)
6310	cg44016415	1881	AGCGGCATAGG CCCTCTGACTTG CA[AG]TGAGGT TGATCCATCCTG ACAGAT	A	G	Ile	Thr (8481)	NON- CONSER VATIVE	polymera se	Human Gene SWISSPROT-ID:P09884 DNA POLYMERASE ALPHA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1462 aa.	0	X
6311	cg4393893	1310	CTCAAAGTTTGC GAGTCTGTGAG CA[TT]GTCGGTG ATTCCCCCGTTG AGAGT	A	T	Met	Lys (8482)	NON- CONSER VATIVE	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.   pcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)
6312	cg4393893	680	CATGAACCTTTGT CTCACCCCTTTGA CA[CG]GGGTATCT GTGATAAAATGA ACCTT	A	C	Leu	Arg (8483)	NON- CONSER VATIVE	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.   pcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)
6313	cg43916712	3743	TTCTCGGGCTT GGGTACACTGT GT[G]GCCTCAG GGCATTGCTCG ATCGTA	T	G	His	Pro (8484)	NON- CONSER VATIVE	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	

6314	cg43916712	3744	TCCTCGGGCTTG GGGTACACTGTG T[G/T]CCTCAGG GCATTGTCTGGA TCGTAT	G	T	His	Asn (8485)	NON- CONSER VATIVE	polymera se	Human Gene Homologous to SWISSNEW-ID:P19387 DNA-DIRECTED RNA POLYMERASE II 33 KD POLYPEPTIDE (EC 2.7.7.6) (RPB3) (RPB33) (RPB31) - HOMO SAPIENS (HUMAN), 275 aa.	6.2E-148	
6315	cg42534568	911	ATTAAAGAAGAG GAGAAGCCCT GC[C/T]CCGCA CGAGTTCACGG CCAGGTG	C	T	Pro	Leu (8486)	NON- CONSER VATIVE	potassiu m_chann el	Human Gene SWISSPROT-ID:P22460 VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV1.5 (HK2) (HPCN1) - HOMO SAPIENS (HUMAN), 613 aa.	0	12 (12p13)
6316	cg43262191	1277	GAAAGCGCTTTGT TTTCTCTCTACAA [G/A]CCATTCCCC GCATAGCTACCA CCAT	G	A	Ala	Thr (8487)	NON- CONSER VATIVE	prostagla ndin	Human Gene SWISSNEW-ID:Q92959 PROSTAGLANDIN TRANSPORTER (PGT) - HOMO SAPIENS (HUMAN), 643 aa.lpcis:SPTREMBL-ID:Q92959 PROSTAGLANDIN TRANSPORTER HPGT - HOMO SAPIENS (HUMAN), 643 aa.	0	3
6317	cg42697980	479	GTTGGGGGCAG GTATGTCACCGT TC[G/T]CGTGGA CCCACAGTCCTA GGACACG	G	T	Arg	Leu (8488)	NON- CONSER VATIVE	prostagla ndin	Human Gene SWISSNEW-ID:Q16647 PROSTACYCLIN SYNTHASE (EC 5.3.99.4) (PROSTAGLANDIN I2 SYNTHASE) - HOMO SAPIENS (HUMAN), 500 aa.lpcis:SWISSPROT- ID:Q16647 PROSTACYCLIN SYNTHASE (EC 5.3.99.4) (PROSTAGLANDIN I2 SYNTHASE) - HOMO SAPIENS (HUMAN), 500 aa.	5.9E-262	
6318	cg38427250	754	GTTGAGCAATGT GCACTTCACTGA A[A/G]AGAAAGAA CTGGAATTTTCG TCTGG	A	G	Lys	Glu (8489)	NON- CONSER VATIVE	protease	Human Gene SWISSPROT-ID:P42575 CASPASE-2 PRECURSOR (EC 3.4.22.-) (CASP-2) (ICH-1 PROTEASE) (ICH- 1L/1S) - HOMO SAPIENS (HUMAN), 435 aa.	4.9E-226	7

6319	cg43306871	605	GCGTATGACTTT ATTGATCCAGGA C[A/G]TGATTG CAGATCTGGGTG TAGAC	A	G	Met	Thr (8490)	NON- CONSER VATIVE	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. lpcis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.1E-153	19
6320	cg43074055	584	CCCAGCCAAACCT CAGTGCCCTCCGT C[G/A]CCACAGT CCAGCTGCCACA GCAGGA	G	A	Ala	Thr (8491)	NON- CONSER VATIVE	protease	Human Gene Homologous to SWISSPROT-ID:P24158 MYELOBLASTIN PRECURSOR (EC 3.4.21.76) (LEUKOCYTE PROTEINASE 3) (PR-3) (PR3) (AGP7) (WEGENER'S AUTOANTIGEN) (P29) (C-ANCA ANTIGEN) - HOMO SAPIENS (HUMAN), 256 aa.	5.7E-138	19 (19p13.3)
6321	cg44031287	393	TGGTTTCACTG ACAGGGGAGAC AC[G/T]AGAGTCA TTGTAGACATGC CAAGCA	G	T	Arg	Ser (8492)	NON- CONSER VATIVE	protease	Human Gene Similar to TREMBLNEW- ID:G2736084 UBIQUITIN SPECIFIC PROTEASE 41 - GALLUS GALLUS (CHICKEN), 357 aa.	8.1E-67	1
6322	cg35817832	780	AACTTCTAAGCT CACCCGTGCTGA G[G/A]CTGTTTT CCTGATGTGGAC TATGT	G	A	Ala	Thr (8493)	NON- CONSER VATIVE	protease	Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	2.1E-63	X

6323	cg42914280	434	ATATCTAGAAA CTACTACGACCT C[G]A/JAAAAAGAT GTGAAACAGTTT GTTAG	G	A	Glu	Lys (8494)	NON- CONSER VATIVE	protease	Human Gene Similar to SWISSNEW- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa. [pcis:SWISSPROT- ID:P09237 MATRILYSIN PRECURSOR (EC 3.4.24.23) (PUMP-1 PROTEASE) (UTERINE METALLOPROTEINASE) (MATRIX METALLOPROTEINASE-7) (MMP-7) (MATRIN) - HOMO SAPIENS (HUMAN), 267 aa.	2.3E-63	11 (11q23)
6324	cg43979831	1346	GCACCGAGGCT GCAGCAGCCAC CAG[C/G]TTGCG GATCAAAATCTT CTCTGCC	C	G	Ser	Arg (8495)	NON- CONSER VATIVE	protease nhib	Human Gene SWISSPROT-ID:P29622 KALLISTATIN PRECURSOR (KALLIKREIN INHIBITOR) (PROTEASE INHIBITOR 4) - HOMO SAPIENS (HUMAN), 427 aa.	1.1E-228	14
6325	cg43511784	1247	CTATCCCCCCCCG AGGTCAAGTTCA A[C]A/JAAACCCCTT TGCTTCTTAAT GATTG	C	A	Asn	Lys (8496)	NON- CONSER VATIVE	protease nhib	Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1- ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa.	9.2E-212	
6326	cg43268468	1080	GGAGGCACCTCTT GAGGTTCTTCTG G[C]G/GGGCAGT GACCGTGCAAG GAGCTC	G	C	Pro	Arg (8497)	NON- CONSER VATIVE	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188 (17p13.3)	17
6327	cg43268468	1260	CAGGAGCACGTT GGTCGTGGGC TC[A/G]TGCTGGA TCGCACCCGGTA CAGGTC	A	G	Met	Thr (8498)	NON- CONSER VATIVE	protease nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1=SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188 (17p13.3)	17
6328	cg43932980	261	TGGGAAGTGGT GACACACGGTTA CTG/TJCGGCTTG GGTGTCGGTGA CCAGCCG	G	T	Cys	Phe (8499)	NON- CONSER VATIVE	protease nhib	Human Gene SPTREMBL-ID:Q92530 PROTEASOME INHIBITOR HPI31 SUBUNIT - HOMO SAPIENS (HUMAN), 271 aa.	1.7E-152	20



6329	cg43060282	1245	TACTACAGAAGG GATGGGTGACT T[G/I]TTTGTCC AAAGTTTTCATT TCTG	G	T	Leu	Phe (8500)	NON- CONSER VATIVE	protease inhib	Human Gene Similar to SWISSPROT- ID:P09006 CONTRAPSIN-LIKE PROTEASE INHIBITOR 6 PRECURSOR (CPI-26) (SERINE PROTEASE INHIBITOR 3) (SPI-3) (SPI-2.2) - RATTUS NORVEGICUS (RAT), 418 aa.	2.2E-83	X (Xq22.2)
6330	cg44921824	1452	CAGCACCACAGC GTGGTAGGCCTC C[C/I]GCAGCTC CGGCACCGTCA CGTCCCT	C	T	Arg	Gln (8501)	NON- CONSER VATIVE	reductase	Human Gene SPTREMBL-ID:Q13716 ADRENODOXIN REDUCTASE - HOMO SAPIENS (HUMAN), 491 aa.	3.2E-270	
6331	cg44921824	1741	TGTGTGGAGAA TGGTGGCAGAA GC[T/C]CGGGT GCTCCCGGGG GAGGCAGC	T	C	Ser	Gly (8502)	NON- CONSER VATIVE	reductase	Human Gene SPTREMBL-ID:Q13716 ADRENODOXIN REDUCTASE - HOMO SAPIENS (HUMAN), 491 aa.	3.2E-270	
6332	cg43941472	771	AGGGGATGTCG CCAAAGCCTTG GA[G/A]CTGGAG CAGATTTGTCA TGCTGGG	G	A	Ala	Thr (8503)	NON- CONSER VATIVE	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.4E-184	X (Xq28)
6333	cg43941472	837	TCATACGGAGTG TGCTGGAGAAGT G[T/A]TTGAGAGG AACGGACGGAA GCTCAA	T	A	Phe	Ile (8504)	NON- CONSER VATIVE	reductase	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.4E-184	X (Xq28)
6334	cg43286949	1008	ACGCCAACTTC CTCTCGGGCTCT G[T/C]ATTTCATCT TGGTCTCTCCT TCGGT	T	C	Thr	Ala (8505)	NON- CONSER VATIVE	reductase	Human Gene SWISSNEW-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa. aa.pcds:SWISSPROT-ID:P53004 BILIVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILIVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.	1.3E-152	7

6335	cg43286949	848	GGAAAGAGCATC CTCCAAAGAAAT CTTCTGCTGGACT CCATCAATGCTC CCGAG	T	C	Gln	Arg (8506)	NON- CONSER VATIVE	reductas e	Human Gene SWISSNEW-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.lpcis:SWISSPROT-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.	1.3E-152	7
6336	cg43925599	570	GGGTACCTGGAA GAGTGAGCCTG GTCTA/JAGGTAA AGCAGCTGTTAA GTATGC	C	A	Gln	Lys (8507)	NON- CONSER VATIVE	reductas e	Human Gene Homologous to TREMBLNEW-ID:G2707824 ALDEHYDE REDUCTASE - HOMO SAPIENS (HUMAN), 325 aa.	5.6E-140	1
6337	cg43255045	5442	CGCGAGGAGGA ACAGCTCCGCCA GGTJGJAAGGA GGAACAGCAGCT GCGCAGC	A	G	Glu	Gly (8508)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0	1
6338	cg43255045	5801	GAGGCACCGCC AAGTCGGGGAG ATAJAJAATCCC AAGAAGGGAAG GGCCATGG	A	C	Lys	Gln (8509)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0	1
6339	cg43957646	3048	GTGTTCATTGCT GTACGTGATAAG AIGTJGCGTGAG GGGTGGACAT GGTGAGG	G	T	Pro	His (8510)	NON- CONSER VATIVE	struct	Human Gene SPTREMBL-ID:O00185 BETA CATENIN - HOMO SAPIENS (HUMAN), 596 aa.	0	10
6340	cg42719763	755	TTCTACAACCCAG CACAACTCTGC TTTCTACAACC AGCACAACTCT GGTCC	T	C	Ser	Pro (8511)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P98088 TRACHEOBRONCHIAL MUCIN (TBM) (MAJOR AIRWAY GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 1056 aa (fragment).	0	11 (11p15)

6341	cg42491601	1247	CAGATTCGAGT AACATGGAACGC C/A/CJGAACAAC GAATACCATATC CTTCTT	A	C	Gln	Pro (8512)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.4E-215	17
6342	cg42491601	1394	GAAGAGAGAGAT ATAAAGAAAACC A/G/CJGAAGATT AGACAGTCGTGC AAGAA	G	C	Arg	Thr (8513)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.4E-215	17
6343	cg42491601	1395	AAGAGAGAGATA TAAAGAAAACCA G/G/CJAGATTAA GACAGTCGTGCA AGAAG	G	C	Arg	Ser (8514)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P35900 KERATIN, TYPE I CYTOSKELETAL 20 (CYTOKERATIN 20) (K20) (CK 20) - HOMO SAPIENS (HUMAN), 424 aa.	1.4E-215	17
6344	cg43956325	1195	TGCATTTGACCT CTCAGTCAGAAT G/C/JTTGATGAGC ATTTCTCATCA GTTCC	C	T	Ser	Asn (8515)	NON- CONSER VATIVE	struct	Human Gene SWISSPROT-ID:P12429 ANNEXIN III (LIPOCORTIN III) (PLACENTAL ANTICOAGULANT PROTEIN III) (PAP-III) (35-ALPHA CALCIMEDIN) (INOSITOL 1,2-CYCLIC PHOSPHATE 2- PHOSPHOHYDROLASE) - HOMO SAPIENS (HUMAN), 323 aa.	3.1E-169	4 (4q21)
6345	cg43985529	972	CCATCCGAGTCC TGGTTGAATAGG C/G/JTTTGGCAG CTGAGAAAGTTCC TGGAG	G	T	Arg	Ser (8516)	NON- CONSER VATIVE	struct	Human Gene SPTREMBL-ID:Q95264 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE II ISOFORM GAMMA- E - SUS SCROFA (PIG), 334 aa (fragment).	1E-163	
6346	cg43051155	1027	TCAGCACCCATG ACAGTGCCATTG C/G/JCTCCTTGT CAAAGACACGCA GGCCC	C	T	Gly	Ser (8517)	NON- CONSER VATIVE	struct	Human Gene Homologous to SWISSPROT-ID:P12829 MYOSIN LIGHT CHAIN 1, EMBRYONIC MUSCLE/ATRIAL ISOFORM - HOMO SAPIENS (HUMAN), 196 aa.	5.3E-103	17
6347	cg42475997	512	ACTTTAACAGGT GGGACTTCAGG CTT/CJTTTAGGA GGAGCCCACTGG CGCTTTC	T	C	Lys	Glu (8518)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q10465 TITIN, SKELETAL MUSCLE ISOFORM (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 7962 aa (fragment).	8.6E-98	

6348	cg44014373	674	TAACATGTTTTC CAAAGCAGATTT C[G/T]TGCTGTAC TGTGCCTGCAGG TCAAT	G	T	Thr	Lys (8519)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.1E-70	17
6349	cg44014373	675	AACATGTTTTC AAAGCAGATTTTC GT[G/G]CTGTACT GTGCCTGCAGGT CAATC	T	G	Thr	Pro (8520)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.1E-70	17
6350	cg44014373	687	AAAGCAGATTTTC GTGCTGTACTGT G[C/T]CTGCAGG TCAATCTCCAGG GCCTGG	C	T	Ala	Thr (8521)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.1E-70	17
6351	cg43961860	1781	GTCTTCTCTAGG CTTCTGTGACC CT[C/G]CTTTTA GCCTCCTTCTT AATT	T	C	Gln	Arg (8522)	NON- CONSER VATIVE	struct	Human Gene Similar to SPTREMBL- ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.5E-51	
6352	cg43918310	232	TCCAGCAGCAGT AAGCAGCCCTGC ATT[C]CCACCCC CTCAGCTTCAGC AGCAG	T	C	Ile	Thr (8523)	NON- CONSER VATIVE	struct	Human Gene Similar to SWISSPROT- ID:P22528 CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) - HOMO SAPIENS (HUMAN), 89 aa.	4E-50 1 (1q21)	
6353	cg43999676	535	ATTGGGTATACA GCACTCAGTGAA A[C/G]GGAGAGT CCACGTTTATTC TCCTCC	C	G	Thr	Arg (8524)	NON- CONSER VATIVE	sulfotran sferase	Human Gene SWISSPROT-ID:Q06520 ALCOHOL SULFOTRANSFERASE (EC 2.8.2.2) (HYDROXYSTEROID SULFOTRANSFERASE) (HST) (DEHYDROEPIANDROSTERONE SULFOTRANSFERASE) (DHEA-ST) (ST2) (ST2A3) - HOMO SAPIENS (HUMAN), 284 aa.	7.8E-157 2 (2q12)	
6354	cg40388639	2168	TCATCCGCTACG CTGGCTACAAGC A[G/C]CCTGACG GCTCCACCCCTGG GGGACC	G	C	Gln	His (8525)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0 (12q24.2)	12

6355	cg40388639	2170	ATCCGCTACGCT C GGCTACAAGCAG C[C/G]TGACGGC TCCACCCTGGG GGACCCA	G	Pro	Arg (8526)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
6356	cg40388639	4911	TATTTTGGAGT T CACCTCTGCGAAC G[T/A]ACGAAGTG ACCAACCGCCTT AGATC	A	Tyr	Asn (8527)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
6357	cg43987111	1807	ACAGAGGCATAG T GAGTCTGAGAAC TTT[C/G]GTGATT TGCCACACAAGG GCAATA	C	Lys	Glu (8528)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0	18 (1p34.1)
6358	cg43971304	1348	GCAACACAGCTTT A GGACACAGGCC AA[A/C]CGCGTG AAGGAAAGTTC GGAGGA	C	Lys	Asn (8529)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0	19 (19q13.3)
6359	cg43971304	1349	CAACACAGCTTTG C GGACACGGCCA AA[C/A]GCGTGAA GGGAAAGTTCG GGAGGAA	A	Arg	Ser (8530)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0	19 (19q13.3)
6360	cg43971304	1359	TGGACACGGC G CAAACGCGTGAA GG[G/A]AAAGTTC GGAGGGAAGCT TTATGAA	A	Gly	Glu (8531)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0	19 (19q13.3)
6361	cg43971304	2282	GTCCTGCACCTC A CTCCACCAGCG GC[A/C]GCAAGC GCAACTCTGTGG ACACGGC	C	Ser	Arg (8532)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P13807 GLYCOGEN (STARCH) SYNTHASE, MUSCLE (EC 2.4.1.11) - HOMO SAPIENS (HUMAN), 737 aa.	0	19 (19q13.3)

6362	cg43948262	1103	GGCTTCTTCCTT GTGCTGCTGGAT A[T/C]CCCTCAGA ATCTGCTCTGTC TGCTC	T	C	Asp	Gly (8533)	NON- CONSER VATIVE	synthase	Human Gene SWISSPROT-ID:P22102 PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE) / PHOSPHORIBOSYLFORMYLGLYCINA MIDINE CYCLO-LIGASE (EC 6.3.3.1) (AIRS) (PHOSPHORIBOSYL- AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2) (GART) (GAR TRANSFORMYLASE) (5'- PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE) - HOMO SAPIENS (HUMAN), 1010 aa	0	21 (21q22.1 )
6363	cg43983214	594	TCCCACTCACTC ATGAGCTCAAAG T[G/T]TACAGGAC GGCGACAGAAAT TGACAG	G	T	His	Asn (8534)	NON- CONSER VATIVE	synthase	Human Gene SPTREMBL-ID:Q13735 5- AMINOLEVULINATE SYNTHASE PRECURSOR - HOMO SAPIENS (HUMAN), 587 aa.	0	X (Xp11.2 1)
6364	cg42721903	318	CCTAAATGACAT CACGAAAAGGGA A[G/A]AATTCTCT CCGCTGACGGC CAACCT	G	A	Glu	Lys (8535)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSPROT- ID:Q06847 ATP SYNTHASE OLIGOMYCIN SENSITIVITY CONFERRAL PROTEIN PRECURSOR, MITOCHONDRIAL (EC 3.6.1.34) (OSCP) - RATTUS NORVEGICUS (RAT), 213 aa.	7.4E-79	

6365	cg43261057	1186	CATGTCATCAAT CCTGCCAGTGAT C/A/CJAGTAATAG CCATCCTGGTCC CGCTG	A	C	Leu	Trp (8536)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. Jcds:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.1E-76	20
6366	cg43933068	534	TTTAATGCGCTG AAGGTTCCCGTG C/C/JAGAGGATA AATATACTGCC AGGTG	C	T	Pro	Leu (8537)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.9E-75	12
6367	cg43064068	1386	CTCGGAGGTAGA GAATGCACTGAT G/A/GJAGACCC TGCTGTGGTTGA GACGGC	A	G	Lys	Glu (8538)	NON- CONSER VATIVE	synthase	Human Gene Similar to SWISSNEW- ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE- COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa. Jcds:SWISSPROT-ID:P39062 ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME) (ACETYL-COA SYNTHASE) - BACILLUS SUBTILIS, 572 aa.	7.4E-65	
6368	cg43958927	2793	GTTGATGTTCTT GTTAATTTATAG G/C/AJGTTTTTG GGGATGTGGAG GTAGT	C	A	Ala	Ser (8539)	NON- CONSER VATIVE	tgf	Human Gene SPTREMBL-ID:Q13118 TGF-BETA INDUCIBLE EARLY PROTEIN - HOMO SAPIENS (HUMAN), 480 aa.	1.2E-246	
6369	cg43980446	3858	ATCTACACATTC ATTCCTGCTAG A/A/GJTATAACCA AAGGGACACTCG CAGCG	A	G	Ile	Thr (8540)	NON- CONSER VATIVE	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166	15 (15q21.1)

6370	cg42711317	1113	TGCTGCATCTAT GGTCTTTAAAGA T[G]ATGGGATTG AAAAAAGAAGAT ATTGC	G	A	Val	Met (8541)	NON- CONSER VATIVE	thiolase	Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa.	2.9E-221	11 (11q22.3)
6371	cg42711317	1233	CCAAAAAGTGAA TATCAATGGAGG A[G]TCTGTTTCT CTGGGACATCCA ATTGG	G	T	Ala	Ser (8542)	NON- CONSER VATIVE	thiolase	Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa.	2.9E-221	11 (11q22.3)
6372	cg42711317	1329	GCAAGGAGAATA CGGCTTGCCAG T[A]TTTGCAAT GGAGGAGGAGG TGCTTC	A	T	Ile	Phe (8543)	NON- CONSER VATIVE	thiolase	Human Gene SWISSPROT-ID:P24752 ACETYL-COA ACETYLTRANSFERASE PRECURSOR, MITOCHONDRIAL (EC 2.3.1.9) (ACETOACETYL-COA THIOLASE) (T2) - HOMO SAPIENS (HUMAN), 427 aa.	2.9E-221	11 (11q22.3)
6373	cg43278427	1119	CCTTGATGTGTA ATGAGAGCAGTA T[G/C]CAGAGCTT GCGCCAGAGAA AATCTG	G	C	Met	Ile (8544)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa.	0	14 (14q31)
6374	cg43278427	1125	TGTGTAATGAGA GCAGTATGCAGA G[C/G]TTGCGCC AGAGAAAATCTG TGAATG	C	G	Ser	Arg (8545)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa.	0	14 (14q31)
6375	cg43278427	2002	TGCCTTCGTCAT CGTCTGCTGCTG TT[C]ATGTGAAG ATCTACATCACA GTCCG	T	C	Tyr	His (8546)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P16473 THYROTROPIN RECEPTOR PRECURSOR (TSH-R) (THYROID STIMULATING HORMONE RECEPTOR) - HOMO SAPIENS (HUMAN), 764 aa.	0	14 (14q31)



6376	cg36988276	2239	TGCTCTTCAGCT CCCAGAGTCACC A[GA]TGGTTCCA CTTACATACCTG TCCCT	G	A	Ser	Asn (8547)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)
6377	cg42899808	1092	CTGGCCACGAAC AGCAGGAAGT GG[C/T]GGCCGA GCGGCGGCGTC GCAGGCGG	C	T	Ala	Thr (8548)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P34995 PROSTAGLANDIN E2 RECEPTOR, EP1 SUBTYPE (PROSTANOID EP1 RECEPTOR) (PGE RECEPTOR, EP1 SUBTYPE) - HOMO SAPIENS (HUMAN), 402 aa.	2.9E-212	19 (1p13.1)
6378	cg43308266	316	CTACACAGGCAT GTGGCGGCCCG AG[C/G]GTTCCG CCGAGGCGCGG GGCAACCT	C	G	Arg	Gly (8549)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	4.8E-212	1 (1p31.2)
6379	cg43284978	153	GATGGATCTGCA CCTCTTCGACTA CTT[G/C]CAGAGCC AGGGAACCTTCTC GGACAT	T	G	Ser	Ala (8550)	NON- CONSER VATIVE	tm7	Human Gene TREMBLNEW- ID:G2736282 G PROTEIN COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 362 aa.	1.4E-196	
6380	cg3001696	1341	CCCGTCCGATG GTCCCGGCGGT GG[C/G]GTGCC GCCTGACCAGG CCATCCGGC	G	C	Gly	Arg (8551)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P41143 DELTA-TYPE OPIOID RECEPTOR (DOR-1) - HOMO SAPIENS (HUMAN), 372 aa.	2.1E-195	1 (1p36.1)
6381	cg42704846	312	CTACACAGGCAT GTGGCGGCCCG AG[C/G]GTTCCG CCGAGGCGCGG GGCAACCT	C	G	Arg	Gly (8552)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P43115 PROSTAGLANDIN E2 RECEPTOR, EP3 SUBTYPE (PROSTANOID EP3 RECEPTOR) (PGE RECEPTOR, EP3 SUBTYPE) - HOMO SAPIENS (HUMAN), 390 aa.	3.1E-194	1 (1p31.2)
6382	cg2514276	645	GTACGTCACCAT CTTCTACGCCCT G[G/C]GCTACCA CCACATCATGAC GGCGAG	G	C	Gly	Arg (8553)	NON- CONSER VATIVE	tm7	Human Gene SWISSPROT-ID:P33032 MELANOCORTIN-5 RECEPTOR (MC5- R) (MC-2) - HOMO SAPIENS (HUMAN), 325 aa.	7E-172	

6383	cg43040271	1300	GCTTCCTCATCT CTATCCCGCCCA TIGCJCTGGGCT GGCGACCCCG GAAGACC	G	C	Met	Ile (8554)	NON- CONSER VATIVE	tm7	Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. lpcis:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.9E-74	
6384	cg38841806	112	CAGCTGGCAGCT GGCACTGTGGG CA[C/A]CAGCCTA CCTGGCCCTGGT GCTGGT	C	A	Pro	Thr (8555)	NON- CONSER VATIVE	tm7	Human Gene Similar to SWISSPROT- ID:P30975 TACHYKININ-LIKE PEPTIDES RECEPTOR 99D (DTKR) - DROSOPHILA MELANOGASTER (FRUIT FLY), 519 aa.	2.1E-67	
6385	cg1408914	623	ATCACTCATGTT AAGTTATCATCT G[A/C]TTGGTATA TGGGTCAGGGG AAGTTT	A	C	Asp	Ala (8556)	NON- CONSER VATIVE	tm7	Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2E-62	
6386	cg1408914	671	TTTCTCTCAGTG TTTTACACAAAT G[A/T]GGTACCCA TGCTGAACCCCT TCATC	A	T	Glu	Val (8557)	NON- CONSER VATIVE	tm7	Human Gene Similar to SPTREMBL- ID:Q63395 OLFACTORY RECEPTOR - RATTUS NORVEGICUS (RAT), 309 aa.	2E-62	
6387	cg43958312	1989	GACGATTGGTGA GATGGTGGCCC G[A/C]GTAGCCT CTCCGTGGCCCT CAAGTT	A	C	Ser	Arg (8558)	NON- CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q15361 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 886 aa.	0	9

6388	cg43948839	1029	GCGGAAGCCTG GGGCTGCTGC TGGC/TGCCCT GGGCTGCTGGG GCCGGGGCC	C	T	Ala	Thr (8559)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa. lpcis:SWISSPROT-ID:P36956 STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREBP-1) (STEROL REGULATORY ELEMENT- BINDING TRANSCRIPTION FACTOR 1) HOMO SAPIENS (HUMAN), 1147 aa.	0	17
6389	cg43328754	934	AAGGACGTCGG GCATCCCCCGTT TC/C/GGCTTCTT GTCCACGCCGTA GCTGTC	C	G	Arg	Pro (8560)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01201 TRANSCRIPTION FACTOR RELB (I- REL) - HOMO SAPIENS (HUMAN), 579 aa.	0	19
6390	cg43328754	935	AGGACGTCGGG CATCCCCCGTTT CC/G/CJCTCTTG TCCACGCCCGTAG CTGICA	G	C	Arg	Gly (8561)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01201 TRANSCRIPTION FACTOR RELB (I- REL) - HOMO SAPIENS (HUMAN), 579 aa.	0	19
6391	cg43962797	770	TCTACAGGATT GCAGGGTCAAAT TTC/AJAGCTCATT TCTGCAGGTAAT AATCA	C	A	Gln	Lys (8562)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q02446 TRANSCRIPTION FACTOR SP4 (SPR- 1) - HOMO SAPIENS (HUMAN), 784 aa.	0	7 (7p15)
6392	cg44925200	651	GTGCCGGTGGT GCTCAGGGAGG GGG/G/CJATGGG GAGAGCTGAAA TCCAGGAC	G	C	Ile	Met (8563)	NON- CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q81191 TRANSCRIPTION FACTOR C1 (HCF) - MUS MUSCULUS (MOUSE), 2045 aa.	0	X

6393	cg43921342	2582	TGCTGCTCCAGC CCCAGGATGACC T[G/A]CACGGCC TGCTGCAGGATG AGCAGC	G	A	Gln	End (8564)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.lpcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	0	0
6394	cg43921342	2592	GCCCCAGGATG ACCTGCACGGC CTG[C/G]TGCAG GATGAGCAGCTT GGTCTGCG	C	G	Gln	His (8565)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSNEW-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa.lpcis:SWISSPROT-ID:P15923 TRANSCRIPTION FACTOR E2-ALPHA (IMMUNOGLOBULIN ENHANCER BINDING FACTOR E12) (TRANSCRIPTION FACTOR-3) (TCF-3) (TRANSCRIPTION FACTOR ITF-1) - HOMO SAPIENS (HUMAN), 654 aa	0	0
6395	cg44130900	1153	TGATCCTATAGC TAAATGGCAAA A[A/G]CTGTTAAG TACGATGTACAA GCTGT	A	G	Thr	Ala (8566)	NON- CONSER VATIVE	transcript factor	HOMO SAPIENS (HUMAN), 654 aa Human Gene SPTREMBL-ID:Q15574 TRANSCRIPTION FACTOR SL1 - HOMO SAPIENS (HUMAN), 556 aa (fragment).	7.5e-310	2
6396	cg43011561	987	CAGACGACGAG GCCTTCGAGGAC AG[G/C]GGTGAT GGGGACTTCGA GGGCCAAG	G	C	Arg	Ser (8567)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:P35269 TRANSCRIPTION INITIATION FACTOR IIF, ALPHA SUBUNIT (TIF-ALPHA) (TRANSCRIPTION INITIATION FACTOR RAP74) - HOMO SAPIENS (HUMAN), 517 aa.	4.3E-275	19 (19p13.3 )

6397	cg44024015	1547	TGCCCTGGCTG GACACATGGCAC CTG ATGGGCC ACCTCCCGCCCT TCAGCCA	G	A	Val	Met (8568)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:P23769 ENDOTHELIAL TRANSCRIPTION FACTOR GATA-2 - HOMO SAPIENS (HUMAN), 480 aa.	1.6E-250	3
6398	cg43129605	1073	GGGATCAGCCCT GGGAAGACCCC ATC A CCAGGA GGTCACCTTCTGA GGAGGAG	C	A	Ser	Tyr (8569)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
6399	cg43129605	1100	CAGGAGGTCACT TCTGAGGAGGA GA A C CAGGGC CACTGACTCTGC CACCATA	A	C	Asn	Thr (8570)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
6400	cg43129605	1121	GAGAACAGGGC CACTGACTCTGC CA C A CATAGTG TCACCACCACCA TCATCT	C	A	Thr	Asn (8571)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
6401	cg43129605	400	GCCCGCGCTCG GCCGCCCGCCG GTG A C AGCCGG AGGCTGGACCT GGAAACTGA	A	C	Lys	Gln (8572)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20

6402	cg43129605	443	GAAACTGACCAT CAGTACCTGGCC G[A/C]GAGCAGT GGCCAGCTCG GGGCAGA	A	C	Glu	Ala (8573)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
6403	cg43129605	445	AACTGACCATCA GTACCTGGCCGA G[A/C]GCAGTGG GCCAGCTCGG GCAGAGG	A	C	Ser	Arg (8574)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:Q01094 TRANSCRIPTION FACTOR E2F1 (E2F- 1) (RETINOBLASTOMA BINDING PROTEIN 3) (RBBP-3) (PRB-BINDING PROTEIN E2F-1) (PBR3) (RETINOBLASTOMA-ASSOCIATED PROTEIN 1) (RBAP-1) - HOMO SAPIENS (HUMAN), 437 aa.	2.8E-232	20
6404	cg43257305	921	CATTGAGGTTCT TGCCAGAAGGAA A[G/T]CTCGTGAT TTTCATGCCAAG CTAAA	G	T	Ala	Ser (8575)	NON- CONSER VATIVE	transcript factor	Human Gene SWISSPROT-ID:P28347 TRANSCRIPTIONAL ENHANCER FACTOR TEF-1 (PROTEIN GT-IIC) (TRANSCRIPTION FACTOR 13) (NTEF- 1) - HOMO SAPIENS (HUMAN), 426 aa.	2.9E-228	9
6405	cg43929348	743	AAGGCCAGGGA TAAATTTCAAGA GTT[A]GCTTTTCG GACACTTCCCTT TCTGCT	T	A	Gln	Leu (8576)	NON- CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa.	6.5E-169	2
6406	cg43929348	930	ATAAAGCACTCA TCATCTGTACTC TT[G]CTGCCGAC TGAAGGCACCCC TGCTG	T	G	Lys	Gln (8577)	NON- CONSER VATIVE	transcript factor	Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa.	6.5E-169	2

6407	cg43051067	1324	TCAAACCTGCAC ATCCACCAGCGA GT/TAACACACAG GAGAGAGGCC TACAAG	A	Val	Glu (8578)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.lpcis:SWISSPROT- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.3E-91	
6408	cg43051067	1648	TTCAGCCAGAGC TCCAACTTCAC AT/GCCACCCAG CGGGTTCACAAG AAAGAT	G	Ile	Ser (8579)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.lpcis:SWISSPROT- ID:Q02975 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - RATTUS NORVEGICUS (RAT), 576 aa.	1.3E-91	
6409	cg42849540	1840	CTCCAGAAAGAG CTCTGCAGGCG GA/GCJCAAAGG CAGGGCAGCCG GAAAGCAG	C	Ala	Pro (8580)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	2E-88	20 (20q13)
6410	cg42532030	317	TTATAAATGTGAT GAGTGTGGGAAA [G]JCCTTCAGTC AGAGCTCAGATC TTAT	A	Ala	Thr (8581)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.lpcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	1.9E-57	

6411	cg43984952	1026	CTCGGTCCCCGT CCCTGTCCCCCA A/C/G/T/CACCCCT CCCTTCTGAACA CAGAA	C	G	Asn	Lys (8582)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	9.6E-53	12 (12q23)
6412	cg43984952	767	CCAGACGCC TTC AAGCCCATCAAG A/C/G/GGAGAAG CTGGAGGAGCC GCCCGAA	C	G	Thr	Arg (8583)	NON- CONSER VATIVE	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2896154 TRANSCRIPTION FACTOR GETS-1 - CARASSIUS AURATUS (GOLDFISH), 471 aa.	9.6E-53	12 (12q23)
6413	cg43946772	1682	ATCTGGTCCAG TTCTTTTATTTT A/C/TATCAATAT TAATATACTGGC TAC	A	C	Tyr	End (8584)	NON- CONSER VATIVE	transferase	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0	18
6414	cg43946772	2216	TCTAATGCTGGG CACCTGGCTATC C/T/C/TCTCTGTG GCTTATCCAGG CACTG	T	C	Glu	Gly (8585)	NON- CONSER VATIVE	transferase	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0	18
6415	cg43916882	674	AAGATGAAGAGC CCCAGCATCATG G/A/G/GAAGCG CTGGCGTAGTAG GGGTAG	A	G	Ser	Pro (8586)	NON- CONSER VATIVE	transferase	Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0643) - HOMO SAPIENS (HUMAN), 456 aa.	5.3E-245	1
6416	cg44017777	364	AAACTGTGGAAG CAGCAGTTTGCC C/G/A/GAGGATGC AGAAGGATGGCT TTTGGG	G	A	Ser	Leu (8587)	NON- CONSER VATIVE	transferase	Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)+)- ARGININE ADP- RIBOSYLTRANSFERASE (TESTIS MONO(ADP-RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa.	9E-195	



6417	cg44017777	469	CACACCATGGTC TTCAAGCTTCTG GATTTTCTCA CCATGGTCTTCA AGCTT	A	T	Ile	Asn (8588)	NON- CONSER VATIVE	transfere se	Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)(+)- ARGININE ADP- RIBOSYLTRANSFERASE) (TESTIS MONO(ADP- RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa.	9E-195	
6418	cg44017777	526	TTTCTCACTATG GTCTTCAAGCTT CATTGGTTTTC TCACCAGGGTTG TAGAC	A	T	Leu	Gln (8589)	NON- CONSER VATIVE	transfere se	Human Gene SWISSPROT-ID:Q13508 TESTIS ECTO-ADP- RIBOSYLTRANSFERASE PRECURSOR (EC 2.4.2.31) (TESTIS NAD(P)(+)- ARGININE ADP- RIBOSYLTRANSFERASE) (TESTIS MONO(ADP- RIBOSYL)TRANSFERASE) - HOMO SAPIENS (HUMAN), 367 aa.	9E-195	
6419	cg44000740	721	TGCCAGTGTCTG GGGAGATACTG GCTTCACCCCA GGAAACACAGGG AACATCAC	T	C	Glu	Gly (8590)	NON- CONSER VATIVE	transfere se	Human Gene Homologous to SWISSPROT-ID:P30711 GLUTATHIONE S-TRANSFERASE THETA 1 (EC 2.5.1.18) (CLASS-THETA) - HOMO SAPIENS (HUMAN), 239 aa.	1.6E-117	16
6420	cg42344304	154	ATCTCACTGCAC CGCCGCCCTGCC CGATTGCGCTG GAACCCGCTGTG CAAAGAG	A	T	Glu	Val (8591)	NON- CONSER VATIVE	transfere se	Human Gene Homologous to SPTREMBL-ID:O08832 POLYPEPTIDE GALNAC TRANSFERASE-T4 - MUS MUSCULUS (MOUSE), 578 aa.	1.2E-101	
6421	cg43954704	888	TCGGATATTGCC CTTCTGGATGGA GATGACTCCTTG GGGATGCTGAGT TCAGG	A	G	Phe	Ser (8592)	NON- CONSER VATIVE	transfere se	Human Gene Similar to SPTREMBL- ID:Q29121 UDP- GALNAC:POLYPEPTIDE ALFA-1,0 N- ACETYLGALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	1.1E-68	2

6422	cg43020771	438	ATGGACATCTGG GGGGAGAGAA TT[C/T]TGAGCTC TCCTTCAAGGTG TGGATG	C	T	Ser	Phe (8593)	NON- CONSER VATIVE	transport	Human Gene Similar to SPTREMBL- ID:O08912 POLYPEPTIDE GALNAC TRANSFERASE-T1 - MUS MUSCULUS (MOUSE), 559 aa.	9.2E-51	
6423	cg38869466	218	CGGCGGAAGGT GGTGGACTGTAG CC[G/C]GGAGGA GACGCGGCTGT CTCGCTGC	G	C	Arg	Pro (8594)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P30825 HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (CAT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC RETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS RECEPTOR HOMOLOG) HOMO SAPIENS (HUMAN), 629 aa.	0	13
6424	cg43998978	4040	GGCGCCCTGGC AAATCCAGGAGA CA[G/C]CTCCGC CCAGCAGCTGG CCCCAGGT	G	C	Ala	Pro (8595)	NON- CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q92798 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER - HOMO SAPIENS (HUMAN), 1545 aa.	0	16
6425	cg43935986	1982	CTCCGGTTCTGT GAGGAACAACAT T[G/A]CTTATGGG CTGCAGAGCTGC GAAGA	G	A	Ala	Thr (8596)	NON- CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0 (6p21.3)	6 (6p21.3)
6426	cg43935986	2282	GCTGGTGATTGC TCACAGGCTGCA G[A/G]CAGTTCA GCGCGCCACC AGATCCT	A	G	Thr	Ala (8597)	NON- CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0 (6p21.3)	6 (6p21.3)
6427	cg43935986	2348	CAAGCTGCAGAA GCTTGCCCGAGCT C[T/C]AGGAGGG ACAGGACCTCTA TTCCCG	T	C	End	Gln (8598)	NON- CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q28437 ABC-TRANSPORTER - GORILLA GORILLA GORILLA (LOWLAND GORILLA), 703 aa.	0 (6p21.3)	6 (6p21.3)

6428	cg43112765	4285	GCTCTGATGCTT C TCTATTGTTATCC [C/T]TCCCTTTGG CGAATACCCCGC TTTG	T	Pro	Leu (8599)	NON- CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:G2959843 RIM ABC TRANSPORTER HOMO SAPIENS (HUMAN), 2273 aa.	0	
6429	cg44008864	3409	CAAGGACACAGAT CACAAAGGCCTT C[T/C]CGGCGTC CAGCACATTGTT TGGGTC	C	Glu	Gly (8600)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa. pcis:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0	
6430	cg44008864	3410	AAGGACACAGAC C ACAAAGGCCTTC T[C/T]GGCGTCCA GCACATTGTTG GGTCC	T	Glu	Lys (8601)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa. pcis:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0	

6431	cg44008864	599	ATGAGGTTGGCT GGAGAATCAAAT TTT/CJAGCTACTA CTCCTTTGTCCA GGACC	T	C	Lys	Glu (8602)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q63120 CANALICULAR MULTISPECIFIC ORGANIC ANION TRANSPORTER (MULTIDRUG RESISTANCE- ASSOCIATED PROTEIN 2) (CANALICULAR MULTIDRUG RESISTANCE PROTEIN) - RATTUS NORVEGICUS (RAT), 1541 aa. Jpcls:SPTREMBL-ID:Q63120 ORGANIC ANION TRANSPORTER - RATTUS NORVEGICUS (RAT), 1541 aa.	0	
6432	cg43300953	244	GGCATGCGGA CTACGACGAGGT GAT/CJCGCCTTC CTGGGCGAGTG GGGGCC	T	C	Ile	Thr (8603)	NON- CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.6E-261	5
6433	cg43300953	336	CCCCAATGGCTT CAATGGTATGTC AIG/TJTCGTGTTT CTGGCGGGGAC CCCGGA	G	T	Val	Phe (8604)	NON- CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.6E-261	5
6434	cg43300953	414	GAACCTGAGCAG CGCCTGGCGCA AC[A/C]ACAGTGT CCCGCTGCGGC TGCGGGA	A	C	Asn	His (8605)	NON- CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.6E-261	5
6435	cg43300953	465	CGGCCGCGAGG TGCCCCACAGCT GC[A/C]GCCGCT ACCGGCTCGCC ACCATCGC	A	C	Ser	Arg (8606)	NON- CONSER VATIVE	transport	Human Gene TREMBLNEW- ID:E1284850 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 557 aa.	1.6E-261	5
6436	cg43964039	2693	TGCAGGGTGCC CAGGGCCCCAC GAA[G/A]GGCTG TGGGTGACACTT CACCCACA	G	A	Leu	Phe (8607)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P11166 GLUCOSE TRANSPORTER TYPE 1, ERYTHROCYTE/BRAIN - HOMO SAPIENS (HUMAN), 492 aa.	1.6E-259	1

6437	cg43992017	1612	CAGCAGGAGGC CGAGAAAGACAA CG[G/A]TGACCA CGCGGCGCTCC GGCGGCTG	G	A	Thr	Ile (8608)	NON- CONSER VATIVE	transport	Human Gene SPTREMBL-ID:Q14728 TETRACYCLINE TRANSPORTER-LIKE PROTEIN MRNA - HOMO SAPIENS (HUMAN), 455 aa.	4.4E-241	
6438	cg43919867	3399	TCGTGTATGTCA CAGGCCGGCCC GA[A/T]AAGAAGA AGCACCGCGTG GTGGCAT	A	T	Lys	Ile (8609)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P43125 RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1054 aa.	8.8E-208	11
6439	cg43919867	3401	GTGTATGTGACA GGCCGGCCCGA AA[A/T]GAAGAAG CACCGCGTGGT GGCATGG	A	T	Arg	End (8610)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P43125 RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1054 aa.	8.8E-208	11
6440	cg43919867	3456	CGCAGCACAACT TCCCCACGGC GT[G/C]GTCTCCT TCTGCGACGGC CTCACCC	G	C	Trp	Ser (8611)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P43125 RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDGB) - DROSOPHILA MELANOGASTER (FRUIT FLY), 1054 aa.	8.8E-208	11
6441	cg42876412	531	GATGCCTCTCCT CCTATACATCTA C[A/T]GCAAAGG GATCTACGACGG AGACCT	A	T	Ser	Cys (8612)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:Q14973 SODIUM/BILE ACID COTRANSPORTER (NA(+)/BILE ACID COTRANSPORTER) (NA(+)/TAUROCHOLATE TRANSPORT PROTEIN) (SODIUM/TAUROCHOLATE COTRANSPORTING POLYPEPTIDE) - HOMO SAPIENS (HUMAN), 349 aa.	1.3E-184	14
6442	cg43924839	1242	TCACCCAAAGAG AAGTATCTGAAC T[C/A]TTTAAAC TTTTTCAAAATAT ACTC	C	A	Lys	Asn (8613)	NON- CONSER VATIVE	transport	Human Gene SWISSPROT-ID:P78382 CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR) - HOMO SAPIENS (HUMAN), 337 aa.	1.6E-172	6

6443	cg43945806	600	AATCCTTCCACA GGGACGGAATG ATG/CJCTGCCA GTTCACTGTCAG CATGGGT	G	C	His	Asp (8614)	NON- CONSER VATIVE	transport	Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, QDB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa.	2.2E-145	6
6444	cg43945806	601	ATCCTTCCACAG GGACGGAATGAT G/C/GJTGCCAGT TCACTGTCAGCA TGGGTG	C	G	Gln	His (8615)	NON- CONSER VATIVE	transport	Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, QDB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa.	2.2E-145	6
6445	cg42726186	821	ATCCAGCAGTTG GTTCAATCCACA G/C/GJAAATCTG AGGATCTCTCTAA AATGG	G	C	Phe	Leu (8616)	NON- CONSER VATIVE	transport	Human Gene Similar to SPTREMBL- ID:Q92473 ABC-C TRANSPORTER - HOMO SAPIENS (HUMAN), 1704 aa.	2.5E-60	17
6446	cg43120117	1168	ATCATAATAACC GAACAACGCAGT TIG/TJACAGACCC AAGGTTACACCA CATCA	G	T	Leu	Phe (8617)	NON- CONSER VATIVE	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P39940 UBIQUITIN- PROTEIN LIGASE RSP5 (EC 6.3.2.-) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 809 aa.	7E-121	
6447	cg43262192	3285	CCCACTGGCACC AAATACTGGGCT C/A/TJCCGGTCTG GGACACATATCT GGAGA	A	T	Val	Glu (8618)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75068 KIAA0480 PROTEIN - HOMO SAPIENS (HUMAN), 1252 aa.	0	1
6448	cg43917756	889	GTCATCATAACC ATATACITGTGG C/G/TJGGTAGGC ATGTAACAGCCC TGGAGC	G	T	Pro	Gln (8619)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14157 HYPOTHETICAL PROTEIN KIAA0144 - Homo sapiens (Human), 983 aa.	0	1
6449	cg43929067	3507	ACCTTGCTTCTT AGATTTTTCCTTC T/AJTTTTCTTG ACTTAATTTCTCG AAG	T	A	Lys	Met (8620)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1

6450	cg43948542	1110	TGAAAAAAGGGA GCCAGTTTGGTC AIG/CITCCTGTTG TTTGCAGCAAA AATTG	G	C	Gln	His (8621)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
6451	cg43948542	1890	AAATCATATCTCT TGATGCAAAGTT G/TAAITTTGGAA AACAAAGACTAC AAGA	G	T	Leu	Phe (8622)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
6452	cg43948542	517	AAAAGGAAATGC TGCCTGGCAAGA AIC/TAGTTGAAA CAGAAAGAAAGCT CCAGT	C	T	Gln	End (8623)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07814 MULTIFUNCTIONAL AMINOACYL- TRNA SYNTHETASE [INCLUDES: GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE); PROLYL-TRNA SYNTHETASE (EC 6.1.1.15) (PROLINE--TRNA LIGASE)] - Homo sapiens (Human), 1440 aa.	0	1
6453	cg43950151	3235	CACTTCCTCCGT AATCTGCTTAAT IACIGCAGCTTAT AGTCTTGAGCCA AGAG	A	C	Leu	Arg (8624)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1
6454	cg43950151	4084	CTCATGGCCATC TGTGCCCTCTAC CIG/CJGCAGGAA GCAATTGGTGGT GTGGCC	G	C	Pro	Arg (8625)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O09013 HYPERTENSION-RELATED PROTEIN - RATTUS NORVEGICUS (RAT), 661 aa.	0	1

6455	cg43926985	1450	CATCACATGGAT CCTCATCCAGTT TGTTCATTAGG AGGACTGACAAA TGGA	G	T	Leu	Phe (8626)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00234 KIAA0235 - HOMO SAPIENS (HUMAN), 850 aa (fragment).	0	2
6456	cg43961763	1528	CTCATCGTTGAT TTGTTCAATTTTT TTCCTATATCT CTTGCTGTCTC TCAC	T	C	Glu	Gly (8627)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P13521 SECRETORANIN II PRECURSOR (SGII) (CHROMOGANIN C) - Homo sapiens (Human), 617 aa.	0	2
6457	cg43301812	3665	GGCACTGTCTTA TCCTCCTCCCTG C[AT]GACCTCTG GGTTGCGTCTT TCTCC	A	T	Cys	Ser (8628)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0	3
6458	cg43301812	3980	TGACCCTCAGCT TCAGCTGCAAT TTTCJAGAGTTTG TGGAGTTATGAG AACTA	T	C	Lys	Glu (8629)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q93075 HYPOTHETICAL PROTEIN KIAA0218 - Homo sapiens (Human), 761 aa.	0	3
6459	cg43925942	2191	GGTTGCTTGGGA GACCCTACAAGA A[AG]AATTTCC CGCTTTATGACA GAACC	A	G	Lys	Glu (8630)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60313 KIAA0567 PROTEIN - HOMO SAPIENS (HUMAN), 978 aa (fragment).	0	3
6460	cg43931104	825	GTGTGTTTCATG TGGACATTGTTT ATTCJGGCTGGC ACTTTGGCAACC TTTGTG	T	C	Met	Val (8631)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75329 ATAXIN-7 - HOMO SAPIENS (HUMAN), 892 aa.	0	3
6461	cg43939697	314	GGCCGCTCAA GCCGGGAGATC GAC[G]TGTGTA GCCCCGAAGCG CAGAAGCT	G	T	Gly	Cys (8632)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa.	0	3



6462	cg43940975	315	TCTGGATCCACG GAGAAATATCCA A[G/A]ACGCTCAA ACTGGAACCTGT CGAAG	G	A	Leu	Phe (8633)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE-TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
6463	cg43917191	3407	TCCTTTAATACT GAAGTTGTATCC TC[A]AGGCAGC CGGCTGTTAGCA TTATCT	C	A	Glu	End (8634)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBL-NEW- ACC:BAA74849 KIAA0826 PROTEIN - HOMO SAPIENS (HUMAN), 1236 aa (fragment).	0	4
6464	cg43934651	1011	AGGATTTTGATA ATTTCTCATAATA [G/C]AATCCAGTA TCTTGATATCAG TGTT	G	C	Arg	Thr (8635)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15399 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 786 aa.	0	4
6465	cg43934651	2577	GCTGTGACTGTG ACCTCCCTCTGC A[G/T]CTACTTGG ATCTGCCCTGGT ATCTC	G	T	Ser	Ile (8636)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15399 ORF, COMPLETE CDS - HOMO SAPIENS (HUMAN), 786 aa.	0	4
6466	cg44035533	1188	GAGAGCGACAG CCCAGATAGCCA CTT[C]GGACCTG GAATCCAAACGTG GAGAGT	T	C	Leu	Ser (8637)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78316 HYPOTHETICAL 99.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 873 aa (fragment).	0	4
6467	cg43933355	1258	GTCTTGAAACA TTCCTCCATCCG G[A/T]CATGGAAG GGTCGCAAGTTA TCTGA	A	T	Val	Asp (8638)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92608 MYELOBLAST KIAA0209 - HOMO SAPIENS (HUMAN), 1842 aa (fragment).	0	5
6468	cg44026925	3702	CCCTGTGTGCTC TAGGGTTGGCAA TT[G/C]CAGGATGC TACACTGTCAA AGCAG	T	G	Ile	Met (8639)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15077 KIAA0372 - HOMO SAPIENS (HUMAN), 1564 aa.	0	5

6469	cg43924112	4800	GGTTTAAAGGAT TGAAGAAATTCAC G[C/A]GTGAAGG GGAAAGTGTTCC AAAGGC	C	A	Arg	Leu (8640)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
6470	cg43975893	517	CTTTGGTGAGC TTCAGTATTCTC A[C/A]AAGAATCT TGGGTAGGTTTC TTGGT	C	A	Cys	Phe (8641)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45157 FLASH - HOMO SAPIENS (HUMAN), 1269 aa (fragment).	0	6
6471	cg43918128	2125	TCATCAAGGGCT CCGTCTCTCCC TT/CJCTCGCCGC CTTCGTCATCAT CCTCA	T	C	Lys	Glu (8642)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14137 HYPOTHETICAL PROTEIN KIAA0124 - Homo sapiens (Human), 682 aa (fragment).	0	8
6472	cg43968274	1803	AATGACTGAAGT GGACCTCTTCAT T[C/T]TTACCCAG AGAATCAAAGTG CTGAA	C	T	Leu	Phe (8643)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14914 NEURONAL MUNC18-1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 837 aa.	0	9
6473	cg43968274	1804	ATGACTGAAGTG GACCTCTTCATT CT/CJTACCCAGA GAATCAAAGTGC TGAAC	T	C	Leu	Pro (8644)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14914 NEURONAL MUNC18-1 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 837 aa.	0	9
6474	cg43287069	2139	ATACTCTATCTG GATCTTCTCTCA G[A/T]CAGGCAC CATCTCATATGT ATGGCA	A	T	Arg	Ser (8645)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P55197 AF-10 PROTEIN - Homo sapiens (Human), 1027 aa.	0	11
6475	cg43925880	1137	CTTCTCTCAGTC TTGGTCTGAAAT TTT/CJAGCAGCAT TGGTCCAAACA CGTCC	T	C	Lys	Glu (8646)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13435 SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150) - Homo sapiens (Human), 872 aa.	0	11

6476	cg43916884	2403	GATCCCTTTTGG TAGCTTTCCAGG C(A/G)ATGGTTTG GCCTCAGGAGA CTTATT	A	G	Leu	Ser (8647)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
6477	cg43916884	340	GCAGCTTTCTCA AAAGGCTGCTCT G(G/C)CAACTGC TGCTTCTCAACC CCCTTG	G	C	Pro	Ala (8648)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
6478	cg43916884	341	CAGCTTTCTCAA AAGGCTGCTCTG G(C/G)AACTGCT GCTTCTCAACCC CCTTGG	C	G	Leu	Phe (8649)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
6479	cg43924701	1114	AGAACTTCGGCA CTGTTTCGTAGG A(A/T)CGCGTGAA GTTTCAGGAAAC AGTCC	A	T	Phe	Ile (8650)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13099 TG737 - HOMO SAPIENS (HUMAN), 824 aa.	0	13
6480	cg43929104	2468	TGGTGGCCATAG AGGACGTGGAG GAT/CJTCAATAT GCGTGGTGGAA ATTTCAG	T	C	Phe	Leu (8651)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q00839 HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U) (SCAFFOLD ATTACHMENT FACTOR A) (SAFA) - Homo sapiens (Human), 806 aa.	0	14
6481	cg44018598	4168	GCAGGATACCAT TCAGTCCTCTCC G(C/T)TCAGACA CCACACTTACAA CTTTT	C	T	Ala	Thr (8652)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29374 RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) - Homo sapiens (Human), 1257 aa.	0	14
6482	cg43936094	1825	ACTCGGGGCAC GACACGCCTGAA GG(G/A)TTTATCA TCTGGTGACAAG TTAGGT	G	A	Pro	Ser (8653)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC62018 P53 TUMOR SUPPRESSOR-BINDING PROTEIN 1 - HOMO SAPIENS (HUMAN), 1972 aa.	0	15

6483	cg43928515	508	GCATTTTCTACA CTTGTTGTGAAC ATTCJGTGGCTCA GGGAAAGGGGT AGGATC	T	C	Met	Val (8654)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14687 HYPOTHETICAL PROTEIN KIAA0182 - Homo sapiens (Human), 1157 aa (fragment).	0	16
6484	cg43945577	2253	GTTGACAAGCCG GCTACAGGGAGT CJG/CJGCCGCT CGGCCAGGCAG CCTCTGA	G	C	Gly	Arg (8655)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
6485	cg43945577	408	GGAGGTGGAAG TGCTGGAGGATG ACJG/ATGTCTGC AGTTGAGTTCAG GCAGAC	G	A	Val	Met (8656)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15155 PM5 PROTEIN - HOMO SAPIENS (HUMAN), 1190 aa.	0	16
6486	cg43964911	2441	AAGCAGAACAGG CACAGGATGTAG GJG/JGGTAGTC AGGAGTGGCGG CAGCTGG	G	T	Pro	Thr (8657)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q12767 HYPOTHETICAL PROTEIN KIAA0195 - Homo sapiens (Human), 1356 aa.	0	17
6487	cg43983241	1570	ACCAACCAGCAG TTTAAAGTTTAC JCA/JAGAAATATCT TGAAATATGGT AATA	C	A	Pro	Gln (8658)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa.	0	18
6488	cg43983241	402	TACTTGGAAATC AAATACATTCTAT TTGJCTGCTGGG AAAAATTACTTAC TAGC	T	G	Ser	Ala (8659)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15219 PROTEIN P84 - HOMO SAPIENS (HUMAN), 657 aa.	0	18
6489	cg43991657	2076	CCAGGCCCCCT CAGCGGCTCC AGGJCTJGCGGC TGAGGAGGCC ATCACTGGG	C	T	Ala	Thr (8660)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0	19

6490	cg43918691	1205	CTTTCCAGCTC TGCCTCCAAATG C[A/G]ACGTGTG CTCCCTCACCTG GTCCGA	A	G	Leu	Ser (8661)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
6491	cg43918691	830	GAGCTTCTCCAA TTCTTCTTGTAAAG [C/A]GACATGCC GAGGTCTGAGC CTCCTC	C	A	Arg	Leu (8662)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
6492	cg43949984	1626	AGGAACACCCAC AACATCTTCCAA A[A/G]TCTTAGTA GGCAAGGTCT GGAATG	A	G	Ile	Thr (8663)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76931 FLS353 - HOMO SAPIENS (HUMAN), 747 aa.	0	20
6493	cg43981483	439	GGCAGCCCAGG TGATGTTGAGGT TG[G/A]AATTCTT GGAGGCATTGAT GAACAT	G	A	Ser	Phe (8664)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75882 ATTRACTIN - HOMO SAPIENS (HUMAN), 1198 aa.	0	20
6494	cg43955358	2797	TTTTCTGCAATCT CCAAAGCTTTCC[ A/C]TGCTTTTCT GTAGTAAAGAGC TCA	A	C	Trp	Gly (8665)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P35573 GLYCOGEN DEBRANCHING ENZYME (GLYCOGEN DEBRANCHER) [INCLUDES: 4-ALPHA- GLUCANOTRANSFERASE (EC 2.4.1.25) (OLIGO-1,4-1,4- GLUCANTRANSFERASE) AMYLO-1,6- GLUCOSIDASE (EC 3.2.1.33) (DEXTRIN 6-ALPHA-D-GLUCOSIDASE)] - Homo sapiens (Human), 1515 aa.	0	1 (1p21)
6495	cg17663981	361	GGCCGGCACCC GGAAGGCCGCC TGC[A/G]CCTGC GACCAAAAACCC TGCAGCTG	A	G	Thr	Ala (8666)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0	10 (10p11.2 3)

6496	cg17663981	388	CTGCGACCAAAA ACCCTGCAGCTG C/C/TTCAAAGG GGATGTCAACTA CGCGTT	C	T	Pro	Ser (8667)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q05329 GLUTAMATE DECARBOXYLASE, 65 KD ISOFORM (EC 4.1.1.15) (GAD-65) (65 KD GLUTAMIC ACID DECARBOXYLASE) - Homo sapiens (Human), 585 aa.	0	10 (10p11.2 3)
6497	cg43968854	9932	GACAATGTGTGT GTCAAGAAAATA A/G/CJAACCAGAA GTCATAGGGACA GTGAA	G	C	Arg	Thr (8668)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
6498	cg43968854	5060	GCCTGCAATCT TCACAACCAGAC C/C/TJAGACAAAA ACCCAGCAAGCT CCAAG	C	T	Pro	Leu (8669)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
6499	cg43968854	8018	ACAAAGAGATGC CCCAAGACACGT C/C/TJCAGGAAA GAAGTAAAAGAG GAGCTC	C	T	Pro	Leu (8670)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
6500	cg43269831	1626	GTGGCGATCATC ATGAAGAAGGGC T/C/AJAAAGTTGG ACTTGTAGTCCA GAAAG	C	A	Glu	End (8671)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15586 N-ACETYLGUCOSAMINE-6- SULFATASE PRECURSOR (EC 3.1.6.14) (G6S) (GLUCOSAMINE-6- SULFATASE) - Homo sapiens (Human), 552 aa.	0	12 (12q14)
6501	cg44920831	1083	CTAGAAGGGGTA ACAGCTCTGTTC G/C/AJTGACAGA CTAGCAGGCGTA GGAGAT	C	A	Ala	Ser (8672)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99493 SCA2 PROTEIN - HOMO SAPIENS (HUMAN), 914 aa (fragment).	0	12 (12q24)

6502	cg43979900	2115	GGTCTCTATGTA AACATCACACTT TTAGJTAGTCAGA TTGGTCCAGTTG TAGTC	A	G	Ile	Thr (8673)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
6503	cg43979900	2601	AAATTGTTGTGA CACATTGAAATA A[G/A]GAAGAAAT GGCCGTATGCAC TTAGA	G	A	Pro	Leu (8674)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54803 GALACTOCEREBROSIDASE PRECURSOR (EC 3.2.1.46) (GALCERASE) (GALACTOSYLCERAMIDASE) (GALACTOSYLCERAMIDE BETA- GALACTOSIDASE) (GALACTOCEREBROSIDE BETA- GALACTOSIDASE) - Homo sapiens (Human), 669 aa.	0	14 (14q24.3)
6504	cg43980198	1948	GAACACGATCTG GTTTCATGTGACC A[G/T]GAAGAACC ACGCCAGGCAG GCGGGA	G	T	Arg	Met (8675)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
6505	cg43980198	1978	AACACGCCAG GCAGGCGGGAG TTC[G/T]AGGTCT TGGACATCAAAG CTGAGTC	G	T	Arg	Leu (8676)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P07199 MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN B) (CENP- B) - Homo sapiens (Human), 599 aa.	0	20 (20p13)
6506	cg43973129	1847	CAACTATGACTG GTGGGAGAAAAA G[C/G]CCTTCTCT GAGGATGTGAAC TGGGG	C	G	Pro	Ala (8677)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P05060 SECRETORANIN I PRECURSOR (SGI) (CHROMOGANIN B) - Homo sapiens (Human), 677 aa.	0	20 (20pter)

6507	cg43973129	657	GGAGAGAACTAT CAAAAAGGGGA GCJA/GJAGGGGA AGATAGCAGTGA AGAGAAA	A	G	Gln (8678)	Arg (8678)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P05060 SECRETOGRANIN I PRECURSOR (SGI) (CHROMOGRANIN B) - Homo sapiens (Human), 677 aa.	0	20 (20pter)
6508	cg43955813	1322	CTGGATACAACT TATGCTTTGATA GIGAJTGAAACA GTAAATAATTATA GATCT	G	A	Gly (8679)	Asp (8679)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa.	0	4 (4q12)
6509	cg43955813	691	ACAAAATGTTATT CCATCTAGTGCC JACJAAAAGAGAG AGACTTACACTT TTGA	A	C	Lys (8680)	Gln (8680)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q03188 CENTROMERE PROTEIN C (CENP-C) (CENTROMERE AUTOANTIGEN C) - Homo sapiens (Human), 943 aa.	0	4 (4q12)
6510	cg25268354	1654	CTCTGTTCCCTG GAACCTCCTCAA CIC/TJGCGACGT ACTGAAGGCCCT GTACAG	C	T	Arg (8681)	Cys (8681)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P09172 DOPAMINE BETA-MONOOXYGENASE PRECURSOR (EC 1.14.17.1) (DOPAMINE BETA- HYDROXYLASE) (DBH) - Homo sapiens (Human), 603 aa.	0	9 (9q34)
6511	cg43311566	794	AAGAGCGAGTG GGCCACGCGAG CGAJA/GJCCCTG AGGACCTGGAAT TCATCCGC	A	G	Asn (8682)	Ser (8682)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment).	0	X
6512	cg43992229	1269	CCAGCCAGACTG TGACTATGTTGT GIGAJAATTGCAA GCCATAACGTAC TGGGG	G	A	Glu (8683)	Lys (8683)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P23352 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE- LIKE X-LINKED) - Homo sapiens (Human), 680 aa.	0	X (Xp22.3)
6513	cg43992229	1770	CAAGCCTATTGG CTGCCCTGGGCG AAIC/GJGAGGTC ATGTTCTTTCTAA GGTCT	C	G	Arg (8684)	Gly (8684)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P23352 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE- LIKE X-LINKED) - Homo sapiens (Human), 680 aa.	0	X (Xp22.3)



6514	cg43992229	1771	AAGCCTATTGGC TGCCTGGCGA AC[G/C]AGGTCAT GTTCTTTCTAAG GTGCTA	C	Arg	Pro (8685)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P23352 KALLMANN SYNDROME PROTEIN PRECURSOR (ADHESION MOLECULE- LIKE X-LINKED) - Homo sapiens (Human), 680 aa.	0	X (Xp22.3)
6515	cg42681986	1609	GCCAGTGGTGG CGGGGAAGAGA ATT[C/T]GCGACA CAGACGTGGGG ATTGCCA	T	Glu	Lys (8686)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14827 RAS-GRF2 - HOMO SAPIENS (HUMAN), 1237 aa (fragment).	0	
6516	cg42682094	3090	GACTGCTGTGAG GACAGGGCTGG CG[C/T]AGAGCG AGCAGTCACAGG TGGGTGA	T	Cys	Tyr (8687)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14674 KIAA0165 PROTEIN - HOMO SAPIENS (HUMAN), 1795 aa.	0	
6517	cg43054046	717	TTTTAAGTGA GTTCAAGAGTTT TTTAAAGAAATGT GGCAGTGATCCC TCCTG	A	Phe	Leu (8688)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48200 IRON-RESPONSIVE ELEMENT BINDING PROTEIN 2 (IRE-BP 2) (IRON REGULATORY PROTEIN 2) (IRP2) - Homo sapiens (Human), 963 aa.	0	
6518	cg43139712	1735	TAAGACCAGGGA AAGGGGGGAGC AG[G/C]GGACAA AGAGGGGCCGG GGCAAGCA	C	Gly	Arg (8689)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60378 F23858_1 - HOMO SAPIENS (HUMAN), 608 aa (fragment).	0	
6519	cg43139712	1745	GAAAGGGGGGA GCAGGGGACAA AGA[G/T]GGGCC GGGGCAAGCAC TTCATCGGA	T	Arg	Met (8690)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60378 F23858_1 - HOMO SAPIENS (HUMAN), 608 aa (fragment).	0	

6520	cg43920875	2051	CCTATACTGAGA TAAAGCAGCCCC AIGTTTGAGCACA TCTGTTGGCCAG GGCCA	G	T	Thr	Asn (8691)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46199 TRANSLATION INITIATION FACTOR IF- 2. MITOCHONDRIAL PRECURSOR (IF- 2MT) (IF-2(MT)) - Homo sapiens (Human), 727 aa.	0	
6521	cg43932090	251	GACTTTAAGGCC TTGTCCTTTACCTT [C/T]ATCCTTTAT GAAGGAAGCTTT GCCA	C	T	Glu	Lys (8692)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0	
6522	cg43934688	1393	GGTTCAGTTAA CCTACTCAAAC A[A/T]TGCTGTTA AAGAATCATTGA CTACA	A	T	Asn	Ile (8693)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	0	
6523	cg43992835	1306	TTCATCATTGTC CGAGTCCACAAC C[A/C]CTGCACTG ATACCGTCCGCT ACAGT	A	C	His	Pro (8694)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60292 KIAA0545 PROTEIN - HOMO SAPIENS (HUMAN), 1129 aa (fragment).	0	
6524	cg44016445	1774	TCCTCCCGGG GACATGGCTGTC GA[A/T]GAAGTCA ATCTGCACAGGG TCCCG	A	T	Phe	Ile (8695)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75427 LEUCIN RICH NEURONAL PROTEIN - HOMO SAPIENS (HUMAN), 832 aa.	0	
6525	cg44024279	1391	TGAATGCCAAGA TAAAGGAGAAGA A[G/T]AATTACAG AAATACATCCAG GAGAG	G	T	Glu	End (8696)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOGLOBULIN) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	
6526	cg44130923	2147	CCAGTTTCTCAA GATATGCCTGGC TTA/GAAGACGAA GGGCTCCTCACC ACTGA	A	G	Lys	Glu (8697)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q62383 SUPPRESSOR OF TY 6 (S. CEREVISIAE) HOMOLOG (SUPT6H) - MUS MUSCULUS (MOUSE), 1726 aa.	0	

6527	cg43957199	801	CCCATGAGGTTG GGGGTGACTCG ACT/CJGATGTCA ATGGTCAAGATG TCCCGG	T	C	Ser	Gly (8698)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa.	1.0e-313	1
6528	cg43978095	1436	GTGCCTCTTCAC CAAGAATGCTGC A/GTCGGAGCA CGCAGACCACAA ACGACG	G	T	Gln	His (8699)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15326 BS69 PROTEIN - HOMO SAPIENS (HUMAN), 562 aa.	2.0e-317	10
6529	cg43937128	2000	GTTTCTGGCACC CACTTGAGTCCG G/A/GJCTGCAGT CTCTGGAAGAAG GAGCGG	A	G	Ser	Pro (8700)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	4.0e-317	X
6530	cg43956210	1439	CCCTGTAATCCT TTCTGCTCCTTG G/T/AJACTTAGAT TTGATTAGCTAT GGACA	T	A	Tyr	Asn (8701)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA- GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)
6531	cg43956210	1477	TTAGCTATGGAC AAGATTGGAGGA A/A/CJTACTATAA AGTGGAACCTCT TGATT	A	C	Lys	Asn (8702)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P07686 BETA-HEXOSAMINIDASE BETA CHAIN PRECURSOR (EC 3.2.1.52) (N-ACETYL- BETA- GLUCOSAMINIDASE) (BETA-N- ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 556 aa.	3E-307	5 (5q13)
6532	cg43254411	1198	TGTGGGATTTT CAGAGGACAGT GC/T/CJGACGTG CATACCAATCTT GAGAATA	T	C	Gln	Arg (8703)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P35810 STEROL O-ACYLTRANSFERASE (EC 2.3.1.26) (CHOLESTEROL ACYLTRANSFERASE) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) - Homo sapiens (Human), 550 aa.	5E-305	1 (1q25)

6533	cg43917155	256	AGTGACATTTGG AAGCTTTTCAAA C[G/A]TGGTTCCC TGTAAGTCATCCA TATAT	G	A	Val	Met (8704)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB87763 EMBRYONIC LUNG PROTEIN - HOMO SAPIENS (HUMAN), 568 aa.	2E-301	
6534	cg43998124	2794	TCGCACAGGTCT CCATTCTCTCC TTACJTGCAATTAC ACGTGCTCTTAA GACCT	A	C	His	Gln (8705)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75174 KIAA0689 PROTEIN - HOMO SAPIENS (HUMAN), 547 aa (fragment).	4.7E-293	
6535	cg40918088	1870	ATTAAACCTCTG GATGTCGCCACC A[T/A]CGTCTCCA GTGCAAAAGCCA CAGAG	T	A	Ile	Asn (8706)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51854 TRANSKETOLASE 2 (EC 2.2.1.1) (TK 2) (TRANSKETOLASE RELATED PROTEIN) - Homo sapiens (Human), 557 aa.	1.8E-287	X (Xq28)
6536	cg43931056	975	AAGCACTACAGC AGCTGGAGAAAT A[A/T]AAACCCTA TGAAGAAGCACT GTTC	A	T	End	Tyr (8707)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15020 ORF - HOMO SAPIENS (HUMAN), 963 aa.	4.5E-286	12
6537	cg42709686	1613	CATCTCTGACTG GCTGCCAACACT C[A/G]TGAAGCT GGCCAGGGGAC ACACCAA	A	G	Met	Val (8708)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15848 ARYLSULFATASE B PRECURSOR (EC 3.1.6.12) (ASB) (N- ACETYL GALACTOSAMINE- 4- SULFATASE) (G4S) - Homo sapiens (Human), 533 aa.	4.3E-283	
6538	cg42709686	1667	CACAAAGCCTCT GGATGGCTTCGA C[G/A]TGTGGAAA ACCATCAGTGAA GGAAG	G	A	Val	Met (8709)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P15848 ARYLSULFATASE B PRECURSOR (EC 3.1.6.12) (ASB) (N- ACETYL GALACTOSAMINE- 4- SULFATASE) (G4S) - Homo sapiens (Human), 533 aa.	4.3E-283	
6539	cg43949830	1097	ACTTTTCTGGA TTCACCAATTCAG A[C/G]AATGTTTC AGGCTGGCACTC TTACA	C	G	Cys	Ser (8710)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16

6540	cg43949830	1106	GGATTACCATTA CAGACAATGTTT C/A/GGGCTGGC ACTCTTACACCC AGCACT	A	G	Leu	Pro (8711)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16
6541	cg43949830	852	AACAATTCTAATT GCTCGGTACATT C/T/GACAAATTT CCAGACTCAAAG CTG	C	T	Glu	Lys (8712)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92617 MYELOBLAST KIAA0220 - HOMO SAPIENS (HUMAN), 553 aa (fragment).	2.7E-281	16
6542	cg44910813	515	AGCACCTCCTGT TATTCCAAATGT G/C/GJCTTTCCTC TGGCCTGGAAT GCCCC	C	G	Pro	Ala (8713)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P38567 HYALURONIDASE PRECURSOR (EC 3.2.1.35) (SPERM SURFACE PROTEIN PH-20) (SPERM ADHESION MOLECULE 1) - Homo sapiens (Human), 509 aa.	1.2E-280	7
6543	cg43963979	1906	AGGAGCGTTTG TCTTGGTAGCGC C/G/AJ/CAGAGCA GACAGACGCTG CTGGCGA	G	A	Arg	Trp (8714)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60559 BREAKPOINT CLUSTER REGION PROTEIN 2 - HOMO SAPIENS (HUMAN), 510 aa (fragment).	2E-276	14
6544	cg43333012	1030	CCATACCTTGTC TCTGAGATCCTA A/G/AJ/CATGATCA TGCCATGCAACT CCATA	G	A	Leu	Phe (8715)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.5E-272 (11q23.3)	11
6545	cg43333012	1884	AATAAGCCCTCA ATCCGAGTTCGG G/T/GJCATTTCCA CAAACTGTCGAG AAACA	T	G	Thr	Pro (8716)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P48444 COATOMER DELTA SUBUNIT (DELTA- COAT PROTEIN) (DELTA-COP) (ARCHAIN) - Homo sapiens (Human), 511 aa.	3.5E-272 (11q23.3)	11
6546	cg43958878	1321	TGGTGGCGCTC TGGCTGTTTCA G/G/AJ/CTGTTCT CCTTGCTCAGGA GGAAG	G	A	Pro	Ser (8717)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBL-NEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9

6547	cg43313186	417	CCGCGTGACGG TGCGCAAGGCC GAC[AG]CCGGT GGGCTGGGCAT CAGCATCAA	A	G	Thr	Ala (8718)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16438 ALPHA 1 SYNTROPHIN - HOMO SAPIENS (HUMAN), 505 aa.	8.3E-265	20 (20q11.2)
6548	cg43056973	691	AAGTGCCAGTGA AGCCACCCCTGGT G[G/C]CCCTGCT GGCCGCTCGGA CCAAAGT	G	C	Ala	Pro (8719)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20711 AROMATIC-L-AMINO-ACID DECARBOXYLASE (EC 4.1.1.28) (DOPA DECARBOXYLASE) (DDC) - Homo sapiens (Human), 480 aa.	5.2E-262	7 (7p11)
6549	cg43980777	1015	CATGGGCTCTGG TACAATCTGGGG T[C/G]GTGAGCA AGTGGCTTCTTG GCCCTC	C	G	Arg	Pro (8720)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.2E-259	2
6550	cg43980777	1016	ATGGGCTCTGGT ACAACTCTGGGT C[G/C]TGAGCAA GTGGCTTCTTG CCCTCC	G	C	Arg	Gly (8721)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.2E-259	2
6551	cg39711096	943	GTGGAGGTGGA CATGTCGGGAGA CTT[C/G]GGGTG GCTGTTGAACCT CTCCAC	T	C	Leu	Ser (8722)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1E-251	
6552	cg42101957	375	CATGAGATCCAT GTTGGTGTCTGC CTT[G/T]TTTGTTC ATGACTGAGTAG GTCTT	T	G	Lys	Asn (8723)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04279 SEMENOGELIN I PROTEIN PRECURSOR (SGI) [CONTAINS: SEMINAL BASIC PROTEIN; ALPHA- INHIBIN-92; ALPHA-INHIBIN-31] - Homo sapiens (Human), 462 aa.	5.5E-251	20 (20q12)
6553	cg44910581	2259	CTTGAGCCATCT AGCTTCTCACCA CTT[C/G]CAATACC GGTTGGGTACTG TGCCA	T	C	Cys	Arg (8724)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.8E-251	

6554	cg44910581	2780	GGTTAGATAGCT CTTTATTGTCAC G/A/GJATTGGTG AAAATACTTAG GGATG	A	G	Glu	Gly (8725)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.8E-251	
6555	cg43995564	1356	CAGAGGCCGCG AGGACGCAGTG CCC[G/C]CCCCA GCTGGAGGGTG CCTGCCATC	G	C	Arg	Gly (8726)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12794 TUMOR SUPPRESSOR (LUCA-1) - HOMO SAPIENS (HUMAN), 435 aa.	2.9E-245	3
6556	cg43965612	708	TTGATAGATCCT GATCCAAATG C/T/AJCAATCTCC TCCCGGATTTTG CGTTT	T	A	Glu	Val (8727)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O43236 BRAIN PROTEIN H5 (PEANUT-LIKE PROTEIN 2) - Homo sapiens (Human), 478 aa.	6.9E-244	17
6557	cg44021361	332	CCACGACCAAC AACCTGAGCAGG T[G/T]GTGAGCC AGCGTGCAGGC ATGGCC	G	T	His	Ash (8728)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92685 NOT56-LIKE PROTEIN - Homo sapiens (Human), 438 aa.	6.3E-241	3
6558	cg44021361	334	CAGCACCAACAA CCTGAGCAGGT GT[G/T]TGAGCCA GCGTGCAGGCA TGGCCCA	G	T	Thr	Lys (8729)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92685 NOT56-LIKE PROTEIN - Homo sapiens (Human), 438 aa.	6.3E-241	3
6559	cg43950654	111	TCCCTTTCTTG GGCAAGATGGC GG[C/A]GTACGA CTTGACTACTCG CATCGCG	C	A	Ala	Glu (8730)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa.	3.2E-239	6
6560	cg43950654	202	TTCTCTCTGTAA AGGAGATATATA ATT/AJGAAAAGGA ATTATTACAAGG TAAAT	T	A	Asn	Lys (8731)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q64252 VIRAL INTEGRATION SITE PROTEIN INT-6 - Mus musculus (Mouse), 445 aa.	3.2E-239	6

6561	cg42750618	359	ATGCGCATGAAT GCGGGCCAGCC TG[G]GTCAGT GGGGCTGAAAG GGCAGAGG	G	C	Pro	Ala (8732)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99764 HYPOTHETICAL 48.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 437 aa (fragment).	2.9E-238	1
6562	cg43922856	1184	TTTCCATAGCTT GATAGACCAAAA A[C/A]AAAAAAC TGCCACACAAC AAACA	C	A	Leu	Phe (8733)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42167 THYMPOIETINS BETA AND GAMMA (TP BETA AND TP GAMMA) - Homo sapiens (Human), 453 aa.	2E-237 (12q22)	12
6563	cg44013460	1021	ACTGAGTTGAAA AAGCTGGACTTC C[C/G]AGCTCCA ATTGGACCCAGC AGCAGA	C	G	Gly	Arg (8734)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.6E-237	1
6564	cg44013460	621	CACACCAGCGTT TACCAACTCCCT T[C/T]GAATCTT TTGATCTTTACTA TCAT	C	T	Arg	Gln (8735)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14496 HEPATITIS C-ASSOCIATED MICROTUBULAR AGGREGATE PROTEIN P44 - HOMO SAPIENS (HUMAN), 444 aa.	2.6E-237	1
6565	cg41027023	815	AGCAAGAGACAA CTGCAACTGGG GG[T/A]GGTCAC CCTGGACAGCA GCTCTGTT	T	A	His	Leu (8736)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P24278 ZINC FINGER PROTEIN 46 (ZINC FINGER PROTEIN KUP) - Homo sapiens (Human), 433 aa.	3.5E-233	
6566	cg43968343	2741	CTGAATAGGAAG TGTCATGAGGTC T[C/T]GGTCCAAG AAGAGTCTCAGA AGGAA	C	T	Arg	Gln (8737)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22830 FERROCHELATASE PRECURSOR (EC 4.99.1.1) (PROTOHEME FERRO- LYASE) (HEME SYNTHETASE) - Homo sapiens (Human), 423 aa.	9.6E-231 (18q21.3)	18
6567	cg43916785	3089	TCCATGGGTTCT TCTCGTTTTTCTT T[C/T]TTTTCTTG CTTTTCTTCTCC TCC	T	C	Lys	Glu (8738)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.5E-230	14



6568	cg43916785	3425	GCCATTTCTCTT CTTCTTTCTCTT [C/T]CTTTGAGC TTCTTTCTCATAT TCC	C	T	Glu (8739)	Lys (8739)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.5E-230	14
6569	cg43916785	3431	TCTCTTCTCTTT CTTCTTCTCTTT C/T]AGCTTCTTTC TCATATTCCCGG GTT	C	T	Glu (8740)	Lys (8740)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.5E-230	14
6570	cg43918854	1087	CAGTTCCTCATG ACTTCCCCCATG C/G]CTGGGCA GAACTGGGAACA GCATGT	G	C	Arg (8741)	Pro (8741)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228 (22q11.2)	22
6571	cg43918854	1438	TTCACATATGAA ACACAGGCCTCC T/T]C]GTCAGGCC CCTACTTAACCT CCGTG	T	C	Leu (8742)	Ser (8742)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P20062 TRANSCOBALAMIN II PRECURSOR - Homo sapiens (Human), 427 aa.	3.3E-228 (22q11.2)	22
6572	cg43929685	303	CACCAGCTCACT GAGGAGCTTTGT C/T]CTCTGGA TCAAGAGTCCCA CCTGA	T	C	Arg (8743)	Gly (8743)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29080 (2'-5')OLIGOADENYLATE SYNTHETASE 1B (EC 2.7.7.-) ((2'-5')OLIGO(A) SYNTHETASE 1B) (2-5A SYNTHETASE 1B) - Mus musculus (Mouse), 414 aa.	2.4E-225	12
6573	cg43929685	444	CCTGTGGGGTG GATGCTGCCTGG AG/T]C]GTGCTG GGTCTATGAGAG AAATGAG	T	C	Thr (8744)	Ala (8744)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P29080 (2'-5')OLIGOADENYLATE SYNTHETASE 1B (EC 2.7.7.-) ((2'-5')OLIGO(A) SYNTHETASE 1B) (2-5A SYNTHETASE 1B) - Mus musculus (Mouse), 414 aa.	2.4E-225	12
6574	cg43918561	1232	GAAATTGAGAAG CTGTCCACGCTG T/A]C]CTGGTTCA CGGTGGAGTTC GGGCTG	A	C	Tyr (8745)	Ser (8745)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.1E-224 (11p15.5)	11

6575	cg43918561	1233	AAATTGAGAAGC TGTCACACGCTGT A/C/A/TGGTTTAC GGTGGAGTTTCG GGCTGT	C	A	Tyr	End (8746)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.1E-224	11 (11p15.5)
6576	cg43062448	1351	ACAACCTTAAAG GAATCCATAAAA T/G/TGTGAAGTC CCAGGAGCTCCA CAAAAT	G	T	His	Asn (8747)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3 (3q21.3)
6577	cg44021565	1014	CCTCAAGGCCAG AGGTTCTCCTTC C/G/A/TGAAGACT CTGCTGGAGACC TGCAG	G	A	Thr	Met (8748)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92663 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
6578	cg44021565	345	ATGTCTGTCTTC TTGAAGGCTGGA A/A/GTTACCTTC TTCTCATGACCA GAATC	A	G	Ile	Thr (8749)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92663 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
6579	cg44021565	507	ATGAAACCAGAC AGGAGTTGGTAA C/T/C/JGGAGGCC AAGCACTTGAAG CTCCAA	T	C	Gln	Arg (8750)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92663 FC GAMMA RECEPTOR I - HOMO SAPIENS (HUMAN), 374 aa.	1E-203	1
6580	cg43959472	1586	TTGAGCCACACG ATGCCGCAGGTA C/G/A/JCGTGAAG GGTTCTCGTTG ATCTGC	G	A	Arg	Cys (8751)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
6581	cg44128902	1009	CAGGTGGAGTCT GTACAGCTCAAA G/T/A/JCAACATAG CCCCAAAACAGC CCATG	T	A	Val	Asp (8752)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201	1 (1p36.2)

6582	cg44128902	1068	CGCTACTGGCAA GTCTGTCTGGGG CTTGCCCTCGCT GTCCAGAACAGC CCTAA	T	G	Ser	Ala (8753)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201	1 (1p36.2)
6583	cg44128902	81	CGAGGAAGAGG AGGCTCTGCAGA AG[G/A]AATTCAA CAAGCTCAAGAA AAAGAA	G	A	Glu	Lys (8754)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201	1 (1p36.2)
6584	cg43973314	598	ACTGTTTTAACA GGAAATGGTGAC TTA/GTTACAGTA GTGGGAATGATC TGACT	A	G	Tyr	Cys (8755)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O75521 DBI-RELATED PROTEIN 1 (DRS-1) - Homo sapiens (Human), 364 aa.	3.6E-192	6
6585	cg43988090	964	ATTCCTACACCT GCGTATCAGTCC TTC/TACCAGCAG GAGGACATGCAC CAACT	C	T	Ser	Leu (8756)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88695 ALIX - MUS MUSCULUS (MOUSE), 869 aa.	5.8E-192	3
6586	cg43988431	442	GCCTTGTACATC TTCTTCATGGCC TTT/GGGGAGCC AGGAACTGAGAA GATTAA	T	G	Lys	Gln (8757)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
6587	cg43988431	547	ATGACGCAGCTC TTGGGCCCTGTG CTT/CICTGGATGA GGTAGCCCGTCT GGATG	T	C	Ser	Gly (8758)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
6588	cg43988432	1182	GTCTTCACTCCT GATGGAACTGC A/GA/CAGAGAG GCTTTCGACGTG TACCTT	G	A	Ser	Asn (8759)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08754 JM5 PROTEIN - HOMO SAPIENS (HUMAN), 360 aa.	1E-191	

6589	cg43933608	378	CCGAGACCAAT CCTTGAGTTCA G[G/C]AGGGCT GTAAGGTGAAGA AGCATG	G	C	Arg	Ser (8760)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.5E-189	8
6590	cg43933608	380	GAGACCAATCC TTGAGTTTCAGG A[G/C]GGGCTGT AAGGTGAAGAAG CATGAA	G	C	Arg	Thr (8761)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.5E-189	8
6591	cg43933608	386	AAATCCTTGAGT TTCAGGAGGGG CT[G/C]TAAGGTG AAGAAGCATGAA ACTCAG	G	C	Cys	Ser (8762)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75410 TACC1 - HOMO SAPIENS (HUMAN), 805 aa.	4.5E-189	8
6592	cg43957632	1221	GGCCACCGCGG CGGGCGGCGCA ACC[G/C]GCGGG GGCCCGCAGGC GGCCAGGCG	G	C	Pro	Arg (8763)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (BP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185 2 (2q33)	
6593	cg43957632	433	GCGGTCTACTGC ATCCGCTGGGTG T[G/C]CACCCCG CGAGCCTCCTGC TGCTCA	G	C	His	Asp (8764)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (BP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185 2 (2q33)	
6594	cg43957632	442	TGCATCCGCTGG GTGTGCACCCC GC[G/A]AGCCTC CTGCTGCTCATT GTAGAAG	G	A	Arg	Cys (8765)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18065 INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECURSOR (IGFBP-2) (BP-2) (IGF-BINDING PROTEIN 2) - Homo sapiens (Human), 328 aa.	2.2E-185 2 (2q33)	
6595	cg44128927	838	GGGGCTGCCCG AGTGCACGGCT GC[G/T]GCCACG GCATCGTGGGC ACCATCGT	G	T	Gly	Cys (8766)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD38070 REVERSION-INDUCED LIM PROTEIN - HOMO SAPIENS (HUMAN), 330 aa.	2.8E-183	5

6596	cg43249165	770	GGAAGTCCTTGT TCCTGAAGCCTC AAGGJAATTTGAT GAGTGGGAGCC TGAAGG	A	G	Lys	Glu (8767)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	7.5E-183	
6597	cg42733081	806	CTGAGGGTGTGG GCCTCCCTGGG ACCJA/TCCGGTC CAGGCTGTTGCC CCGGTGA	A	T	Trp	Arg (8768)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75791 GADS PROTEIN - HOMO SAPIENS (HUMAN), 330 aa.	1.8E-181	22
6598	cg43918452	391	TAGCCAGTCTC TCCGACCTTCCC TTT/CJACCGCGTG CCCAGTGACTGG CCTCA	T	C	Phe	Ser (8769)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83027 KIAA1075 PROTEIN - HOMO SAPIENS (HUMAN), 1400 aa (fragment).	3E-179	12
6599	cg44035161	712	CAATGCTGGAGC AGAAAGGATCAC A/GC/JATGTGGCT TTGGATTCTGG AGGAG	G	C	Asp	His (8770)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14656 TORSINA - HOMO SAPIENS (HUMAN), 332 aa.	2.1E-178	9
6600	cg43933591	3997	CTGAGATAAAAT TGTGACACCAAT G/C/JTGCAGTAT TCAACACTATCC TGTA	C	A	Ser	Ile (8771)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q18476 C35A5.8 - CAENORHABDITIS ELEGANS, 1078 aa.	1.7E-176	8
6601	cg43285900	288	AAATATGATCCA AGGAAACTACGG A/C/JTTCCTTCT GAACTGCCTGCT GTGG	C	T	Leu	Phe (8772)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34058 CGI-63 PROTEIN - HOMO SAPIENS (HUMAN), 373 aa.	4.1E-175	1
6602	cg43941890	1343	AGGCTGGGCTCT GGGACCTTGTC T/C/JTCCCAGTTG GCCTACTGTTAC ACATT	C	T	Pro	Ser (8773)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD3024 MNUDC PROTEIN - HOMO SAPIENS (HUMAN), 331 aa.	5.2E-175	

6603	cg43918085	1492	AAGGCTTTTGCT TCACTTGAGTGT TTC/AJACATGTT CACGCTCTCTCTG GAGCT	C	A	Glu	End (8774)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45699 HYPOTHETICAL 37.9 KD PROTEIN - HOMO SAPIENS (HUMAN), 361 aa.	1.9E-173	
6604	cg43926685	355	ATGCGCATGACA GTGGCTGACGG CA/C/TJGTATAC ATAGCCCAGCAG ATGCAC	C	T	Thr	Ile (8775)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168 (1p36.33)	
6605	cg43926685	491	TTCACCTACAATT CTAAATACAAGA G/C/GJATGATAT AGCCCAAGATGC GCCGG	C	G	Ser	Arg (8776)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168 (1p36.33)	
6606	cg43926685	857	ATTACCGCAGGA CCCAGCCCTGA A/C/AJACAGAGT GGTGAATCCAA CTTCC	C	A	Asn	Lys (8777)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23280 CARBONIC ANHYDRASE VI PRECURSOR (EC 4.2.1.1) (CARBONATE DEHYDRATASE VI) - Homo sapiens (Human), 308 aa.	2.5E-168 (1p36.33)	
6607	cg43959938	1723	TGTTGCACTTCA CGCAATGCTTGG C/A/CJAACTTGGT CTCATGGCAAGT CACGC	A	C	Phe	Leu (8778)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13642 SKELETAL MUSCLE LIM-PROTEIN 1 (SLIM 1) (SLIM) (FOUR AND A HALF LIM DOMAINS PROTEIN 1) (FHL-1) - Homo sapiens (Human), 280 aa.	5.2E-168	X
6608	cg42477985	863	ATGACACTGAGT CCAGATCTTCAC A/T/CJAGGCAT GGGTGATTCTC GCCTGC	T	C	Met	Thr (8779)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	3.6E-167	17
6609	cg43996522	383	GTCATAGTATGT AGGAAGATTCTGA A/G/TJAGAAAAAC TGCACCTTCACA TCATC	G	T	Ser	Tyr (8780)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P56180 PUTATIVE PROTEIN-TYROSINE PHOSPHATASE TPTE (EC 3.1.3.48) - Homo sapiens (Human), 551 aa.	3.3E-166	

6610	cg44003630	966	GGAAAGTCCAG GCGGGGCTTGTT GGT/CJGGCCGT GTACCACAGGAA GATGCTG	T	C	Thr	Ala (8781)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
6611	cg44003630	1613	GAGCTGCCGAC AGCCAAGACGTA CT[G]GGAGGA GAAAGCGCCGC CGTGAGCC	G	T	Gln	Lys (8782)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
6612	cg42712022	386	CGCTTTTGACCA GAGAGGAAAGC GA/A/GJAATTTGA AAGATATGGTGG GAATGA	A	G	Lys	Glu (8783)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75804 KI-1/57 INTRACELLULAR ANTIGEN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	2.4E-161	9
6613	cg43986534	768	TTCTGCTACGAA TTCCCCCTCCCG C[G/C]GGTGCC ACCACCCACCG CCCCCC	G	C	Arg	Pro (8784)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75900 METALLOPROTEASE MMP21/22A - HOMO SAPIENS (HUMAN), 390 aa.	4.7E-160	
6614	cg43055617	1416	CCTGAGGCTGTGA TACCAGCTCCCA G/A/CJGTGACTG GCTTCTCAGCAG ACCACT	A	C	Ser	Ala (8785)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD27736 CGI-27 PROTEIN - HOMO SAPIENS (HUMAN), 297 aa.	3.7E-158	21
6615	cg43287561	745	CATAGGCCCCAC TTTCAGTTGAGG AT/GJAATCTGCC AGCATCACGTGC CTCTC	T	G	Leu	Phe (8786)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.4E-156 9 (9q34)	
6616	cg43287561	799	CAGGGTCCACCA TGGTCCGAGGC AT/T/CJATGTACA GCTCCTTGAAT GGTCAA	T	C	Ile	Met (8787)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.4E-156 9 (9q34)	

6617	cg41629243	582	CTCCCATGCTCTT GAAGTGCTCTGCG C[C/T]CCTTCACG CGCCACAGCATC TCCAG	C	T	Gly	Glu (8788)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75229 R31449_3 - HOMO SAPIENS (HUMAN), 813 aa (fragment).	7.8E-155	19 (19p13.3)
6618	cg43992304	588	CAGCTGTCCAGCA AAATCGCCATCT G[A/G]AGATCATA GAGATGGAGTG GGACTG	A	G	Phe	Ser (8789)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92503 SEC14-LIKE PROTEIN - Homo sapiens (Human), 715 aa.	1.1E-151	17 (17q25.1)
6619	cg42712956	357	TGTCATCCGACA GCTGGGCAGCC TG[A/G]GTAATA TGCAGAGGACAT TTTTGG	A	G	Ser	Gly (8790)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA81795 WASP-FAMILY PROTEIN - HOMO SAPIENS (HUMAN), 498 aa.	3.1E-151	
6620	cg42197063	739	GGCGCCATTGC CCTCAGCCTCGT GG[A/C]CATGGG GAGTTCTGATGG GGAACG	A	C	Asp	Ala (8791)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75631 UROPLAKIN III - HOMO SAPIENS (HUMAN), 287 aa.	3.3E-150	
6621	cg43919239	396	ACCAGCATTAC ATGCATGGCTGC A[G/T]CATAGAAG CTGCCCACTTCC TCGTT	G	T	Ala	Asp (8792)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
6622	cg43919239	645	GTTGCTCTTGCA CGTGTGGGAGG TG[T/A]GACAATC CTCCCACCAAGG CTGACA	T	A	His	Leu (8793)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	



6623	cg44921374	2813	GTGAAATCTGG ATATAAACTGG TIA/GJGTCCTGAG GATAACGGAATG AGGCA	A	G	Tyr	His (8794)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
6624	cg44921374	3118	TGTAAGATCTTG TGCCACTGCTAA C[G/A]AGCCTCT GGGGCCGCCCTC GGAACAA	G	A	Ser	Leu (8795)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P43307 TRANSLOCIN-ASSOCIATED PROTEIN, ALPHA SUBUNIT PRECURSOR (TRAP-ALPHA) (SIGNAL SEQUENCE RECEPTOR ALPHA SUBUNIT) (SSR-ALPHA) - Homo sapiens (Human), 286 aa.	3.4E-148	12 (12q23)
6625	cg43927534	701	CCAGTCAGGGTC ATGGCCACAGGA GA/A/CJGGGGT TCCCACGATGA TGAGCAG	A	C	Leu	Arg (8796)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P23249 PROTEIN MOV-10 - Mus musculus (Mouse), 1004 aa.	9E-148	1
6626	cg42929454	321	CTCTAAATTTCC CCAGAACTCTCA[ A/GTTCTGTCTT GAAGCCATGGTA CACT	A	G	Ile	Thr (8797)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P78345 RNASEP PROTEIN P38 - HOMO SAPIENS (HUMAN), 283 aa.	1.1E-144	10
6627	cg43946394	239	ACACACTGAATC TGAGCTTCCGG ATT/AJACCGTAGC CCACGGGCACC AGCTTG	T	A	Ile	Phe (8798)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa.	2.8E-144	19
6628	cg43946394	617	TGGCCAGGCGA GCTCTTCTCCAG CA/C/TJGTTTCAGC CGGGCCTCCAG CTTGGAG	C	T	Val	Met (8799)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa.	2.8E-144	19

6628	cg43324690	775	TGTACGAGAAAA ACAAAAAGGAAA TIG/CJAATATCA ACAGCTCACCAA CTACA	G	C	Met	Ile (8800)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P22676 CALRETININ (CR) (29 KD CALBINDIN) - Homo sapiens (Human), 271 aa.	1.6E-143	16 (16q22.1)
6630	cg43024858	1114	TGTGTGTGTCCT GACGGCTTCGAA GIA/GJACGGAA GATGCCGTGTGTG CCGCCG	A	G	Glu	Gly (8801)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:G60438 HT PROTEIN - CRICETULUS GRISEUS (CHINESE HAMSTER), 348 aa.	2.3E-142	22
6631	cg43935709	1680	AGATAAATGCCT TGGAAGTGGCAC AT/CJAGAAACAT TCTGATATTACC ACCAA	T	C	Tyr	Cys (8802)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB41239 DJ971N18.2 PROTEIN - HOMO SAPIENS (HUMAN), 262 aa (fragment).	8E-140	20
6632	cg43973762	594	CCAGGGGCTCA GTGAAGCTATGA ATT/GJAATTAGA TGCTGTCAGCG GGAATA	T	G	End	Glu (8803)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.2E-137	
6633	cg43973762	741	AGAGAAACATCT TGAGGAGCAGAT TIG/CJCTAAAGTT GATAGAGAATAT GAAGA	G	C	Ala	Pro (8804)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O14777 RETINOBLASTOMA-ASSOCIATED PROTEIN HEC - HOMO SAPIENS (HUMAN), 642 aa.	2.2E-137	
6634	cg43948495	677	GCTCCCCCTGCTT GATCGCTCGTGT GIA/TJCCTCGTCA AGCTTGGGCTG GTCCAG	A	T	Val	Asp (8805)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q13722 UNKNOWN PROTEIN - HOMO SAPIENS (HUMAN), 256 aa.	9.7E-135	3
6635	cg42923692	395	ACAGGAAGACCCC AAGGTAACACAA TIC/GJACTTTCAT ATACCGAGAAAA GGACA	C	G	Ile	Met (8806)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to REMTREMBL-ACC:G298105 GAMMA- DELTA T-CELL RECEPTOR - HOMO SAPIENS (HUMAN), 260 aa.	3E-133	14 (14q11.2)

6636	cg43918679	613	CCCGTGCTGCG GCACGAGCCCC CAC/C/G/GCTAC CGCATGACCGTG CTGGGCAC	C	G	Arg	Gly (8807)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3E-131	21
6637	cg43918679	614	CCGTGCTGCGG CACCAGCCCCCA CC/G/C/CTACCG CATGACCGTGCT GCGCACC	G	C	Arg	Pro (8808)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3E-131	21
6638	cg42382358	835	CATGCAGCGG GGGACGACGAC GGC/A/G/CGCTC CACGCCGCTG CCAGGTGCA	A	G	Thr	Ala (8809)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P08294 EXTRACELLULAR SUPEROXIDE DISMUTASE [CU-ZN] PRECURSOR (EC 1.15.1.1) (EC-SOD) - Homo sapiens (Human), 240 aa.	5.7E-130	4 (4pter)
6639	cg44128041	215	CAGAAGGAGCT GCTGGAAAAGG GCA/A/G/CATCAC GCGGCAGGGCA AGAGCCAG	A	G	Asn	Ser (8810)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q61140 V-CRK- ASSOCIATED TYROSINE KINASE SUBSTRATE P130CAS - MUS MUSCULUS (MOUSE), 874 aa.	2.8E-128	
6640	cg43300586	705	CAGGGCACATTC GCCTCCCAGGT GAT/C/GCTGGA GGGGACAAAGT TGAAAGTG	T	C	Met	Thr (8811)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P38117 ELECTRON TRANSFER FLAVOPROTEIN BETA- SUBUNIT (BETA-ETF) - Homo sapiens (Human), 255 aa.	3.6E-128 (19q13.3)	19
6641	cg43949081	408	GCAGGCCACGC ACCACAACCCGG GC/C/G/TGGGGC TGTCGCTCATTC ACCAGTT	C	G	Gln	His (8812)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19

6642	cg43986720	2320	GGGCACACACTC CAGGCCCTCGTC A[C/T]TGACAGCAG CCCCCGCATCG CATCAG	C	T	Ser	Asn (8813)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P15692 VASCULAR ENDOTHELIAL GROWTH FACTOR PRECURSOR (VEGF) (VASCULAR PERMEABILITY FACTOR) (VPF) - Homo sapiens (Human), 215 aa.	1.1E-121	6 (6p12)
6643	cg43943363	167	AGTGTGCGGCA CCAGCAGGCAG CTG[G/C]CTCCG GCTTTGGGGTAT CTGGGCTC	G	C	Ala	Pro (8814)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P04179 SUPEROXIDE DISMUTASE [MN] PRECURSOR (EC 1.15.1.1) - Homo sapiens (Human), 222 aa.	1.7E-120	6 (6q25.3)
6644	cg43933691	286	ACTCTTCAGCAG CTCTCCTAGGT C[A/G]TTCCTTCA CAACGTATATTC CGTTT	A	G	Met	Thr (8815)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14976 PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 248 aa.	4.1E-120	2
6645	cg43933691	881	CATCTTTTCTTT TCCTTCCTTTCT T[C/G]CTGAAGG TGTGCTGGACAC CTCC	T	C	Lys	Glu (8816)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14976 PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 248 aa.	4.1E-120	2
6646	cg42551270	472	GAAGTCTGTGCG GCAACCTACATG A[T/C]GGGGAAT GAGTTGACCTTC CTAGAT	T	C	Met	Thr (8817)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:P16410 CYTOTOXIC T-LYMPHOCYTE PROTEIN 4-1 PRECURSOR (CTLA-4) (CD152 ANTIGEN) - Homo sapiens (Human), 223 aa.	5.4E-118	
6647	cg43067745	155	ATACACACAGAA AGAGATCACAGA C[T/G]CCCTACCT TAGAAGAAGGGA GGTGG	T	G	Ser	Arg (8818)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
6648	cg43067745	164	GAAAGAGATCAC AGACTCCCTACC TT[G]AGAAAGAG GGAGGTGGTAG ATGAA	T	G	Lys	Gln (8819)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	

6649	cg43067745	205	GTAGATGAAATG AACTGTATGAAG AGTTCCTACTAGC CTGGCCACACACA CAGAA	G	T	Ala	Asp (8820)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
6650	cg43067745	227	AGAGCCACTAGC CTGGCCACACACA CAGGGAAGAAG GACTGGCCCGT CTTCTTG	A	G	Cys	Arg (8821)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
6651	cg43067745	260	GACTGGCCCGT CTTCTTGAAGCC CAATTAGCTCTGG TAGAGGGCCATA GCAGAG	T	A	Met	Leu (8822)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
6652	cg43087745	403	CTGACGACGGT GCTCACTGTCCA CA[GA]AGAGAT GAAACAGCTGCA ACCGCTT	G	A	Ser	Phe (8823)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75839 TSC501 PROTEIN - HOMO SAPIENS (HUMAN), 227 aa.	6.9E-118	
6653	cg43919033	1675	CCCAGGCCCAT GGTGACTAGGG GCA[GTT]AAGTAC CCAGAGAAGACT GAGGTQC	G	T	Leu	Met (8824)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46893 DJ797M17.1 (DERMATOPONTIN) - HOMO SAPIENS (HUMAN), 201 aa.	6.2E-117	1 (1q12)
6654	cg43926002	391	GGCACAGAAA CACAGCAGCGG GAG[C/G]AGCAA CACCAGCACTGC CAACAGAT	C	G	Ser	Arg (8825)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P50539 MAX INTERACTING PROTEIN 1 (MXI1 PROTEIN) - Homo sapiens (Human), 228 aa.	1.6E-116	10
6655	cg43268843	781	GACTGCTTCCAG GAAACCTCTGA C[AG]TGGTACTG AAAAGAAAGCAA ACTAA	A	G	Met	Val (8826)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43260 HYPOTHETICAL 25.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 218 aa (fragment).	9E-116	1

6656	cg43298119	420	TGTAGAATGGAT CAAAGCTAGAGT G/A/GjCTGAGTT GAACCCAGACAA GAACCTG	A	G	Thr (8827)	Ala (8827)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34039 CGI-44 PROTEIN - HOMO SAPIENS (HUMAN), 450 aa.	1.3E-114	
6657	cg43971133	312	GCTGAGGCGCG TCTTCGAGAAGT AC/A/GjGGCGG TCGGCGACGTGT ACATCCC	A	G	Arg (8828)	Gly (8828)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q01130 SPLING FACTOR, ARGinine/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN) - Homo sapiens (Human), 221 aa.	6.6E-113	4
6658	cg43942219	293	TTTCGGCGCTGG GTCGCCCAAGC A/G/AjAATGGAGA CGGATAGAGTG GTGGCT	G	A	Ser (8829)	Phe (8829)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
6659	cg43942219	317	AGAATGGAGACG GATAGAGTGGTG G/C/AjTCCAGAA TCCCGAAGAACA TAAGC	C	A	Ser (8830)	Ile (8830)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD31317 APOPTOSIS RELATED PROTEIN APR- 3 - HOMO SAPIENS (HUMAN), 208 aa.	2.2E-111	2
6660	cg43036790	114	TCAACAATCAA GAGAAAGTCATT C/T/AjTGTA CTGT AACATCTTCTC TTCCC	T	A	Gln	His (8831)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.5E-110	
6661	cg43036790	152	TCTTCTCTTCC CCATCGGGGTTG A/A/CjTCTATTGA AATGTATACTGA AATCA	A	C	Phe	Val (8832)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75058 KIAA0470 PROTEIN - HOMO SAPIENS (HUMAN), 1460 aa.	1.5E-110	
6662	cg43116651	752	TCTGTGTGGCAG AAGGATCAGCTG G/T/AjGACACAG CTGCACTGGCAA GAAAT	T	A	Val	Glu (8833)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD28300 DNA- BINDING PROTEIN PREB - RATTUS NORVEGICUS (RAT), 417 aa.	1.6E-109	2

6663	cg43325271	810	ATCCAGCCCCAG CCCCTGCTCTCC CTTAJGGCCCT CTCGCAAGCAC CTGCAG	T	A	Leu	Gln (8834)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43675 HYPOTHETICAL 97.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 892 aa (fragment).	1.5E-108	
6664	cg42657906	257	GAAGGGTGTG GGGGCTCTGA AAGTIAJGGCA GAGGGTGGCT GGCCTGGG	T	A	His	Leu (8835)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14919 NC2.ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 205 aa.	6.2E-108	11
6665	cg43976960	634	TGGCTGGAGACA ACACTTTATCAG TTT/CJTTGACACT GACAGGAGTGG AACAGT	T	C	Phe	Leu (8836)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P30626 SORCIN (22 KD PROTEIN) (CP-22) (V19) - Homo sapiens (Human), 198 aa.	1E-107	7 (7q21.1)
6666	cg43967668	470	TTCTCCGAGCCA GTCTGAGGGT GC/CJTCAGGT GCCCCGCGCG AGATGCAG	C	T	Gly	Ser (8837)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa.	5.6E-107	3 (3p22)
6667	cg43959885	1027	GTCGTTGGAGTC CACTTTGTCTAT GJA/TJGGTAAAG GTACGTCTCCTG GCTCAT	A	T	Leu	His (8838)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43329 HYPOTHETICAL 23.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 206 aa.	2.4E-106	18
6668	cg43932706	197	AGAGATTGATAT TCGTTTGAGAGA GJA/GJAATTTCT AAAATGTGTTTT GAAAC	A	G	Lys	Glu (8839)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:BAA82992 KIAA1040 PROTEIN - HOMO SAPIENS (HUMAN), 544 aa (fragment).	5.2E-104	
6669	cg43941552	757	CCGGCCTTCCTGA GGCATGGCCGT GAJA/GJACCCCT GTGTGGCGAGG TGCCGCTC	A	G	Asn	Ser (8840)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	1.6E-100	

6670	cg43252708	486	CGACCTCAGGA GCGTCCGAAGT GGG[C/T]TCATCA CACAGAATCGGC AAGACCT	C	T	Leu	Phe (8841)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75679 RET FINGER PROTEIN- LIKE 3 - HOMO SAPIENS (HUMAN), 288 aa.	2.1E-100	
6671	cg43049606	457	CAGAAGGAAAGT CAAGTTTACTTG TTT/GJGGAACT GGACTCCGAGG GAAAGAG	T	G	Leu	Trp (8842)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13094 SLP-76 TYROSINE PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 533 aa.	4.3E-100	5
6672	cg43941550	525	GAGCGGCACCT CGCCACACAGG GTG[C/T]TCACG GCCATGCCCGAG GAAGGCCGG	C	T	Ser	Asn (8843)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
6673	cg43941550	669	CATCTGGAAGTT GTGGACTTTTCT A[G/T]TGAGAGC CTCAAGACTGGG GATGCT	G	T	Thr	Asn (8844)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
6674	cg42903839	211	GGACCGGCGGC CCAAGCTGTGGA GA[C/G]GCCGGG CTGGAAGGCCCC GGAGGACG	C	G	Thr	Arg (8845)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32099 SOUL PROTEIN - HOMO SAPIENS (HUMAN), 205 aa.	8.6E-100	6
6675	cg42903839	717	GTCAAATTGCTT AATAGAAATAAT G[A/C]JAGTGTGG TTGATTCAAAA AATGAA	A	C	Glu	Ala (8846)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32099 SOUL PROTEIN - HOMO SAPIENS (HUMAN), 205 aa.	8.6E-100	6



6676	cg43971745	1964	CTCTTATCTGGG AACAGTGCCAGC T[G/T]GTTGATGG GTGGTGGGGCA GCCAGT	G	T	Gln	Lys (8847)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P41271 ZINC FINGER PROTEIN DAN (N03) - Homo sapiens (Human), 180 aa.	2E-95	1
6677	cg43992729	709	CCTGGGCCATAT GTTGCTGGGAAT T[C/T]CCTCCACC CTTCGTCATGCA GTGGA	C	T	Pro	Ser (8848)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70303 CELL DEATH-INDUCING DNA FRAGMENTATION FACTOR, ALPHA SUBUNIT-LIKE EFFECTOR B (CELL DEATH ACTIVATOR CIDE-B) - MUS MUSCULUS (MOUSE), 219 aa.	2.6E-95	14
6678	cg43927693	667	CCCCTACCTGGC CTGGCTGGCCTT C[G/A]CGACCAC ACTCAACTACTG CGTATG	G	A	Ala	Thr (8849)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22
6679	cg36896591	81	TCCGGAGCCATG CAGGCCGAAGG CC[G/A]GGGCAC AGGGGGTTGCA CGGGCGAT	G	A	Arg	Gln (8850)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75637 LAGE-1A PROTEIN - HOMO SAPIENS (HUMAN), 180 aa.	6.8E-95	
6680	cg42914758	224	ATTCACCAGTTC TGGATGAAAGAC T[G/C]ATGTTGAT TTATGCAGCCAT TTTAG	G	C	Ser	End (8851)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O88422 UDP- GALNAC:POLYPEPTIDE N- ACETYL GALACTOSAMINYLTRANSFER ASE T5 (EC 2.4.1.41) - RATTUS NORVEGICUS (RAT), 930 aa.	7.8E-94	
6681	cg42907594	354	GCCAATAATGCA ATCAGGGTTTCT T[C/A]ATCAGGAG CTTGACCACCA CCTTG	C	A	Glu	End (8852)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34142 CGI-147 PROTEIN - HOMO SAPIENS (HUMAN), 179 aa.	3.8E-92	17

6682	cg43964799	743	TACAACAAGACT ACAAATGCTTCTC TTC/AJCAAGCAAT TCGTGCAGTGG GATGAG	C	A	Ser	Tyr (8853)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75935 DYNACTIN SUBUNIT - HOMO SAPIENS (HUMAN), 186 aa.	4.9E-92	9
6683	cg43921592	158	AGGCTGGCTCA GGACTATCTGCA GT[G/AJCGTCCTA CAGATACCACAA CCTGGA	G	A	Cys	Tyr (8854)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16548 BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC- SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) - Homo sapiens (Human), 175 aa.	4.9E-92	15
6684	cg43921592	219	GCAAAACGTCCA GAGTGCTACAAA AT[GJGTTCGTT CTCAGTCCAAA AGAAG	T	G	Asn	Lys (8855)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16548 BCL2-RELATED PROTEIN A1 (BFL-1 PROTEIN) (HEMOPOIETIC- SPECIFIC EARLY RESPONSE PROTEIN) (GRS PROTEIN) - Homo sapiens (Human), 175 aa.	4.9E-92	15
6685	cg43987971	403	AGCTGCAAGCGA ATGAGGTAGAA G[G/AJACACAGA CATGAGATAGAC ATCAGC	G	A	Pro	Ser (8856)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q92535 PHOSPHATIDYLINOSITOL-GLYCAN- CLASS C (PIG-C) - HOMO SAPIENS (HUMAN), 297 aa.	7.2E-91	1
6686	cg25236776	881	CAGTGCCTCCCC TGCGGCCCCGG GG[G/AJCAAAGG CCGCTGCTTCGG GCCCAGC	G	A	Gly	Asp (8857)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01185 VASOPRESSIN- NEUROPHYSIN 2-COPEPTIN PRECURSOR [CONTAINS: ARG- VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN] - Homo sapiens (Human), 164 aa.	7.2E-91	
6687	cg43978148	707	TGTAGCCCATGC TGTTATCAAGC A[A/GJTGCTCAGC TTGAAGAATATT CCTGT	A	G	Met	Val (8858)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4E-90	16

6688	cg43978148	815	CCTGCACAGTCT GCAACTTCTGA G[G/T]CCTGTTCT GAAATAAAACAT GAGGC	G	T	Ala	Ser (8859)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75201 HYPOTHETICAL 64.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 580 aa (fragment).	4E-90	16
6689	cg43963913	707	CAAGTCCGATC CCACAGGACTG G[A/G]AGACTCG CGTCCAGCTGGA GCTTGG	A	G	Phe	Ser (8860)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11
6690	cg43922714	416	CCTCGCTGGATC AATCGACTTGCC T[A/G]CTTCAGCT CCTGTATACCCCT TTCTA	A	G	Tyr	Cys (8861)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34141 CGI-146 PROTEIN - HOMO SAPIENS (HUMAN), 193 aa.	9.8E-87	19
6691	cg43068353	208	CCTGGTCTGCT GCTCCGGGGT CT[C/T]GGCTGC CAAACGAAATC CTTCTCC	C	T	Arg	Gln (8862)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa.	1E-86	2
6692	cg43068353	391	TTTCTTTTCTGA TTTCTCTGGTTCC G[A/AAATGCCAA ATTAAATCCATC AGC	G	A	Ser	Leu (8863)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49792 NUCLEAR PORE COMPLEX PROTEIN NUP358 (NUCLEOPORIN NUP358) (358 KD NUCLEOPORIN) (P270) (RAN-BINDING PROTEIN 2) - Homo sapiens (Human), 3224 aa.	1E-86	2
6693	cg44018226	1252	CCCTGCAGGCAA TTACTCTCACC G[T/A]GGTAAAA TCAATCGCAGCA GAGAA	T	A	His	Leu (8864)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa.	1.6E-86	
6694	cg36842490	547	GGAAAACGTGT AGCAGTAACATC TTC/TAGAAAGACC CTGTACCAGTCA AACGT	C	T	Ser	Leu (8865)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P01282 VASOACTIVE INTESTINAL PEPTIDE PRECURSOR (VIP) - Homo sapiens (Human), 170 aa.	2.3E-85	

6695	cg36842490	606	TGCAGTCTTCAC TGACAACTATAC C[C]G/GCCCTTAG AAACAAATGGC TGTAAG	C		G	Arg	Gly (8866)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P01282 VASOACTIVE INTESTINAL PEPTIDE PRECURSOR (VIP) - Homo sapiens (Human), 170 aa.	2.3E-85	
6696	cg43142459	281	GGGTGGTCACC CTCCAATACAAT AA[G]C/JATGCCA GGAAGAGTAAGT TGCCCTT	G		C	Ser	Cys (8867)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O15205 DIUBIQUITIN - HOMO SAPIENS (HUMAN), 165 aa.	1.9E-83	6
6697	cg43969140	348	GCCATCTGGTTC CACATTCAGGGC C[T]A/JTCACTATG CCATCCTGTACC ACCAT	T		A	Lys	Met (8868)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
6698	cg43969140	441	CGAATCATCTAG TAATAAGTCTGT C[T]G/JCCTTCCCA AAGGCCCCAGT GGGATC	T		G	Glu	Ala (8869)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
6699	cg43969140	730	GGCTCCCTTCA AACACCTCCACT G[C]A/JTGGGATG GCATCTCCCAACC TTGATT	C		A	Ala	Ser (8870)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30044 PUTATIVE PEROXISOMAL ANTIOXIDANT ENZYME (LIVER TISSUE 2D-PAGE SPOT 71B) - Homo sapiens (Human), 161 aa.	1.7E-80	
6700	cg43989505	634	ATCAGCGGCTCT TTGTATGATGAC G[A]T/AAGGATGA GGCGGCAGGGA AGAAGA	A		T	Glu	Val (8871)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75274 F16601_1, PARTIAL CDS - HOMO SAPIENS (HUMAN), 158 aa (fragment).	2.2E-80	
6701	cg43969316	745	CAGCAGCTGAG CTTGAATCAGCA CA[G]A/JCCGAGC CTTTAACATCGA AAGAGCG	G		A	Ser	Asn (8872)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBL/NEW- ACC:CAA19455 Y17G7B.10A PROTEIN CAENORHABDITIS ELEGANS, 514 aa.	7.5E-79	5

6702	cg42331787	384	TCATCCCGCGTG CTCCGGACACAA TTC/ACTTTTGC GCAGTGGATGC CTGCAA	A	Arg	Ser (8873)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75951 LYSOZYME HOMOLOG - HOMO SAPIENS (HUMAN), 148 aa.	7.5E-78	17
6703	cg44936941	897	TTAAGATAATATA TACATGTACACAC A/GTCTTCCATC TCCATTTGGATT ATCA	G	Cys	Arg (8874)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa.	7E-77	1
6704	cg42462901	430	ACTTTATTGGGG AACTGTGGAAT TT/CJTTCAGGCA ACTCAATAAAT GGTG	C	Lys	Glu (8875)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BA83043 KIAA1091 PROTEIN - HOMO SAPIENS (HUMAN), 1359 aa (fragment).	1.4E-75	
6705	cg43989639	955	ATGCCAGACCCC ACTCTGCAGTAA G/GCJTGTTCAC AACAGAAATGC ACAAA	C	Pro	Ala (8876)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME I - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
6706	cg38276737	336	AGACCTCAATGA CAAGAGTGTGCA GT/CJGTGCCCT GGACTTTGCCAT CAGCGA	C	Cys	Arg (8877)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P28325 CYSTATIN D PRECURSOR - Homo sapiens (Human), 142 aa.	3.1E-74	
6707	cg44004729	520	AGTTTCTCGGC CACGAGGCCCT GG/GAJTAACTCT AGACTGATACCT CCTCAT	A	Thr	Ile (8878)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P22749 NKG5 PROTEIN PRECURSOR (LYMPHOKINE LAG-2) (T- CELL ACTIVATION PROTEIN 519) - Homo sapiens (Human), 145 aa.	1.7E-73	
6708	cg43933021	621	ACAGCTATCAAA CTTCTACCACT CT/CJCTGCTGGT CGACGTCGGCG TCTGGC	C	Arg	Gly (8879)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38506 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa.	2.8E-73	13

6709	cg43932428	597	GCTCGATTTC CAAGCACCTGGT TTA/CJTGGGTAT GGCCCGTCCGC TCTCAT	A	C	Asn (8880)	Lys (8880)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60869 EDF-1 PROTEIN - HOMO SAPIENS (HUMAN), 148 aa.	2.5E-72	
6710	cg42691635	483	TAGAGAGAGTTG ACGGTGTCTCG TTT/CJGGGTGG TCGTTGCTGATT TTGAAA	T	C	Gln (8881)	Arg (8881)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16378 PHL E1F1 - HOMO SAPIENS (HUMAN), 134 aa.	1.8E-71	12
6711	cg43271682	339	GGGGCGGACA GGCCCGGCTGC TGG[G/CJGGCTC CCGGAGCTCTC GGGGGGCGG	G	C	Pro (8882)	Arg (8882)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15726 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
6712	cg43917616	146	TTGGCAACTTTT GATGCATTTTC G[A/G]TTTTGGTT CCCAGAGGGCA TTTTTT	A	G	Ser (8883)	Pro (8883)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q13901 C1D DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 141 aa.	6.9E-70	
6713	cg43942922	229	TGAGCCCACTC TCAGGCCCACTAG G[G/A]GCAGAAC AAATAGGTCCTG TGTCAA	G	A	Gly (8884)	Ser (8884)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
6714	cg43942922	265	TAGGTCCTCTGT CAAGACCCCTGA A[A/C]CAGTTGTC CCCACAGCCCT GAGCT	A	C	Thr (8885)	Pro (8885)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
6715	cg43942922	362	TCTCAGGCCACT AGGGGAAGAAA A[A/G]TAGGTCCT CTGTCAAGACCC CTGAA	A	G	Asn (8886)	Ser (8886)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	

6716	cg43942922	407	CCTGAAACAGTT GTGCCACAGC CC[C/T]TGAGCTC CAGCCTTCCACC TCCACA	C	T	Pro	Leu (8887)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
6717	cg43942922	437	CTCCAGCCTTCC ACCTCCACAGAC C[A/G]ACCTGTCA CCTCTGAACCCA CATCT	A	G	Gln	Arg (8888)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14676 KIAA0170 PROTEIN - HOMO SAPIENS (HUMAN), 2089 aa.	2.3E-68	
6718	cg41400057	447	CACCTGGCCTGA ATGCAGCATGGG G[G/C]TTTGGCT GGCAGCAGTGAT TGTGT	G	C	Pro	Ala (8889)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P49901 SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS) - Homo sapiens (Human), 116 aa.	2.7E-68	9
6719	cg43955219	980	GGATCCTCAAAA CTCAGAACGTGG C[C/T]GGGCGTG GTGGCTCAGCG CTGTAAT	C	T	Arg	Trp (8890)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P39194 IIII ALU SUBFAMILY SQ WARNING ENTRY IIII - Homo sapiens (Human), 593 aa.	6.4E-68	
6720	cg42831353	787	TGCACCGCGGC GGTGGTGAGGA CAC[A/G]GGCTG CGGTGTAAGCCC GCGTCACC	A	G	Cys	Arg (8891)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa.	1.3E-67	22
6721	cg43927424	353	TCCCTGTCTGCA AGTCGGGCAGG AA[C/T]AGAAACA CACCTACCTGCC ACTAGA	C	T	Gln	End (8892)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O77503 TRANSLATION INITIATION FACTOR EIF2C - ORYCTOLAGUS CUNICULUS (RABBIT), 813 aa.	1.9E-65	
6722	cg42381630	244	GAGTTGCGGAG GAAGATCGACCT ATT[C/A]TTGGCC TAGACCAAGGCG CTATGT	T	C	Tyr	His (8893)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O78087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.9E-64	

6723	cg42381630	439	AGGTCAAGGC CGAAGCCTGAAG CTC/GIATAGCCA GGAACAGGGTC ACCCACA	C	G	His	Asp (8894)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:076087 GAGE-8 - HOMO SAPIENS (HUMAN), 117 aa.	5.9E-64	
6724	cg43950549	273	CTTATTGTACA TTCTTCTTGGGA AIA/TTACAGTGT TGCTGTTGCTGA TGCAA	A	T	Lys	Asn (8895)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.4E-62	
6725	cg43950549	485	CAAGAACTTCAG AATGGGTCAGAA TTACJGGAAAGTG GTGATGGAACCA GCCCTG	A	C	End	Ser (8896)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	1.4E-62	
6726	cg43308257	773	GACCCTGTACCC CTGTTCAAGATC TTA/GTGTGGCG GAGCTGATCCAG CAGCTG	A	G	Tyr	Cys (8897)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q13084 MELANOMA ANTIGEN P15 - Homo sapiens (Human), 128 aa.	2.9E-62	
6727	cg42686636	719	GGTTATACCACA AGCTGTGCTTGC AIA/TJGGAGACT GAGCAAAAGGAA ATGTG	A	T	Gln	His (8898)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:008904 BRAIN X-LINKED GENE (BRX PROTEIN) - MUS MUSCULUS (MOUSE), 216 aa (fragment).	4.4E-59	
6728	cg42566513	351	TTCTACCCTGAG TGCGAGATAAGA AIC/TJGATGGGT GGAAGAGAGCA ACGCCAG	C	T	Thr	Met (8899)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:070576 NUCLEAR PROTEIN SA3 - MUS MUSCULUS (MOUSE), 1240 aa.	9.6E-59	
6729	cg43930685	1007	CAGCGATTCTTT TTTTGTTTCGGTT TTA/TJTTCAAGAGA CTTGCTTTGCTC TTCA	T	A	Lys	End (8900)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:076080 ZINC-FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa.	4E-58	



6730	cg43930685	821	GGAGTTCAAATC TTTTGGATCTTTT [C/T]ACCAACAAC TACTGGATTTTC TTTT	C	T	Glu	Lys (8901)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76080 ZINC FINGER PROTEIN 216 - HOMO SAPIENS (HUMAN), 213 aa.	4E-58	
6731	cg40968986	251	TGTGCAGATGAA GGCCAGTGAGC TG[G/A]JAGCAGG AGCAAGAGAGA GAGGGCTC	G	A	Glu	Lys (8902)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.1E-58	11 (11p15.2)
6732	cg40968986	267	AGTGAGCTGGA GCAGGAGCAAG AGA[G/C]JAGAGG GCTCCAGAAATCA TTGCCCAG	G	C	Arg	Thr (8903)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.1E-58	11 (11p15.2)
6733	cg40968986	372	AGCAGATCAGG GGGTGTGGTGA AGA[A/G]CAACTT TGTGCCACCAAC TGTGGGT	A	G	Asn	Ser (8904)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P06881 CALCITONIN GENE- RELATED PEPTIDE I PRECURSOR (CGRP-I) (ALPHA-TYPE CGRP) - Homo sapiens (Human), 128 aa.	5.1E-58	11 (11p15.2)
6734	cg43934461	766	TCGGGGACCCC AAGAGAATTCAT AT[G/T]CTGGTGG ATTGGTGTGAGG CAQCCG	G	T	Ala	Glu (8905)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD3392 BREAST CANCER ASSOCIATED GENE 1 PROTEIN - HOMO SAPIENS (HUMAN), 606 aa.	8.8E-57	3
6735	cg43968980	1126	TGCTTCCCTTGA CTGAAGAATAAA C[A/C]TTCCTCCT ACACCTTCATAC ATGTT	A	C	Met	Arg (8906)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60925 PREFOLDIN SUBUNIT 1 - HOMO SAPIENS (HUMAN), 122 aa.	2.5E-56	5
6736	cg44011808	554	AACCACATGAGT CCGCTGAAGAAC T[C/T]GCTCTGGA ACACCTGGGATC TGGTC	C	T	Glu	Lys (8907)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O85178 NADH-UBIQUINONE OXIDOREDUCTASE AGGG SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-AGGG) (CI-AGGG) - Homo sapiens (Human), 105 aa.	2.5E-56	

6737	cg43916991	120	GACATCTGGCCAC GGTCCATCTCTG A/C/TJCGGCTCCT GGTCAACCCCA GGGAG	T	Thr	Ile (8908)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33400 CARBOXY TERMINUS OF HSP70-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	3E-55	16
6738	cg43916991	74	AATGTGGGAAGT TGTGGATGTTAG CT/GICTGAGATT GGGGTGTGGTC AGACAT	G	Ser	Ala (8909)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33400 CARBOXY TERMINUS OF HSP70-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	3E-55	16
6739	cg39895368	203	CGGGATGGCTTA CATTGATATCAT C/A/GJTACGTAG GTCCTTCATCA GATGTC	G	Met	Thr (8910)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33910 HYPOTHETICAL 21.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 190 aa.	1.7E-50	X
6740	cg40357240	240	ACGGATGTCCT CGGCCAGTGCT GA/A/GJGGGAC TGACTGGGGATA CAGCTTT	G	Leu	Pro (8911)	NON- CONSER VATIVE	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45741 HYPOTHETICAL 112.7 KD PROTEIN - HOMO SAPIENS (HUMAN), 1008 aa (fragment).	5.4E-50	
6741	cg44917490	1621	GGGACCGTTTCC TCTTCCTCTTCA G/C/gap]CTGCGG AGGCTCCACGAA GTAATCA	gap	Ala	Leu (8912)	FRAMES HIFT	amyloid	Human Gene SWISSPROT-ID:P51693 AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP) - HOMO SAPIENS (HUMAN), 650 aa.	0	19
6742	cg44917490	873	GGGGGTGTCAT CCTTGGAATCTG GA[G/gap]GCTGC AGCCACCCCTTG TCCTCGCT	gap	Pro	Leu (8913)	FRAMES HIFT	amyloid	Human Gene SWISSPROT-ID:P51693 AMYLOID-LIKE PROTEIN 1 PRECURSOR (APLP) - HOMO SAPIENS (HUMAN), 650 aa.	0	19
6743	cg42663825	2303	GACAAAACACTG TTTGTTGGGTTTA C[C/gap]GCCCCC TGCAGATCGCCT TGCCATC	gap	Pro	Arg (8914)	FRAMES HIFT	ATPase_ associate d	Human Gene TREMBLNEW- ID:G2406580 NUCLEAR VCP-LIKE PROTEIN NVLP.1 - HOMO SAPIENS (HUMAN), 750 aa.	0	1

6744	cg43987714	2730	TGGTTACGTTTG ATGAGGAGCTGC G[G/gap]CCATTG CCAGTGTCTGTC CGTGTGG	G	gap	Pro	His (8915)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.lpcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909.aa	0	3
6745	cg43987714	2785	GGCAGTGGATGT GGTGGGCCAGG CT[G/gap]GCAAG CCGAAGACTATC ACAGGGTT	G	gap	Gly	Ala (8916)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.lpcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909.aa	0	3
6746	cg43987714	2786	GCAGTGGATGTG GTGGGCCAGGC TG[G/gap]CAAGC CGAAGACTATCA CAGGGTTC	G	gap	Gly	Ala (8917)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.lpcis:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909.aa	0	3

6747	cg43987714	2914	CCCCATTCTGGA AGGTTTTGTTAT C[G/gap]TTCGGA AGAACCCCAATT ATGATCT	gap	Leu	Phe (8918)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSNEW-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.pcls:SWISSPROT-ID:Q13200 26S PROTEASOME REGULATORY SUBUNIT S2 (P97) (TUMOR NECROSIS FACTOR TYPE 1 RECEPTOR ASSOCIATED PROTEIN 2) (55.11 PROTEIN) - HOMO SAPIENS (HUMAN), 909 aa.	0	3
6748	cg43277632	1676	GCAAATATCGGT GTCCTTTGGCCGA A[G/gap]GGACTG CAACAGTTCCTT ATAATCC	gap	Gly	Gly (8919)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSPROT-ID:P35670 COPPER-TRANSPORTING ATPASE 2 (EC 3.6.1.36) (COPPER PUMP 2) (WILSON DISEASE-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 1465 aa.	0	13 (13q14.3)
6749	cg43933946	1781	AGCCAAATCCCA GAGTGCTGGTG GG[G/gap]CCAGG CCAGTGTCAGAT TCITTAAT	gap	Ala	Ala (8920)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSPROT-ID:P35998 26S PROTEASE REGULATORY SUBUNIT 7 (MSS1 PROTEIN) - HOMO SAPIENS (HUMAN), 433 aa.	5.2E-231	7
6750	cg43958825	343	GGATCTGCATGA TTCGTGGCCCGG GC[G/gap]TCCTC ATTGGGCATCGG GAACCTCTA	gap	Glu	Glu (8921)	FRAMES HIFT	ATPase_ associate d	Human Gene SPTRMBL-ID:P97638 SPERMATOGENIC CELL/SPERM- ASSOCIATED TAT-BINDING PROTEIN HOMOLOG SATA - RATTUS NORVEGICUS (RAT), 442 aa.	7.8E-228	11
6751	cg43933600	1192	TGCCCCCGACG AAGATCCACTTC AG[G/gap]CTGCG CTGCTCGATGAT GTTGCTAA	gap	Ser	Ser (8922)	FRAMES HIFT	ATPase_ associate d	Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa.	4E-185	19
6752	cg43933600	348	CGCACCTCATGG GGTAACAGCGG CA[G/gap]CTTCA CGATGTGGAAGT CTTCATAC	gap	Leu	Cys (8923)	FRAMES HIFT	ATPase_ associate d	Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa.	4E-185	19

6753	cg43933600	556	CATACAGGGACA GGAAGCTCAGCAA T[G/gap]CATACG CAGATGAAAGTT GTCCTGCT	gap	Cys	End (8924)	FRAMES HIFT	ATPase_ associate d	Human Gene TREMBLNEW- ID:G2745900 ARSENITE- TRANSLOCATING ATPASE - MUS MUSCULUS (MOUSE), 350 aa.	4E-185	19
6754	cg43916747	1057	GAATCCGGGGC ACCAGCTACCAG AG[C/gap]CCTCA CGGCATCCCCAT AGACCTGC	gap	Pro	Leu (8925)	FRAMES HIFT	ATPase_ associate d	Human Gene SPTRMBL-ID:Q12464 CHROMOSOME XVI READING FRAME ORF YPL235W - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 471 aa.	4E-163	19
6755	cg43947105	1581	AGAGCAAGATCA AACCCAGCTCT T[G/gap]GCGGTG CGCCCCAGGAAT TCTCCGG	gap	Ala	Ala (8926)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.6E-152	
6756	cg43947105	1582	GAGCAAGATCAA ACCCAGCTCTT G[G/gap]CGGTGC GCCCCAGGAATT CTCCGGT	gap	Ala	Ala (8927)	FRAMES HIFT	ATPase_ associate d	Human Gene SWISSPROT-ID:P54709 SODIUM/POTASSIUM-TRANSPORTING ATPASE BETA-3 CHAIN (EC 3.6.1.37) (SODIUM/POTASSIUM-DEPENDENT ATPASE) (ATPB-3) - HOMO SAPIENS (HUMAN), 279 aa.	4.6E-152	
6757	cg43927442	1437	CACAGCAAATTT GTTCTCTAGGGG G[G/gap]ACCACT TCACAAAAGTAG CTGCGCG	gap	Ser	Ser (8928)	FRAMES HIFT	ATPase_ associate d	Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.   pcls: SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.	6.4E-146	17

6758	cg43927442	653	TCACTCAGCTTC ACATTATCCGGA G[G/gap]CCCTGG ATGGAAGACTCG AGGGTCT	gap	Gly	Gly	(8929)	FRAMES HIFT	ATPase_ associate d	Human Gene Homologous to SWISSNEW-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.pcls:SWISSPROT-ID:O15143 ARP2/3 COMPLEX 41 KD SUBUNIT (P41-ARC) - HOMO SAPIENS (HUMAN), 372 aa.	6.4E-146	17
6759	cg43967912	1267	AGCTGCAAAACAC CCGGCCACGCA CT[gap/]GCACA TACTGCGAACTA TCACTTGA	T gap	Gln	Gln	(8930)	FRAMES HIFT	ATPase_ associate d	Human Gene Homologous to SPTREMBL-ID:Q22494 SIMILAR TOS. CEREVISIAE VACUOLAR H(+)-ATPASE 54 KD SUBUNIT - CAENORHABDITIS ELEGANS, 470 aa.	5.6E-108	8
6760	cg43304881	1413	CAGGGCCAGCT GCCGGAGGCGC TCC[C/gap/]TGGC GTCACGGTGTCT CTCGGAGGA	gap	Arg	Arg	(8931)	FRAMES HIFT	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q19335 F11A10.2 - CAENORHABDITIS ELEGANS, 610 aa.	8.7E-94	
6761	cg43132502	208	GGCACGAGGCA GGAGTTGGCGAT GC[C/gap/]ACCTG GGGTCACATTG AGTCTGGA	gap	Pro	His	(8932)	FRAMES HIFT	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.4E-58	11
6762	cg43132502	309	CAGGGAAGAAG GGGAGGCGCCA GAG[G/gap/]CAGG GCCATGCTTGGC TTCCCAGCT	gap	Ala	Gln	(8933)	FRAMES HIFT	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.4E-58	11
6763	cg43132502	346	TGGCTTCCAGC TGGCCCCAGTG CA[gap/]AGTGGG TGGCACCGCGG AGGCTGCTG	A gap	Gln	Gln	(8934)	FRAMES HIFT	ATPase_ associate d	Human Gene Similar to SPTREMBL- ID:Q15332 GAMMA SUBUNIT OF SODIUM POTASSIUM ATPASE LIKE - HOMO SAPIENS (HUMAN), 126 aa.	9.4E-58	11

6764	cg44015998	469	TGGCTGTTGAAG TCGGGCGAGGA GC[C]gap]GAGGA GCAGGCCAATGA TGGCCAGG	C	gap	Gly	Ala (8935)	FRAMES HIFT	ATPase_ associate d	Human Gene Similar to SWISSPROT- ID:P39986 PROBABLE CALCIUM- TRANSPORTING ATPASE 6 (EC 3.6.1.38) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 1215 aa.	1.5E-53	
6765	cg43918042	1862	GCTGACCCCTGC GAGTGCGCGAC GGC[ap]GJCGGA CCCGCTCGCTCC TCGCAGGCC	gap	G	Ala	Ala (8936)	FRAMES HIFT	cadherin	Human Gene TREMBLNEW- ID:G2852363 NF-PROTODCADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	0	4
6766	cg43918042	2009	ACCCCCATCCTG CAACTGCGCGCA G[C]gap]CGACTT GGACGTGGGG TCAACGGG	C	gap	Ala	Ala (8937)	FRAMES HIFT	cadherin	Human Gene TREMBLNEW- ID:G2852363 NF-PROTODCADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	0	4
6767	cg43957225	2825	TTGCTACATAGC AGGTGCCAACTG G[G]gap]TCCTTT TCTGGTGTCGGT TTAAGAG	G	gap	Asp	Asp (8938)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa.	0	10
6768	cg43957225	2832	TAGCAGGTGCCA ACTGGGTCCTTT T[ap]TCTGGTG TCGGTTTAAGAG TTCTCCA	gap	T	Glu	Glu (8939)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P53708 INTEGRIN ALPHA-8 - HOMO SAPIENS (HUMAN), 1025 aa.	0	10
6769	cg43977440	3175	GCATCACACTGC CACCGAGCCCTC T[G]gap]CCCCCT GGGCAAGGGG ACACGGAC	G	gap	Gln	Arg (8940)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P11215 CELL SURFACE GLYCOPROTEIN MAC- 1 ALPHA SUBUNIT PRECURSOR (CR-3 ALPHA CHAIN) (CD11B) (LEUKOCYTE ADHESION RECEPTOR MO1) (INTEGRIN ALPHA-M) (NEUTROPHIL ADHERENCE RECEPTOR) - HOMO SAPIENS (HUMAN), 1152 aa.	0	16 (16p11.2 )

6770	cg44026834	1087	CGGCCGCTCGC ACCGCGGCTCCT GC[C/gap]AGCTC ACTCTGAGAGAT GTGGGCCC	C	gap	Trp	Cys (8941)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
6771	cg44026834	1320	GGGGCACGTGT GGGCTCAGGTG GGT[G/gap]CCAT AGGCAGCAGCA CTGGTCGTGG	G	gap	Gly	Gly (8942)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
6772	cg44026834	1433	TGCTCAGTGTC TCGGAGACGCT GG[G/gap]CCTCT GGCTGCCCGAT GGAGAGCGT	G	gap	Pro	Pro (8943)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P16144 INTEGRIN BETA-4 SUBUNIT PRECURSOR (GP150) (CD104) - HOMO SAPIENS (HUMAN), 1875 aa.	0	17 (17q11)
6773	cg40310734	1060	CTCAACACTACA GAATATGTCGTC G[G/gap]TGCCCC CACTTGGAGCTG GACCCCTG	G	gap	Gly	Val (8944)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
6774	cg40310734	3291	CTTCTCAAGCG GAACCGGCCAC CC[C/gap]TGGAA GAAGATGATGAA GAGGGGGA	C	gap	Leu	Trp (8945)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P08514 PLATELET MEMBRANE GLYCOPROTEIN IIB PRECURSOR (GPIIB) (INTEGRIN ALPHA- IIB) (CD41) - HOMO SAPIENS (HUMAN), 1039 aa.	0	17 (17q21.3 2)
6775	cg42558238	2563	TCCTCAGAGATG CAGAGACCTCCC C[C/gap]GGACTG CGATGACACGGT CACTTAT	C	gap	Pro	Arg (8946)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa. Jpts:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1 )



6776	cg42558238	2567	AGAGATGCAGAG ACCTCCCCCGGA C[gap/C]TGCGAT GACACGGTCACT TATTCAG	gap	C	Cys	Leu (8947)	FRAMES HIFT	cadherin	Human Gene SWISSNEW-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.   pcis:SWISSPROT-ID:Q01665 B- CELL RECEPTOR CD22-BETA PRECURSOR (LEU-14) (B- LYMPHOCYTE CELL ADHESION MOLECULE) (BL-CAM) - HOMO SAPIENS (HUMAN), 847 aa.	0	19 (19q13.1)
6777	cg43303099	1216	TCTTGCACAGGA ACAGTAGCGTCC A[G/gap]CTGCCA GTCCTGTATGGT CCCCAAA	G	gap	Leu	Cys (8948)	FRAMES HIFT	cadherin	Human Gene SWISSPROT-ID:P32942 INTERCELLULAR ADHESION MOLECULE-3 PRECURSOR (ICAM-3) (CDW50) (CD50 ANTIGEN) (ICAM-R) - HOMO SAPIENS (HUMAN), 547 aa.	8.7E-158	19 (19p13.3)
6778	cg42528468	283	TGCTCCTGCCTG GGAACAACCGG AA[G/gap]GTGTA TGAACGTAGCAA TGTGCAAG	G	gap	Val	Cys (8949)	FRAMES HIFT	cadherin	Human Gene Similar to SWISSPROT- ID:P05362 INTERCELLULAR ADHESION MOLECULE-1 PRECURSOR (ICAM-1) (MAJOR GROUP RHINOVIRUS RECEPTOR) (CD54) - HOMO SAPIENS (HUMAN), 532 aa.	8.4E-78	19 (19p13.3)
6779	cg43976467	882	TGGTGGTCAACA TAAGTGACCTGG G[G/gap]TACCCT AAGTCTTTGCAC ACGCTTG	G	gap	Tyr	Thr (8950)	FRAMES HIFT	cadherin	Human Gene Similar to TREMBLNEW- ID:G2852363 NF-PROTODADHERIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 1035 aa.	1.2E-64	13
6780	cg43307361	1212	CACAGGCACTAG GGAAGGCGGCT GC[C/gap]ACATA GCGCCTTCTTCC CTGCAGGG	C	gap	Val	Val (8951)	FRAMES HIFT	carboxylase	Human Gene SWISSPROT-ID:Q16822 PHOSPHOENOLPYRUVATE CARBOXYKINASE, MITOCHONDRIAL PRECURSOR (GTP) (EC 4.1.1.32) (PHOSPHOENOLPYRUVATE CARBOXYLASE) (PEPCK-M) - HOMO SAPIENS (HUMAN), 640 aa.	0	14

6781	cg43264626	637	CATCTTGGGAA GCTGGCCAGGT G[G/gap]CAATGC CACAGGCGTTGT TCTTATT	G	gap	Ala (8952)	Ala	FRAMES HIFT	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.1E-183	1
6782	cg43264626	642	TGGGAAGCTG GCCAGGTGGC AAT[G/gap]CCAC AGCGTTGTTCT TATTTCGAG	G	gap	Gly (8953)	Gly	FRAMES HIFT	cathepsin	Human Gene SWISSPROT-ID:P43235 CATHEPSIN K PRECURSOR (EC 3.4.22.38) (CATHEPSIN O) (CATHEPSIN X) (CATHEPSIN O2) - HOMO SAPIENS (HUMAN), 329 aa.	4.1E-183	1
6783	cg42094324	596	AGATGTTGTGAA GGTCCTGGCC TG[C/gap]CCACC CAGGAGCCAGC ACTGGGGAC	C	gap	Pro (8954)	Pro	FRAMES HIFT	cathepsin	Human Gene Homologous to SWISSPROT-ID:P20151 GLANDULAR KALLIKREIN 2 PRECURSOR (EC 3.4.21.35) (TISSUE KALLIKREIN) (PROSTATE) (HGK-1) - HOMO SAPIENS (HUMAN), 261 aa.	2.1E-147 (19q13.2)	19
6784	cg43970982	2435	GGGATAGTTGGA CAGAAGGGAGA CC[C/gap]TGGCT ACCCAGGACCA GCTGGTCCC	C	gap	Leu (8955)	Pro	FRAMES HIFT	collagen	Human Gene SWISSPROT-ID:P12111 COLLAGEN ALPHA 3(VI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 3176 aa.	0	2
6785	cg43011543	1879	TTGATGGCGTGA AACCCCCCATG C[C/gap]TACGGG GGCTAAGAAAGG CAAGAAAT	C	gap	Thr (8956)	Tyr	FRAMES HIFT	collagen	Human Gene SWISSPROT-ID:P27658 COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN) - HOMO SAPIENS (HUMAN), 744 aa.	0	
6786	cg43998782	110	ACCTGATTGTGG TGACCGACGGG CA[C/gap]CCCCCT GGAGGGCTACA AGGAACCCCT	C	gap	Thr (8957)	Thr	FRAMES HIFT	collagen	Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa.	1.5E-103	

6787	cg43998782	138	CCTGGAGGGCT ACAAGGAACCT GT[G/gap]GGGG GCTGGAGGATG CTGTGAACG	G	gap	Gly	Gly (8958)	FRAMES HIFT	collagen	Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa.	1.5E-103	
6788	cg43998782	144	GGGCTACAAGG AACCCTGTGGG GGG[G/gap]CTGG AGGATGCTGTGA ACGAGGCCA	G	gap	Leu	Trp (8959)	FRAMES HIFT	collagen	Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa.	1.5E-103	
6789	cg43998782	446	GACCCCGGCTTT GAGGGAGAACG AG[G/gap]CAAGC CGGGCTCCCA GGAGAGAAG	G	gap	Gly	Ala (8960)	FRAMES HIFT	collagen	Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa.	1.5E-103	
6790	cg43998782	66	GGAGCAGCTCCT CGTGGGGGGCT CC[C/gap]ACCTG AAGGAGATAAG TACCTGAT	C	gap	His	Thr (8961)	FRAMES HIFT	collagen	Human Gene Homologous to SWISSPROT-ID:Q04857 COLLAGEN ALPHA 1(VI) CHAIN PRECURSOR - MUS MUSCULUS (MOUSE), 1025 aa.	1.5E-103	
6791	cg439981318	3976	CCCAATGACACA GATCTCTCCTGG C[C/gap]GGCCGT CCCGGCCTGGC TTTCCCGG	C	gap	Arg	Gly (8962)	FRAMES HIFT	collagen	Human Gene Similar to SWISSPROT- ID:Q07092 COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 1603 aa.	1.3E-73	1 (1p34)
6792	cg43938820	1581	TCCTCTGGCAG CGCGAGACGAG GC[C/gap]TCGCG GTAGAAGCGGG TCACATAGC	C	gap	Glu	Glu (8963)	FRAMES HIFT	collagen	Human Gene Similar to SPTREMBL- ID:Q14040 ALPHA-1 COLLAGEN VI (AA 574-1009) - HOMO SAPIENS (HUMAN), 438 aa (fragment).	5E-59	21 (21q22.3 )

6793	cg43063256	258	TGGCATCTCCTG TCACATTGGGAA A[A/gap]TGAAGA ATTCCAGGACAT GGGCTTG	A	gap	Met	End (8964)	FRAMES HIFT	complem ent	Human Gene SWISSNEW-ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa. ID:P07358 COMPLEMENT COMPONENT C8 BETA CHAIN PRECURSOR - HOMO SAPIENS (HUMAN), 591 aa.	0 1 (1p32)
6794	cg43933757	2462	CAGACGATGTCT GAGTGTGAGGC GG[G/gap]CGCTC TGAGATGCAGAG GGCAGAGC	G	gap	Gly	Ala (8965)	FRAMES HIFT	complem ent	Human Gene SWISSPROT-ID:P10643 COMPLEMENT COMPONENT C7 PRECURSOR - HOMO SAPIENS (HUMAN), 843 aa.	0 5 (5p13)
6795	cg43029289	1158	CCTATTACTGTG ATGAACATTTTG A[gap/A]GACTCC GTCAGGAAGTTA CTGGGAT	gap	A	Glu	Glu (8966)	FRAMES HIFT	complem ent	Human Gene SPTREMBL-ID:Q14570 COMPLEMENT FACTOR H PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	6.4E-265
6796	cg21644442	1562	TAACCTCCGTTCC TTTGACTGACAC A[G/gap]GCCATG AGAGGCAGTCC GAGGGATC	G	gap	Gly	Ala (8967)	FRAMES HIFT	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	5E-304 1 (1p21)
6797	cg21644442	1563	AACTCCGTTCTT TTGACTGACACA G[G/gap]CCATGA GAGGCAGTCCG AGGGATCC	G	gap	Gly	Ala (8968)	FRAMES HIFT	csf	Human Gene SWISSPROT-ID:P09603 MACROPHAGE COLONY STIMULATING FACTOR-1 PRECURSOR (CSF-1) (MCSF) - HOMO SAPIENS (HUMAN), 554 aa.	5E-304 1 (1p21)
6798	cg43920512	779	CCTTAGGGAAT GGAGGTTAAATG TT[A/gap]AACCTAA AGTGGGTTACAT GAAGAA	A	gap	Lys	Asn (8969)	FRAMES HIFT	cyclin	Human Gene SWISSPROT-ID:P20248 G2/MITOTIC-SPECIFIC CYCLIN A - HOMO SAPIENS (HUMAN), 432 aa.	4.1E-231 4 (4q27)

6799	cg43998855	4913	CAGGGCCTGGT GGATGGCGCGC TCG[C/gap]CATT CAGCACCACTAT GGGCGAGCT	C	gap	Gly	Ala (8970)	FRAMES HIFT	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.2E-293	2 (2p22)
6800	cg43998855	4941	TCAGCACCACTA TGGGGCAGCTG CC[gap]CJAGGCG GATCTGGAAAC GTCGCCGT	gap	C	Gly	Gly (8971)	FRAMES HIFT	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.2E-293	2 (2p22)
6801	cg43998855	5050	TCCGATCAGTGG CCACGCAACG GG[C/gap]CCGGG GGCGCGGACCG GAGCTGCCG	C	gap	Gly	Ala (8972)	FRAMES HIFT	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.2E-293	2 (2p22)
6802	cg43998855	5205	GGTCGTCGGG CTGAGGCTGGT GCC[C/gap]ATGC TGCGGGGAGGT GCGGTTTCCA	C	gap	Met	Met (8973)	FRAMES HIFT	cyto450	Human Gene SPTREMBL-ID:Q93089 DIOXIN-INDUCIBLE CYTOCHROME P450 (EC 1.14.14.1) - HOMO SAPIENS (HUMAN), 543 aa.	3.2E-293	2 (2p22)
6803	cg43316849	1727	CAAGGAAGGGC AGGCGCCAGGG CCC[C/gap]GGCG GGTAGTTCTTTG GGCGCCGTC	C	gap	Pro	Pro (8974)	FRAMES HIFT	cyto450	Human Gene SWISSNEW-ID:P51589 CYTOCHROME P450 2J2 (EC 1.14.14.1) (CYP1J2) (ARACHIDONIC ACID EPOXYGENASE) - HOMO SAPIENS (HUMAN), 502 aa.   pdis:SWISSPROT- ID:P51589 CYTOCHROME P450 1J2 (EC 1.14.14.1) (ARACHIDONIC ACID EPOXYGENASE) - HOMO SAPIENS (HUMAN), 502 aa.	7.2E-257	1 (1p31.3)
6804	cg439988704	905	CGCTGTCTCCTC TCCACAGATGTA G[G/gap]CCCCAG CCCCGCGCACC ACAAACAC	G	gap	Ala	Ala (8975)	FRAMES HIFT	cytochrome	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11

6805	cg43966704	134	GGTGGTGGGCT AAGAGGCAGCCT GC[C/gap]GGGCC TGATGCTGCTGG GCAAACCG	C	gap	Arg (8976)	FRAMES HIFT	cytochro me	Human Gene SPTREMBL-ID:Q43840 NADH DEHYDROGENASE (EC 1.6.99.3) (CYTOCHROME C REDUCTASE) (TYPE I DEHYDROGENASE) - SOLANUM TUBEROSUM (POTATO), 487 aa.	5.8E-184	11
6806	cg42717303	320	GGGGATTGAGC GTAGAATGGCGT AT[G/gap]CAAAT AGGAAATATCAT TCGGGTTT	G	gap	Ala	FRAMES HIFT	cytochro me	Human Gene SWISSPROT-ID:P00158 CYTOCHROME B (EC 1.10.2.2) - MUS MUSCULUS (MOUSE), 381 aa.	1.4E-175	
6807	cg43935752	1098	GCCCCAGTGAC CATGAAGAGTGA GG[gap]GICTGCA GCCAGGGAATA GTCCATCGC	gap	G	Ser (8978)	FRAMES HIFT	cytochro me	Human Gene Similar to SWISSNEW- ID:O14521 SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE- UBIQUINONE REDUCTASE MEMBRANE ANCHOR SUBUNIT) - HOMO SAPIENS (HUMAN), 159 aa.	4E-82	11
6808	cg43935752	1238	TGGAGCCAGAAT GGTGGCTCGGT GA[C/gap]AAGTG TATGTGCTGCAC TCCACACC	C	gap	Phe (8979)	FRAMES HIFT	cytochro me	Human Gene Similar to SWISSNEW- ID:O14521 SUCCINATE DEHYDROGENASE [UBIQUINONE] CYTOCHROME B SMALL SUBUNIT PRECURSOR (CYBS) (SUCCINATE- UBIQUINONE REDUCTASE MEMBRANE ANCHOR SUBUNIT) - HOMO SAPIENS (HUMAN), 159 aa.	4E-82	11
6809	cg43962888	502	CCATACAATGTA CTGGCCCCAAAG G[G/gap]AGCTTC AGGCACACAGG AAGACCCCT	G	gap	Gly (8980)	FRAMES HIFT	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)
6810	cg43962888	627	GTTTGGCTGCA CAAAGCGAGG CC[C/gap]AGCGA TGCCCCCGCTGT GGAGCCCCA	C	gap	Gln (8981)	FRAMES HIFT	cytochro me	Human Gene Similar to SWISSPROT- ID:P10606 CYTOCHROME C OXIDASE POLYPEPTIDE VB PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 129 aa.	5.1E-66	2 (2cen)

6811	cg43941766	557	GCCATGGGCGC CACTCGACATAG GC[C/gap]GCCCC AGCTGTGGGCG GGACCGACC	C	gap	Arg (8982)	Arg (8982)	FRAMES HIFT	cytochrome	Human Gene Similar to TREMBLNEW- ID:E1248288 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) - HOMO SAPIENS (HUMAN), 109 aa.	1.5E-57	6
6812	cg43955586	144	TCTTCTGGTCA AAATGGCTGGTA A[G/gap]CAGGCC GTTTCAGCATCA GGCAAGT	G	gap	Gln (8983)	Arg (8983)	FRAMES HIFT	cytochrome	Human Gene Similar to SWISSPROT- ID:P14927 UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD PROTEIN (EC 1.10.2.2) (COMPLEX III SUBUNIT VI) - HOMO SAPIENS (HUMAN), 110 aa.	5.2E-57	8
6813	cg43923430	2583	GCCACTGTTCCA CTGCAGACCAG GA[G/gap]CCATC GGCCACACAC CGCTCAGCA	G	gap	Leu (8984)	Ser (8984)	FRAMES HIFT	cytochrome	Human Gene Similar to SWISSPROT- ID:P40086 CYTOCHROME C OXIDASE ASSEMBLY PROTEIN COX15 - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 486 aa.	3.7E-54	10
6814	cg42719440	383	TTGAGCATGCTC ACTCCACCCCG G[G/gap]CAGCGC CACGAAGTAGGT GAGGGCC	G	gap	Pro (8985)	Pro (8985)	FRAMES HIFT	cytochrome	Human Gene Similar to SWISSNEW- ID:P43024 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) - MUS MUSCULUS (MOUSE), 111 aa. lpcds:SWISSPROT-ID:P43024 CYTOCHROME C OXIDASE POLYPEPTIDE VIA-LIVER PRECURSOR (EC 1.9.3.1) - MUS MUSCULUS (MOUSE), 111 aa.	1.3E-51	
6815	cg43967318	1787	GACCAAAGGCC CCCAGCTCCTTG AG[G/gap]CCCTG CCAAGTGGTCTC CTCCACCA	G	gap	Gly (8986)	Gly (8986)	FRAMES HIFT	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0 (17p11.2)	17
6816	cg43967318	336	CTGCCAGGGGT CAGACTGCAGG GCG[G/gap]CCAT GCCCTCTCGGAT CCGAGCTGC	G	gap	Ala (8987)	Ala (8987)	FRAMES HIFT	dehydrogenase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0 (17p11.2)	17

6817	cg43967318	417	TTTCTCATGCTG GGCCGTGGGT GG[C/gap]CCTCA CTCAGGGATCTT GAGGCCCT	C	gap	Gly	Ala (8988)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
6818	cg43967318	419	TCTCATGCTGGG CCGTGGGTGG CC[C/gap]TCACT CAGGGATCTTGA GGCCCTCG	C	gap	Glu	Glu (8989)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P49748 ACYL-COA DEHYDROGENASE, VERY- LONG-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.-) (VLCAD) - HOMO SAPIENS (HUMAN), 655 aa.	0	17 (17p11.2)
6819	cg44028421	390	TCGAAGGTCAC TCTTGACCCGC A[G/gap]GTACTC GTTACAGAGCCGC CTCTCCT	G	gap	Leu	Cys (8990)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P28037 10-FORMYLTETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.6) (FBP- C) - RATTUS NORVEGICUS (RAT), 902 aa.	0	
6820	cg44028421	391	CGAAGGTCAC TCTTGACCCGCA G[G/gap]TACTCG TTCAGAGCCGC TCTCCTA	G	gap	Tyr	Tyr (8991)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P28037 10-FORMYLTETRAHYDROFOLATE DEHYDROGENASE (EC 1.5.1.6) (FBP- C) - RATTUS NORVEGICUS (RAT), 902 aa.	0	
6821	cg43962405	1134	ATGGGAAGACGA TTGAGGCTGAGG C[C/gap]GCTCAT GGACCCGTCAC CCGCCACT	C	gap	Ala	Leu (8992)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P48735 ISOCITRATE DEHYDROGENASE (NADP), MITOCHONDRIAL PRECURSOR (EC 1.1.1.42) (OXALOSUCCINATE DECARBOXYLASE) (IDH) (NADP+- SPECIFIC ICDH) (IDP) (ICD-M) - HOMO SAPIENS (HUMAN), 452 aa.	8.2E-249	15 (15q26.1)
6822	cg43255016	1088	ATTAGGATTTTA GCCAGTAGTTTTT G/gap]GGTCAAG CCCTAACCTGAT TCCAAG	G	gap	Pro	Gln (8993)	FRAMES HIFT	dehydrog enase	Human Gene SWISSPROT-ID:P29266 3- HYDROXYISOBUTYRATE DEHYDROGENASE PRECURSOR (EC 1.1.1.31) (HIBADH) - RATTUS NORVEGICUS (RAT), 346 aa (fragment).	3.4E-156	



6823	cg43969759	949	GCAGCAACACCT ATGATGGCTGTG G[Gap]CTTCAC CAGCCTCACCAC CTCCTCC	G	gap	Pro (8994)	FRAMES HIFT	dehydrog enase	Human Gene Homologous to SPTREMBL-ID:Q16797 NADP- DEPENDENT MALIC ENZYME (EC 1.1.1.40) (MALATE DEHYDROGENASE (OXALOACETATE DECARBOXYLATING) (NADP+)) (PYRUVIC-MALIC CARBOXYLASE) - HOMO SAPIENS (HUMAN), 572 aa.	1.8E-109	11
6824	cg44000219	741	GCACTGCCTGCC CTACTCCGCAA G[Gap]GCGCAGG GCCACGAGCTG GGCGCCAC	gap	G	Ala (8995)	FRAMES HIFT	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q64644 CHOLINE DEHYDROGENASE (EC 1.1.99.1) - RATTUS NORVEGICUS (RAT), 441 aa (fragment).	3.3E-93	
6825	cg42717162	370	GCCCTATCCATA AACTAGGCCTC G[C/gap]CCCAT CCACTTCTGATT ACCAGAA	C	gap	Ala (8996)	FRAMES HIFT	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q34799 NADH DEHYDROGENASE SUBUNIT 2 (ND2) - SYMPHALANGUS SYNDACTYLUS (SIAMANG), 347 aa.	1.3E-90	
6826	cg42717162	373	CTATCCATAAAA CTAGGCCTCGCC C[C/gap]ATTCCA CTTCTGATTACC AGAAAGTA	C	gap	Pro (8997)	FRAMES HIFT	dehydrog enase	Human Gene Similar to SPTREMBL- ID:Q34799 NADH DEHYDROGENASE SUBUNIT 2 (ND2) - SYMPHALANGUS SYNDACTYLUS (SIAMANG), 347 aa.	1.3E-90	
6827	cg43248620	2674	CTTTTTTTTGGG AGGAGAAAGGG G[Gap]TTTTTTTG GGACAGCTGAA GGCGGGCG	gap	T	Thr (8998)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q14550 ZINC-FINGER DNA-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 1482 aa.	0	1
6828	cg42175288	1619	GAGGTACGGA GGAGATCGAGG AGG[G/gap]TTAT GGAGGAGATCG AGGAGGCTAT	G	gap	Tyr (8999)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0	17

6829	cg42175288	1813	AGGTGGGGACG GAGAGACCGAG GTG[G/gap]CTAT GGAGGCAAAATG GGAGGAAGA	G	gap	Gly	Ala (9000)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q92804 PUTATIVE RNA BINDING PROTEIN RBP56 - HOMO SAPIENS (HUMAN), 592 aa.	0	17
6830	cg43962927	1470	GGCACTGGCTG GAGAGGGGCTG GGC[C/gap]ACCG GTCCCTGCTGG GGGTCCCAGG	C	gap	Gly	Ala (9001)	FRAMES HIFT	dna_ma_ bind	Human Gene SWISSPROT-ID:P38935 DNA-BINDING PROTEIN SMUBP-2 (GLIAL FACTOR-1) (GF-1) - HOMO SAPIENS (HUMAN), 993 aa.	0	11 (11q13.2 )
6831	cg44005808	816	CAACCACAGATG GCACCTGCCAACA G[C/gap]AGATGG CCCATACCTTCA AATATTA	C	gap	Ala	Glu (9002)	FRAMES HIFT	dna_ma_ bind	Human Gene SWISSNEW-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (DNA-BINDING FACTOR KBF1) (EBP- 1) [CONTAINS: NUCLEAR FACTOR NF-KAPPA-B P50 SUBUNIT] - HOMO SAPIENS (HUMAN), 969 aa.lpcis:SWISSPROT-ID:P19838 NUCLEAR FACTOR NF-KAPPA-B P105 SUBUNIT (CONTAINS: NUCLEAR FACTOR NF- KAPPA-B P50 SUBUNIT) (DNA-BINDING FACTOR KBF1) (EBP-1) HOMO SAPIENS (HUMAN), 969 aa.	0	
6832	cg43931615	2554	CAGGTCTCTGTTT GGTTGTTTTCCA TT[G/gap]GGAGAC CCAACACTATTA AATCGGA	G	gap	Pro	His (9003)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q13148 TAR DNA-BINDING PROTEIN-43 - HOMO SAPIENS (HUMAN), 414 aa.	4.3E-227	20
6833	cg43956159	1718	CACCTCTCTCCT GCCGTCGGGG AG[G/gap]CATCG CCATTTCCTTG TCACCTGG	G	gap	Ala	Ala (9004)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.4E-159	10

6834	cg43956159	1725	CTCCTGCCGTCG GGGGAGGCATC GC[C/gap]ATTC CCTTGTCACCTG GCTTCCCC	C	gap	Gly	Ala (9005)	FRAMES HIFT	dna_ma_ bind	Human Gene SPTREMBL-ID:Q99612 DNA-BINDING PROTEIN CPBP - HOMO SAPIENS (HUMAN), 290 aa (fragment).	1.4E-159	10
6835	cg43917883	1246	ATCACCAGGGG CCCCCGCCCG GCG[G/gap]GCCC GGCGCCGCAG CGAGGAGAAG	G	gap	Gly	Gly (9006)	FRAMES HIFT	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.7E-138	1
6836	cg43917883	1247	TCACCAGGGG CCCCCGCCCG CGG[G/gap]CCCG GCGGCCGCAGC GAGGAGAAGA	G	gap	Pro	Pro (9007)	FRAMES HIFT	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.7E-138	1
6837	cg43917883	1984	GAAAAACAGCAA AGGGAACAAGTT G[A/gap]AAAAAA CATGAAAGATGC AAAAGAC	A	gap	Glu	Glu (9008)	FRAMES HIFT	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.7E-138	1
6838	cg43917883	1990	AGCAAAGGGAAC AAGTTGAAAAAA A[gap/A]CATGAA AGATGCAAAAGA CAAATTG	gap	A	Asn	Lys (9009)	FRAMES HIFT	dna_ma_ bind	Human Gene Homologous to SWISSPROT-ID:Q15233 54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)) - HOMO SAPIENS (HUMAN), 471 aa.	2.7E-138	1
6839	cg43947431	2147	CCACCAAGGACC GAAGTACCCTGT T[G/gap]GCGATG TCGCCCCCCATC TTATACT	G	gap	Ala	Ala (9010)	FRAMES HIFT	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q96327 PUTATIVE NUCLEAR DNA- BINDING PROTEIN G2P (ATG2) - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 392 aa.	1.2E-91	
6840	cg43947431	2148	CACCAAGGACC GAAGTACCCTGT TG[G/gap]CGATG TCGCCCCCCATC TTATACTT	G	gap	Ala	Ala (9011)	FRAMES HIFT	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q96327 PUTATIVE NUCLEAR DNA- BINDING PROTEIN G2P (ATG2) - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 392 aa.	1.2E-91	

6841	cg43940815	436	GAGAACTCTCTCC AGTGTGAGGTTT TTT/gap/ATTGTTG TAAAAAAGAAGA GTTTTG	T	gap	End	End (9012)	FRAMES HIFT	dna_ma_ bind	Human Gene Similar to SPTREMBL- ID:Q61491 DNA-BINDING PROTEIN - MUS MUSCULUS (MOUSE), 546 aa.	1E-89	6
6842	cg43269833	295	TGTGCTGGGCA GGACGAGGCTG CGG[C/gap]CCCC GGGGCAGCGT TGGGGCGGGC	C	gap	Pro	Pro (9013)	FRAMES HIFT	dna_ma_ bind	Human Gene Similar to SWISSPROT- ID:O00287 REGULATORY FACTOR X- ASSOCIATED PROTEIN (RFX DNA- BINDING COMPLEX 36 KD SUBUNIT) (RFX-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 272 aa.	6.6E-89	13
6843	cg43269833	412	ACCTGTTAGACA CTTCGGACCCTC C[G/gap]GGGGGA GGCGAGACGCG GCTAGTTT	G	gap	Gly	Gly (9014)	FRAMES HIFT	dna_ma_ bind	Human Gene Similar to SWISSPROT- ID:O00287 REGULATORY FACTOR X- ASSOCIATED PROTEIN (RFX DNA- BINDING COMPLEX 36 KD SUBUNIT) (RFX-ASSOCIATED PROTEIN) - HOMO SAPIENS (HUMAN), 272 aa.	6.6E-89	13
6844	cg43299462	971	TGAGGGTGGTCA GCGGCGTCCTG GA[gap]GJCGCCT GGTTCTGCCCG GGTCTCTGG	gap	G	Ser	Leu (9015)	FRAMES HIFT	dna_ma_ bind_inhi b	Human Gene Similar to SWISSNEW- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa. pcis:SWISSPROT- ID:Q02363 DNA-BINDING PROTEIN INHIBITOR ID-2 - HOMO SAPIENS (HUMAN), 134 aa.	9.2E-67	3 (2p25)
6845	cg43947402	594	CTTTCATGTTTG GATCAATTTTTT T[gap]GACCCAG CAGGAATGGGT GACACGC	T	gap	Ser	Ser (9016)	FRAMES HIFT	dynein	Human Gene SWISSPROT-ID:Q90828 DYNEIN LIGHT INTERMEDIATE CHAIN 1. CYTOSOLIC (LIC57/59) (DYNEIN LIGHT CHAIN A) (DLC-A) - GALLUS GALLUS (CHICKEN), 515 aa.	3.7E-214	3
6846	cg43932150	190	CGGACGTGTCG GTGCTGCAGAAG CA[C/gap]CTGCG CAACTGGTGCG GCTGCTGCT	C	gap	Leu	Cys (9017)	FRAMES HIFT	dynein	Human Gene Similar to SWISSPROT- ID:P38650 DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C) - RATTUS NORVEGICUS (RAT), 4644 aa.	1.1E-89	

6847	cg43958656	2145	TACAAAGCGGAG GACGAGGTGCA GC[G/gap]CGAGA GGGTGTCAGCC AAGAAGGCC	gap	Arg	Pro (9018)	FRAMES HIFT	eph	Human Gene SWISSPROT-ID:P08107 HEAT SHOCK 70 KD PROTEIN 1 (HSP70.1) (HSP70-1/HSP70-2) - HOMO SAPIENS (HUMAN), 641 aa.	0	6
6848	cg44017749	14201	CCAGCCAGCCCT TCCCTGGCCCC GC[G/gap]GGATG TATAAATGTAAAA ATGAAGG	gap	Arg	Gly (9019)	FRAMES HIFT	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0	12
6849	cg44017749	5045	CAACACCCAGCC CTTTGACCTGCA G[G/gap]GTGACC ACCCCTCCCGCC AGCCCAT	gap	Val	Cys (9020)	FRAMES HIFT	eph	Human Gene SWISSPROT-ID:Q07954 LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN 1 PRECURSOR (LRP) (ALPHA-2- MACROGLOBULIN RECEPTOR) (A2MR) (APOLIPOPROTEIN E RECEPTOR) (APOER) (CD91) - HOMO SAPIENS (HUMAN), 4544 aa.	0	12
6850	cg43950268	1346	AGCTGAGCCAG GCCAGGCTCGC TTG[C/gap]GCGC AGCTGATTCAGC TTCTTGATG	gap	Ala	Gln (9021)	FRAMES HIFT	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16
6851	cg43950268	1476	TGCGCAGGAAGT GGCGGGCAGCC CC[C/gap]ATCTC CAGCACGGTGA CCATGGCAG	gap	Met	Met (9022)	FRAMES HIFT	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16

6852	cg43950268	1895	GAGAGGCTGGTT AGCTGCCCGGA GG[G/gap]CAGCG CCGAGGACTCGT AGCGCAGC	G	gap	Pro	Pro (9023)	FRAMES HIFT	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16
6853	cg43950268	2239	TTTGCGGCTGTA CAGTGCAACGCT G[G/gap]AGCCCA GCTCCCGGCTCA CATCAAA	G	gap	Ser	Ser (9024)	FRAMES HIFT	eph	Human Gene TREMBLNEW- ID:G2865466 HEAT SHOCK PROTEIN 75 - HOMO SAPIENS (HUMAN), 649 aa.	0	16
6854	cg43945212	1867	AGAACATTGCG AACTGGCCGCG AG[G/gap]ATGCT CTCAGCGCGGT CGAGTGGG	G	gap	Met	Cys (9025)	FRAMES HIFT	eph	Human Gene SWISSPROT-ID:P43135 APOLIPOPROTEIN AI REGULATORY PROTEIN-1 (ARP-1) (COUP-TF II) - MUS MUSCULUS (MOUSE), 414 aa.	5.8E-232	7
6855	cg43985169	659	GCCTCAAAACAAG ATCCTCCAGTTA TTT[gap]CATGAA CTTAGAGATATCA CTTGAAG	T	gap	His	Met (9026)	FRAMES HIFT	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	
6856	cg43985169	738	AAGATTCTCGA AAAAGGCTAAAC G[gap]TCTGATG GAAGGAGTTACA GATCTGA	gap	T	Ala	Val (9027)	FRAMES HIFT	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	
6857	cg43985169	843	ACTTTTCCAAGA GAAGGAGATGAA A[gap]A[CACCAA ATAGTATCCAG CAGACAT	gap	A	Thr	Asn (9028)	FRAMES HIFT	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	
6858	cg43985169	933	AAGGGATGGATC AAATATAATTAT [A/gap]CTGCTAA AATTAGTTTACG AGAGGC	A	gap	Thr	Leu (9029)	FRAMES HIFT	eph	Human Gene Homologous to SWISSPROT-ID:P25685 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	

6859	cg43985169	968	TAGTTTACGAGA GGCATTGTGTGG C[gap/G]TGCTCA ATTAATGTACCA ACACTGG	gap	gap	Cys	Val (9030)	FRAMES HIFT	eph	Human Gene Homologous to SWISSPROT-ID:P25885 DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40) - HOMO SAPIENS (HUMAN), 340 aa.	2.4E-123	
6860	cg43918531	443	TTCACCCCAATCA GAATAGCCGATG G[C/gap]TATGAG CAGGCTGCTCG CGTTGCTA	C	gap	Tyr	Met (9031)	FRAMES HIFT	eph	Human Gene Homologous to SWISSNEW-ID:Q52500 THERMOSOME SUBUNIT (HEAT-SHOCK PROTEIN) - PYROCOCCLUS KODAKARAENSIS, 546 aa.[pcis:SWISSPROT-ID:Q52500 THERMOSOME SUBUNIT (HEAT- SHOCK PROTEIN) - PYROCOCCLUS SP. (STRAIN KOD1), 546 aa.	1E-104	5
6861	cg43949555	1550	CCCTGCTGTAAA GGACATGCTGGA A[G/gap]CTGGTA TTCTAGATACCTA CCTGGG	G	gap	Ala	Leu (9032)	FRAMES HIFT	eph	Human Gene Similar to SWISSPROT- ID:Q53546 THERMOSOME SUBUNIT (HYPERTHERMOPHILIC HEAT SHOCK PROTEIN) (HHSP) - DESULFUROCOCCLUS SP. (STRAIN SV), 545 aa.[pcis:SPTREMBL-ID:Q53546 HYPERTHERMOPHILIC HEAT SHOCK PROTEIN - UNKNOWN, 545 aa.	6.7E-80	21
6862	cg42889246	496	CTCCAGTGGACT CAGCGGCAGAG AC[G/gap]CCACC CCGAGAAAGCA AATCCCACT	G	gap	Pro	His (9033)	FRAMES HIFT	eph	Human Gene Similar to SPTREMBL- ID:Q12988 HEAT SHOCK PROTEIN 27 - HOMO SAPIENS (HUMAN), 241 aa.	7.5E-73	
6863	cg43972010	2213	ATGCCAGATGGG AGCCTCCCAGAG G[C/gap]CCAGAG CCTGTGGCCAAG GCCACTG	C	gap	Ala	Ala (9034)	FRAMES HIFT	esterase	Human Gene SWISSPROT-ID:P17405 SPHINGOMYELIN PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.12) (ACID SPHINGOMYELINASE) - HOMO SAPIENS (HUMAN), 629 aa.	0	11 (11p15.4)

6864	cg43942273	858	TGGGAGAGTGG ATAGCTCATCAA CT[G/gap]CATTG GAATCAACCAGC CAAACCTCC	G	gap	Gln	Ser (9035)	FRAMES HIFT	esterase	Human Gene SWISSPROT-ID:P23141 LIVER CARBOXYLESTERASE PRECURSOR (EC 3.1.1.1) (ACYL COENZYME A:CHOLESTEROL ACYLTRANSFERASE) (ACAT) (MONOCYTE/MACROPHAGE SERINE ESTERASE) (HMSE) - HOMO SAPIENS (HUMAN), 567 aa.	2.2e-310	16
6865	cg43328419	234	TTACCAAGCTAT ACAGCCGACAAG G[C/gap]TACCAC TTGCAGCTGCAG GCGGATG	C	gap	Tyr	Thr (9036)	FRAMES HIFT	fgf	Human Gene Homologous to SWISSPROT-ID:Q92913 FIBROBLAST GROWTH FACTOR-13 (FGF-13) (FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 2) (FHF-2) - HOMO SAPIENS (HUMAN), 245 aa.   pcds:SPTREMBL-ID:Q92913 FIBROBLAST GROWTH FACTOR HOMOLOGOUS FACTOR 2 - HOMO SAPIENS (HUMAN), 245 aa.	2.2E-119	
6866	cg43249494	602	ACAAGGGACAG GAGCGACCAGC ACA[C/gap]AGAC ACCAAATGAGGA ATGTTTGT	C	gap	Gln	Arg (9037)	FRAMES HIFT	fgf	Human Gene Similar to SWISSPROT- ID:P34004 HEPARIN-BINDING GROWTH FACTOR 1 PRECURSOR (HBGF-1) (ACIDIC FIBROBLAST GROWTH FACTOR) (AFGF) - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 155 aa.	2.3E-61	5 (5q31)
6867	cg43320667	1502	GGTATGCCAGGA ACGCCAGCCCG GG[gap/G]CTGAG GCCGCCACATCA GCAATGGA	gap	G	Pto	Pro (9038)	FRAMES HIFT	gaba	Human Gene SWISSPROT-ID:P30531 SODIUM- AND CHLORIDE- DEPENDENT GABA TRANSPORTER 1 - HOMO SAPIENS (HUMAN), 599 aa.	0	3 (3p25)
6868	cg43969076	1807	CACCCACACGAT GGCATAGGAATG G[G/gap]CACTGC CAATCCTCAGCA CCACTCT	G	gap	Ala	Ala (9039)	FRAMES HIFT	glucuronidase	Human Gene SWISSPROT-ID:P08236 BETA-GLUCURONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1) - HOMO SAPIENS (HUMAN), 651 aa.	0	7 (7q21.11)



6869	cg43286488	553	CAGGCTGGGCT GGGTAGCACAG GCT[G/gap]GCAC AGCCGCTGGGC AGGGGGCTGG	G	gap	Gln	Ser (9040)	FRAMES HIFT	glycoprot ein	Human Gene SWISSNEW-ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20- ANTIGEN) (ME20M/ME20S) (ME20- M/ME20-S) (95 KD MELANOCYTE- SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.   pcis:SWISSPROT- ID:P40967 MELANOCYTE PROTEIN PMEL 17 PRECURSOR (MELANOCYTE LINEAGE-SPECIFIC ANTIGEN GP100) (MELANOMA-ASSOCIATED ME20 ANTIGEN) (ME20M) (ME20-M / ME20-S) (95 KD MELANOCYTE-SPECIFIC SECRETED GLYCOPROTEIN) - HOMO SAPIENS (HUMAN), 661 aa.	0	12
6870	cg43065549	1570	GCTGGATGACG CGGCCTGCCTTG CC[C/gap]CAGGG TTATGATGGATG GCAGATTG	C	gap	Gln	Arg (9041)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
6871	cg43085549	1571	CTGGATGACGC GGCCTGCCCTTG CC[C/gap]AGGGT TATGATGGATGG CAGATTCT	C	gap	Gln	Arg (9042)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)
6872	cg43065549	2126	CTACAACGGTGT CCCTTGCTGCCAA G[C/gap]TCTGGA GGAAGAAGCTG CACCTCAC	C	gap	Leu	Ser (9043)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P16452 ERYTHROCYTE MEMBRANE PROTEIN BAND 4.2 (P4.2) (PALLIDIN) - HOMO SAPIENS (HUMAN), 690 aa.	0	15 (15q15)

6873	cg44034764	586	CAGGCGAGGCA GCCCCCAGGCA GTA[gap/C]AGAG CTGGTAGAAGAT GTGCAACAG	gap	C	Leu	Cys (9044)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0	7 (Xp21.2)
6874	cg44034764	586	CAGGCGAGGCA GCCCCCAGGCA GTA[gap/C]AGAG CTGGTAGAAGAT GTGCAACAG	gap	C	Leu	Cys (9045)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P23276 KELL BLOOD GROUP GLYCOPROTEIN (EC 3.4.24.-) - HOMO SAPIENS (HUMAN), 732 aa.	0	7 (Xp21.2)
6875	cg43010733	1185	TTCCTGGACCAC TTCCCGCCCGG CG[G/gap]CCCGC AGGACGGCTGG ATCGCCGAC	G gap	gap	Gly	Ala (9046)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:Q09327 BETA-1,4-MANNOSYL-GLYCOPROTEIN BETA-1,4-N-ACETYLGLUCOSAMINYL- TRANSFERASE (EC 2.4.1.144) (N- GLYCOSYL-OLIGOSACCHARIDE- GLYCOPROTEIN N- ACETYLGLUCOSAMINYLTRANSFERAS E III) (N- ACETYLGLUCOSAMINYLTRANSFERAS E III) (GNT-III) (GLCNAC-T III) - HOMO SAPIENS (HUMAN), 531 aa.	5E-304	
6876	cg43094362	168	CACTGAGGTGTC AGAAGGCAAAGC C[C/gap]ACTGCT CTACTTCATGGT CACCACCT	C gap	gap	Trp	Trp (9047)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6877	cg43094362	215	CACTCCTGTCCA GGAAGATCAGTG G[C/gap]CCCCAC GGTGACATCTGC TTCTTCT	C gap	gap	Gly	Gly (9048)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7

6878	cg43084362	219	CCTGTCCAGGAA GATCAGTGGCCC C[C/gap]ACGGTG ACATCTGCTTCT TCTGTCA	C	gap	Val	Val (9049)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6879	cg43084362	259	TCCTCTGTACACA TGCCCTGCGGTTA C[gap]A]GGGAAG CAGACGTGGAC CACTGGCT	gap	A	Arg (9050)	Leu (9050)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P21754 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3) - HOMO SAPIENS (HUMAN), 424 aa.	9.7E-230	7
6880	cg43924985	1264	TGCAAAATAACAA TCTCAGCTACTG G[G/gap]ATGCC CCCTGGGAAGTT CTTATAT	G	gap	Asp	Met (9051)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa.	1.2E-222 X (Xq24)	
6881	cg43924985	330	TGTGCTTCCGCC TCTTCCCGGTT C[G/gap]GGCTCA GGCTCGTTCTG GTCTGCC	G	gap	Gly	Ala (9052)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P13473 LYSOSOME-ASSOCIATED MEMBRANE GLYCOPROTEIN 2 PRECURSOR (LAMP-2) (CD107B ANTIGEN) - HOMO SAPIENS (HUMAN), 410 aa.	1.2E-222 X (Xq24)	
6882	cg43987514	339	ACTGGCACATGA GGGGGCCAGC TG[C/gap]CCCGA GGCCAAGGCTG CGCTGAACA	C	gap	Gly	Gly (9053)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-215	
6883	cg43987514	544	ACTGGCCAGGTC CACTTGCTGGCC G[C/gap]CTGCTG GCCCGGCTGGT ACGTTTCAT	C	gap	Gly	Ala (9054)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-215	

6884	cg43987514	833	AAGCTGGCCAG GCCAGGTCCAGT CA[G/gap]GGCCC CCAGCCCCACCCA GTCCTCCG	G	gap	Leu	End (9055)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:Q16186 110 KD CELL MEMBRANE GLYCOPROTEIN - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-215	
6885	cg43958670	2191	AGGCTTGTAAGT AGGCCTAGGAC CT[G/gap]AGGCA CTGGACGCTGG AGATTTTGT	G	gap	Ser	End (9056)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P15529 MEMBRANE COFACTOR PROTEIN PRECURSOR (CD46 ANTIGEN) (TROPHOBLAST LEUCOCYTE COMMON ANTIGEN) (TLX) - HOMO SAPIENS (HUMAN), 377 aa.	9.6E-207	1 (1q32)
6886	cg44034752	1095	TGAGAAGCTTGG TGGGGCAGAGG TT[G/gap]CAGTG ACCTGCACGGTG TTCCAAAC	G	gap	Ala	Gln (9057)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.9E-203	3 (3q27)
6887	cg44034752	1299	TCCTCCAGGACA CCAGTTGCACCG G[G/gap]CGCACT ACGACCTGCGC CACACCTT	G	gap	Ala	Arg (9058)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.9E-203	3 (3q27)
6888	cg44034752	1350	CATGGGTGTGGT CTCATTGGGGTC A[G/gap]CCTCAG GAGAAAGTGTCCG ACCCCCG	C	gap	Pro	Pro (9059)	FRAMES HIFT	glycoprot ein	Human Gene SWISSPROT-ID:P02765 ALPHA-2-HS-GLYCOPROTEIN PRECURSOR (FETUIN) (ALPHA-2-Z- GLOBULIN) - HOMO SAPIENS (HUMAN), 367 aa.	4.9E-203	3 (3q27)
6889	cg43051796	1283	GCCAAAAAAGC AAGGGGAATGA GG[G/gap]TCCCC CCCAGGCATCTG GCACAGCC	G	gap	Thr	Thr (9060)	FRAMES HIFT	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.[pds:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa.	4E-114	3

6890	cg43051796	1301	AATGAGGGTCCC CCCCAGGCATCT G[G/gap]CACAGC CCCCAGTGCACA TTCTGGG	G	gap	Ala	Ala (9061)	FRAMES HIFT	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL-TMP - HOMO SAPIENS (HUMAN), 202 aa.lpcds:SWISSPROT-ID:P48230 TETRASPAN MEMBRANE PROTEIN IL- TMP - HOMO SAPIENS (HUMAN), 202 aa.	4E-114	3
6891	cg43924574	1299	TCTCAGGGGTGA ATTTCTCTGGTT C[C/gap]TGCCGG TCCTGGGACCAG TTGGTAA	C	gap	Gln	Gln (9062)	FRAMES HIFT	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP- 39) (39 KD SYNOVIAL PROTEIN) (YKL- 40) (CHITINASE-3 LIKE 1) - HOMO SAPIENS (HUMAN), 383 aa.lpcds:SWISSPROT-ID:P36222 CARTILAGE GLYCOPROTEIN-39 PRECURSOR (GP-39) (39 KD SYNOVIAL PROTEIN) (YKL-40) - HOMO SAPIENS (HUMAN), 383 aa.	1E-106	1
6892	cg43255952	678	AGAGGCGGGTG CACGGGTACTGT TC[C/gap]TCACG GCAGTCAAGAG GCCCAGGCT	C	gap	Glu	Glu (9063)	FRAMES HIFT	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.lpcds:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101 (1p36.1)	1
6893	cg43255952	935	TCATACTGGCCC TGAGCCAGCAAG C[C/gap]TGCAGG CAGGAATAGCAG GAAGAGG	C	gap	Gly	Ala (9064)	FRAMES HIFT	glycoprot ein	Human Gene Homologous to SWISSNEW-ID:P55001 MICROFIBRIL- ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.lpcds:SWISSPROT-ID:P55001 MICROFIBRIL-ASSOCIATED GLYCOPROTEIN PRECURSOR (MAGP) (MAGP-1) - HOMO SAPIENS (HUMAN), 183 aa.	2.6E-101 (1p36.1)	1

6894	cg43967180	92	GGGGACCTGCC CTCCTGGACGC GGA[G/gap]CCTA AACCTGAGTTAC AACAAACTC	G	gap	Ser	Thr (9065)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SPTREMBL- ID:P70193 MEMBRANE GLYCOPROTEIN - MUS MUSCULUS (MOUSE), 1091 aa.	1.7E-99	
6895	cg43917300	269	TGAGGGCCACC ACCCCACTGTGG GG[G/gap]CTCAC CTCCGGGTGGT GAAAAAGC	G	gap	Ser	Ser (9066)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT- MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	4.4E-99	22 (22q13.3)
6896	cg43917300	527	TCTCAGGGCACT CGAAGGCCAGG CA[G/gap]CGGAA GCCGCCCTGGA TGTTGAAGC	G	gap	Arg	Arg (9067)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q08878 FIBULIN-1, ISOFORM C PRECURSOR (BASEMENT- MEMBRANE PROTEIN 90) (BM-90) - MUS MUSCULUS (MOUSE), 685 aa.	4.4E-99	22 (22q13.3)
6897	cg43252493	320	AATGTAATGCCA CCAACGCCATTG G[C/gap]TCCGCC TCTGTTGTCACT GTCCTCA	C	gap	Ser	Pro (9068)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SPTREMBL- ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	1.8E-84	
6898	cg43252493	326	ATGCCACCAACG CCATTGGCTCCG C[C/gap]TCTGTT GTCACGTGCTCTC AGGGTGC	C	gap	Ser	Leu (9069)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SPTREMBL- ID:P97546 GLYCOPROTEIN 55 PRECURSOR - RATTUS NORVEGICUS (RAT), 281 aa.	1.8E-84	

6898	cg43512398	91	TTGCTATTGCAG GACGGACCTGTC C[C/gap]AAGCCA GATGATTACCA TTTTCCA	C	gap	Lys	Ser (9070)	FRAMES HIFT	glycoprotein	Human Gene Similar to SWISSNEW- ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa.	2.7E-83	17 (17q23)
6900	cg44341920	91	TTGCTATTGCAG GACGGACCTGTC C[C/gap]AAGCCA GATGATTACCA TTTTCCA	C	gap	Lys	Ser (9071)	FRAMES HIFT	glycoprotein	Human Gene Similar to SWISSNEW- ID:P02749 BETA-2-GLYCOPROTEIN I PRECURSOR (APOLOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C- BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:SWISSPROT-ID:P02749 BETA- 2-GLYCOPROTEIN I PRECURSOR (APOLOPROTEIN H) (APO-H) (ACTIVATED PROTEIN C-BINDING PROTEIN) (APC INHIBITOR) - HOMO SAPIENS (HUMAN), 345 aa.lpcis:TREMBLNEW-ID:E308445 BETA-2-GLYCOPROTEIN I PRECURSOR - HOMO SAPIENS (HUMAN), 345 aa.	2.7E-83	17 (17q23)
6901	cg43983795	1467	TGCTTCCATTATC CAGGCAAAATGT G[G/gap]CAAGGC CCCTGGATGCAT CTCTCC	G	gap	Ala	Ala (9072)	FRAMES HIFT	glycoprotein	Human Gene Similar to SPTREMBL- ID:Q95250 STEROID MEMBRANE BINDING PROTEIN - SUS SCROFA (PIG), 194 aa.	1.2E-74	X

6902	cg43056971	238	CAATCCGTCAGC TAAACCCAGTGT GT[ <i>gap</i> ]GGCTGA GATCCAAAATTG GGACAGT	T	<i>gap</i>	Trp	Gly (9073)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SPTREMBL- ID:O04711 P-GLYCOPROTEIN-2 - ARABIDOPSIS THALIANA (MOUSE- EAR CRESS), 1233 aa.	2.2E-72	1
6903	cg43995037	2835	GGCTCAGGAAGT GCGTGGGGCG TA[G/ <i>gap</i> ]CGGGT GAGCATGCTGAT GATGACCA	G	<i>gap</i>	Arg	Arg (9074)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SWISSNEW- ID:P21851 BETA-ADAPTIN (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND BOS TAURUS, 937 aa. ID:P21851 BETA-ADAPTIN (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN BETA SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 BETA LARGE CHAIN) (AP105B) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND BOS TALRUS, 937 aa.	3E-68	15
6904	cg42687075	230	CGGGTGAAGAA GTCAGGGCCTC GGC[C/ <i>gap</i> ]ACAG GGCCCCAGGGA AAAGGAGGCC	C	<i>gap</i>	Pro	His (9075)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SWISSPROT- ID:P13983 EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) - NICOTIANA TABACUM (COMMON TOBACCO), 620 aa.	1.3E-58	
6905	cg43926142	652	TTTAATTAAGAA TGAGTGCTGGG G[C/ <i>gap</i> ]CCTTTT ATTGGGTACTGC ATCTAC	C	<i>gap</i>	Ala	Ala (9076)	FRAMES HIFT	glycoprot ein	Human Gene Similar to SWISSPROT- ID:Q15388 MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM20 HOMOLOG (MITOCHONDRIAL 20 KD OUTER MEMBRANE PROTEIN) (OUTER MITOCHONDRIAL MEMBRANE RECEPTOR TOM20) (KIAA0016) - HOMO SAPIENS (HUMAN), 145 aa.	2.9E-57	1



6906	cg43250682	1070	GCCAAAGAAGCA GGAAAAAGGGG CAG[G/gap]CTTG AGGACGCCTCCA TTCTATGCC	G	gap	Leu	Leu (9077)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6907	cg43250682	1483	TTTCAAGGAAAG CCTAATTTTGAA G[A/gap]ATACTTT GAAATTTCTGACT CCAAAA	A	gap	Glu	Asp (9078)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6908	cg43250682	1484	TTCAAGGAAAGC CTAATTTTGAAG A[A/gap]TACTTTG AAATTTCTGACTC CAAAAA	A	gap	Tyr	Thr (9079)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6909	cg43250682	2104	GATGTCTACAAG GTGGAGACCAAT G[G/gap]CGATGC CTATTGTGTGGC TGGGGGA	G	gap	Gly	Ala (9080)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6910	cg43250682	2123	CATTGGCGATGC CTATTGTGTGGC T[gap/T]GGGGGA TTACACAAAGAG AGTGATA	gap	T	Gly	Trp (9081)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6911	cg43250682	2551	TTCCAAAAGAAA GATGTGGAAGAT G[G/gap]CAATGC CAATTTTITAGG CAAAGCA	G	gap	Gly	Ala (9082)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6912	cg43250682	2555	AAAAGAAAGATG TGGAAGATGGCA A[T/gap]GCCAAT TTTTAGGCAAA GCATCAG	T	gap	Ala	Pro (9083)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4

6913	cg43250682	2574	TGGCAATGCCAA TTTTTTAGGCA A[G/gap]CATCAG GAATAGATTAGC AACCTAT	G	gap	Ala	His (9084)	FRAMES HIFT	Guanylyl	Human Gene SWISSPROT-ID:P19687 GUANYLATE CYCLASE SOLUBLE, ALPHA-1 CHAIN (EC 4.6.1.2) (73 KD CHAIN) - BOS TAURUS (BOVINE), 691 aa.	0	4
6914	cg43956596	2876	AACCAGCGGTCA GGCGGAGCCGG CA[G/gap]GACGG GCCAGGTCAGT GTTTCAGG	G	gap	Arg	Arg (9085)	FRAMES HIFT	helicase	Human Gene SWISSNEW-ID:Q92620 PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa. pcds:SWISSPROT-ID:Q92620 PUTATIVE ATP-DEPENDENT RNA HELICASE KIAA0224 (HA4657) - HOMO SAPIENS (HUMAN), 1227 aa.	0	16
6915	cg43919913	1197	GGTCGATCAGTG TCCGGTAACCCCT C[C/gap]TGCGGG TCTTCTTGGA GCATTAC	C	gap	Gln	Gln (9086)	FRAMES HIFT	helicase	Human Gene SWISSNEW-ID:Q14562 PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN 8) - HOMO SAPIENS (HUMAN), 1220 aa. pcds:SWISSPROT-ID:Q14562 PROBABLE ATP-DEPENDENT RNA HELICASE HRH1 (DEAH BOX PROTEIN 8) - HOMO SAPIENS (HUMAN), 1220 aa. pcds:SPTREMBL-ID:Q14562 PUTATIVE RNA HELICASE HRH1 - HOMO SAPIENS (HUMAN), 1220 aa (fragment).	0	17
6916	cg44026400	245	TTCGCCTATTTC TTCTTGGGCGCC G[C/gap]CTTCTT AGGCTTGACAAC CTTGGGC	C	gap	Ala	Arg (9087)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6917	cg44026400	246	TCGCCTATTTC TCTTGGGCGCC GC[C/gap]TTCCTT AGGCTTGACAAC CTTGGGCT	C	gap	Lys	Lys (9088)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6

6918	cg44026400	282	TGACAACCTTGG GCTTAGCGGCTT T[G/gap]GGCTTC ACAGCCTTAGCA GCACCTT	G	gap	Pro (9089)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6919	cg44026400	356	ACCTTGGCCTTC TTTGGGCTCTTA G[C/gap]CACCTT CTTGGTTACAGT GGCCGGG	C	gap	Ala (9090)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6920	cg44026400	357	CCTTGGCCTTCT TTGGGCTCTTAG C[C/gap]ACTTTCT TGGTTACAGTGG CCGCGG	C	gap	Val (9091)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6921	cg44026400	383	ACTTCTTGGTT ACAGTGGCCGC GG[C/gap]CGGCT TCTTCGCTTCTT CGGTGTT	C	gap	Pro (9092)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6922	cg44026400	384	CTTCTTGGTTA CAGTGGCCGCG GC[C/gap]GGCTT CTTCGCTTCTT CGGTGTT	C	gap	Pro (9093)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6923	cg44026400	532	AACCTTGGGCTT GGCTTCCCCGG AG[G/gap]CTGCC TTCTTGTGAGT TTAAAGGA	G	gap	Ala (9094)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6
6924	cg44026400	720	AAACTCCGCTAC GCTCTTTAGAGG C[G/gap]GCCACA GCCTTGGTGATG AGCTCTG	G	gap	Ala (9095)	FRAMES HIFT	histone	Human Gene Homologous to SWISSPROT-ID:P16403 HISTONE H1D (H1.2) - HOMO SAPIENS (HUMAN), 212 aa.	1.7E-104	6

6925	cg42689883	363	CCAGCTCCAGGA CCTTGGCCGTCA G[G/gap]TACTCA ATAACCGCAGCG AGGTAGA	gap	Tyr	Tyr (9096)	FRAMES HIFT	histone	Human Gene Similar to SWISSPROT- ID:P98176 HYPOTHETICAL 12.7 KD HISTONE H2A RELATED PROTEIN - HOMO SAPIENS (HUMAN), 115 aa.	3.7E-53	
6926	cg42689883	519	CCGCCCCCGGC CGCCAGCACCG GAG[gap]GACCC TCGGCGCTCCT CCTCCTCGG	G	Ser	Ser (9097)	FRAMES HIFT	histone	Human Gene Similar to SWISSPROT- ID:P98176 HYPOTHETICAL 12.7 KD HISTONE H2A RELATED PROTEIN - HOMO SAPIENS (HUMAN), 115 aa.	3.7E-53	
6927	cg43985818	429	AGACGCCGTCAC CTATACGGAGCA C[G/gap]CCAAGC GCAAAACTGTCA CAGCCAT	gap	Ala	Pro (9098)	FRAMES HIFT	histone	Human Gene Similar to TREMBLNEW- ID:G2564108 HISTONE H4 - CHAETOPTERUS VARIOPELATUS, 103 aa. pcis:TREMBLNEW-ID:E314007 HISTONE H4 - MUS MUSCULUS (MOUSE), 103 aa. pcis:TREMBLNEW- ID:G62736 H4 HISTONE - CAIRINA MOSCHATA (MUSCOVY DUCK), 103 aa. pcis:TREMBLNEW-ID:G1493809 HISTONE H4-VI - GALLUS GALLUS (CHICKEN), 103 aa.	4E-50	
6928	cg43988803	464	CTGCCCCCGGC GCGCTCGTGCA CCT[G/gap]GCCG CTGCCACAGCC GGAGTTTAGC	G	Trp	Cys (9099)	FRAMES HIFT	homeobo x	Human Gene SPTREMBL-ID:Q12776 PAX-3-FKHR GENE FUSION - HOMO SAPIENS (HUMAN), 689 aa (fragment).	1.2E-242 (13q14.1 )	13
6929	cg43332152	1175	CAGCTGAGCGC CCTGGGCGCCC GGC[G/gap]CCAC GCCTTCTCCGC AGTCCGCGC	G	Arg	Pro (9100)	FRAMES HIFT	homeobo x	Human Gene SWISSPROT-ID:P36199 HOMEBOX PROTEIN LIM-1 (HOMEBOX PROTEIN LMX-2) - MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND MESOCRICETUS, 406 aa.	3.4E-227	17

6930	cg41637704	1220	GCGCGCGGAGA CAAGGGCAGCG GAC[gap/C]CGCC TGCGGACTTGAG GGACAGTGA	gap	C	Pro	Pro (9101)	FRAMES HIFT	homeobo x	Human Gene SWISSPROT-ID:P50219 HOMEBOX PROTEIN HB9 - HOMO SAPIENS (HUMAN), 401 aa.	1.2E-224	7
6931	cg43983917	1204	CCCGGTGCGGA TCTGGCGGCCTA CA[C/gap]ACGCT GGCTAAGCTGC AACGAAAA	C	gap	Thr	Asn (9102)	FRAMES HIFT	homeobo x	Human Gene SWISSPROT-ID:P50458 HOMEBOX PROTEIN LH-2 - HOMO SAPIENS (HUMAN), 423 aa.	4.3E-216	
6932	cg43143467	406	GCAGAACAGCTGA GAGGAACCTGGA GC[A/gap]CGTTG CTTTGAGAGAA CTCATTAC	A	gap	His	Pro (9103)	FRAMES HIFT	homeobo x	Human Gene SPTREMBL-ID:Q12777 PAX-3 - HOMO SAPIENS (HUMAN), 332 aa (fragment).	2.1E-179	2 (2q35)
6933	cg42908326	783	TGTGGCGCACG CGCACCAACACC TG[C/gap]ATCCG CACCTGGCCGC GCACGCGGCC	C	gap	His	Ile (9104)	FRAMES HIFT	homeobo x	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.8E-136	3
6934	cg42908326	833	CCTACATGATGT TCCCAGCACCGC C[C/gap]TTCGGA CTGCCGCTCGC CAGGCTGG	C	gap	Phe	Ser (9105)	FRAMES HIFT	homeobo x	Human Gene Homologous to SPTREMBL-ID:P70390 OG-12A HOMEODOMAIN PROTEIN - MUS MUSCULUS (MOUSE), 331 aa.	5.8E-136	3
6935	cg42489148	1154	CACACAGCCG CCTCCGCCGCC ACC[C/gap]ACAG CCTCCCCAGCCT CAGCCAGGT	C	gap	Pro	His (9106)	FRAMES HIFT	homeobo x	Human Gene Homologous to SPTREMBL-ID:O00503 CAUDAL-TYPE HOMEBOX PROTEIN 2 - HOMO SAPIENS (HUMAN), 313 aa.	6E-118	13

6936	cg42489148	872	GGAACCTGTGC GAGTGGATGCG GAA[gap]GJCCGG CGCAGCAGTCC CTCGGCAGCC	gap	G	Asn	Lys (9107)	FRAMES HIFT	homeobo x	Human Gene Homologous to SPTREMBL-ID:O00503 CAUDAL-TYPE HOMEODOMAIN PROTEIN 2 - HOMO SAPIENS (HUMAN), 313 aa.	6E-118	13
6937	cg43983244	2275	TGGTGAGTCCCG GCGACTCCAGCA G[G/gap]CTCCGG CCAGCCTCGCC CACGTTCT	gap	G	Ser	Ser (9108)	FRAMES HIFT	homeobo x	Human Gene Homologous to SWISSPROT-ID:P43271 PAIRED MESODERM HOMEODOMAIN PROTEIN 1 (HOMEODOMAIN PROTEIN MHX) (HOMEODOMAIN PROTEIN K-2) (RHOX) - MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT), 217 aa.	2.2E-113	
6938	cg43932912	729	TGACAGCAAGTC CATTAGCTCAA G[G/gap]CAGAAC TGCCTTAAATGT TCATACT	gap	G	Cys	Cys (9109)	FRAMES HIFT	homeobo x	Human Gene Similar to SWISSPROT- ID:P34349 HYPOTHETICAL 30.5 KD PROTEIN C30A5.3 IN CHROMOSOME III - CAENORHABDITIS ELEGANS, 261 aa.	1.3E-81	
6939	cg43988195	3178	TGTCAAATACCA GGAGGGCATCA GC[C/gap]GCAAA CTCCTCTGAGCT GGTGTTACC	gap	C	Ala	Ala (9110)	FRAMES HIFT	homeobo x	Human Gene Similar to SPTREMBL- ID:Q23590 SIMILARITY TO VARIOUS HOMEODOMAIN PROTEINS - CAENORHABDITIS ELEGANS, 1453 aa.	2.6E-53	12
6940	cg42503642	2466	ATGCCAATGCAA ACATTATTCTGA [G/gap]GCCAAGC CCGAAGGACCTA GAGTCA	gap	G	Ala	Pro (9111)	FRAMES HIFT	hydrolas e	Human Gene SWISSPROT-ID:Q92995 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T-3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE T-3) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T-3) (DEUBIQUITINATING ENZYME T-3) (ISOPEPTIDASE T-3) (ISOT-3) - HOMO SAPIENS (HUMAN), 863 aa.	0	

6941	cg42503642	2467	TGCCAATGCAAA CATTATTTCTGA G[G/gap]CCAAGC CCGAAGGACCTA GAGTCAA	G	gap	Ala	Pro (9112)	FRAMES HIFT	hydrolas e	Human Gene SWISSPROT-ID:Q92995 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE T-3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE T-3) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE T-3) (DEUBIQUITINATING ENZYME T-3) (ISOPEPTIDASE T-3) (ISOT-3) - HOMO SAPIENS (HUMAN), 863 aa.	0	
6942	cg43296921	405	TGGAGCCGAAGT TTTCTGGCTCCG G[C/gap]CCGCTG ATGGTCCCAGAA GCCAGGA	C	gap	Gly	Gly (9113)	FRAMES HIFT	hydrolas e	Human Gene SWISSPROT-ID:P16930 FUMARYLACETOACETASE (EC 3.7.1.2) (FUMARYLACETOACETATE HYDROLASE) (BETA-DIKETONASE) (FAA) - HOMO SAPIENS (HUMAN), 419 aa.	3.3E-238	15 (15q23)
6943	cg43933380	1392	ACATGTAAGACT CCTTCTGCTGAA A[C/gap]ACAGTA CTGAGAAATTCAG TGAGGAT	C	gap	Val	Phe (9114)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
6944	cg43933380	300	ACCTAGGAACCA GGAGTACTGGAT A[C/gap]TGTTC GTTACTGGTAAC CTATCTG	C	gap	Gln	His (9115)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
6945	cg43933380	349	TGGATGTAAGG TTCATAAGTTAC A[A/gap]TGCCTTT TTTGTTTAAAAAA AAAAA	A	gap	Ile	Met (9116)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
6946	cg43933380	374	ATGCTTTTTTTGT TTAAAAAATAAA A[gap]AAAGTCTG TACTTTACAAGC CAAAA	A	gap	Phe	Phe (9117)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6

6947	cg43933380	377	CTTTTGTGTTA AAAAA A/gap]GTCTGTAC TTTACAAGCCAA AAGTG	A	gap	Phe (9118)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:P15260 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119) - HOMO SAPIENS (HUMAN), 489 aa.	1.4E-261	6
6948	cg43931810	819	GAACCAGAGGG CATAGCGTGGT AG[C/gap]GTCCG CTTCCTTCCGTG AAGGTAAT	C	gap	Arg (9119)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:Q14653 INTERFERON REGULATORY FACTOR 3 (IRF-3) - HOMO SAPIENS (HUMAN), 427 aa.	1.2E-240	19
6949	cg43956260	570	AGTGTACCTGG AACTTCGGTGG G[G/gap]GCCAG GCCCTGAAAGTA CCTGACC	G	gap	Pro (9120)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
6950	cg43956260	571	GTGTTACCTGGA ACTTCGGTGG GG[G/gap]CCCAG GCCCTGAAAGTA CCTGACCA	G	gap	Gly (9121)	FRAMES HIFT	interferon	Human Gene SWISSPROT-ID:Q00978 TRANSCRIPTIONAL REGULATOR ISGF3 GAMMA SUBUNIT (IFN-ALPHA RESPONSIVE TRANSCRIPTION FACTOR SUBUNIT) (INTERFERON STIMULATED GENE FACTOR 3 GAMMA) (ISGF3 P48 SUBUNIT) (ISGF-3 GAMMA) - HOMO SAPIENS (HUMAN), 393 aa.	2.5E-215	14
6951	cg43926568	1529	CTCTCAGGGCT TCCTCATTCTGG C[C/gap]TTTCAG GTGTTTCACATA GGCTAGT	C	gap	Gly (9122)	FRAMES HIFT	interferon	Human Gene Homologous to SPTREMBL-ID:Q13325 RETINOIC ACID- AND INTERFERON-INDUCIBLE 58K PROTEIN RI58 - HOMO SAPIENS (HUMAN), 482 aa.	4.8E-141	10 (10q23)



6952	cg43922672	1616	GGGACCACGCA CCATGATGCCCT GG[C/gap]CATCC TCCGCCAAGCTC GAGAGCCC	C	gap	Ala	Ala (9123)	FRAMES HIFT	interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15
6953	cg43922672	1687	AAGGAAGCTGAC TCCAGAGGCCAT G[C/gap]CCGACC TCAACTCCTCCA CTGACTC	C	gap	Pro	Pro (9124)	FRAMES HIFT	interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15
6954	cg43922672	1760	AGTGATGTTTCT GTAGAATCTACA G[C/gap]AGAGGC CACAGTCTGCAC GGTGACA	C	gap	Ala	Glu (9125)	FRAMES HIFT	interleukin	Human Gene TREMBLNEW- ID:G2114410 INTERLEUKIN-16 - HOMO SAPIENS (HUMAN), 631 aa.	0	15
6955	cg43930054	1773	CGATCTGGGCGA GTGGATCACTGC T[G/gap]GCCAAC AGCCGCGCCAC TTCGCTGT	G	gap	Ala	Ala (9126)	FRAMES HIFT	isomerase	Human Gene SWISSPROT-ID:P34949 MANNNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2E-222	15 (15q22)
6956	cg43930054	1818	CGCTGTTGGAAC CCATCTTCCCCC A[G/gap]GCATAC TGCTGCACCGCA CAGGAAA	G	gap	Ala	Ala (9127)	FRAMES HIFT	isomerase	Human Gene SWISSPROT-ID:P34949 MANNNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2E-222	15 (15q22)
6957	cg43930054	633	AGCAGGCACGG AATATCAGCAGG TC[C/gap]TTCGG CTCAGTAAGCTT CAGTGAGA	C	gap	Lys	Lys (9128)	FRAMES HIFT	isomerase	Human Gene SWISSPROT-ID:P34949 MANNNOSE-6-PHOSPHATE ISOMERASE (EC 5.3.1.8) (PHOSPHOMANNNOSE ISOMERASE) (PMI) (PHOSPHOHEXOMUTASE) - HOMO SAPIENS (HUMAN), 422 aa.	2E-222	15 (15q22)

6958	cg43297395	1744	GCGCCCCAGCT GCCTCTGGCTGT GG[C/gap]CACAG ACAACTTCATCA GCACCTGT	C	gap	Ala (9129)	Ala	kinase HIFT	Human Gene SWISSPROT-ID:Q15569 TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-) - HOMO SAPIENS (HUMAN), 626 aa.	0	9
6959	cg43259301	1495	GCCCCATCCCCA TCCACACAAGTA C[A/gap]GCGCAG CGTGTCGGCCAA TCCCAAG	A	gap	Gln (9130)	Arg (9130)	kinase HIFT	Human Gene SPTREMBL-ID:Q15524 SERINE/THREONINE PROTEIN KINASE - HOMO SAPIENS (HUMAN), 745 aa.	0	13
6960	cg43299934	1634	TGACCACAATGA CCTCCACGGTGA T[G/gap]CCATCA GGCAGCATGAG CCAGGATG	G	gap	Gly (9131)	Gly (9131)	kinase HIFT	Human Gene SPTREMBL-ID:Q92667 KINASE A ANCHOR PROTEIN - HOMO SAPIENS (HUMAN), 903 aa.	0	17
6961	cg43336163	2426	CTTCCCATCTAG ATGGCCCCCGG GC[C/gap]GTGGC TGTGGGCCAGT GCCCGCTGG	C	gap	Val (9132)	Trp (9132)	kinase HIFT	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0	19
6962	cg43336163	2464	CAGTGCCCGCT GGTGGGGCCAG GCC[C/gap]CATG CACCGCCGCCA CCTGCTGCTC	C	gap	Pro (9133)	Pro (9133)	kinase HIFT	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0	19
6963	cg43336163	2465	AGTGCCCGCTG GTGGGGCCAGG CCC[C/gap]ATGC ACCGCCGCCAC CTGCTGCTCC	C	gap	Met (9134)	Cys (9134)	kinase HIFT	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0	19

6964	cg43336163	944	CCGACTTCTTGC AGTGGCGGAG CC[C/gap]ATCGT GGTGAGGCTTAA GGAGGTCC	C	gap	Ile	Ser (9135)	FRAMES HIFT	kinase	Human Gene TREMBLNEW-ID:G300258 MYOTONIC DYSTROPHY KINASE, DM- KINASE {C-TERMINAL, ALTERNATIVELY SPLICED, CLONE DELTA II} - HOMO SAPIENS, 616 aa.	0	19
6965	cg44929725	2841	AAGAGCAGAATC CAGATATTGTTT C[gap/C]AGAAAA AAAACCCAGCAAC TGAAGTG	gap	C	Ser	Ser (9136)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6966	cg44929725	2851	TCCAGATATTGT TTCAGAAAAAAA A[gap/A]CCAGCA ACTGAAGTGGAC CCCACAC	gap	A	Pro	Thr (9137)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6967	cg44929725	2856	ATATTGTTTCAG AAAAAAACCAG C[gap/C]AACTGA AGTGGACCCAC ACATTTT	gap	C	Ala	Ala (9138)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6968	cg44929725	2964	GAGCTCTGCAG GTATGACCCCGA AG[gap]GGACA ATACAGGGGAG CAGGTGGCT	G	gap	Gly	Gly (9139)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6969	cg44929725	2965	AGCTCTGCAGGT ATGACCCCGAAG G[gap]GACAAT ACAGGGGAGCA GGTGGCTG	G	gap	Asp	Thr (9140)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)
6970	cg44929725	2966	GCTCTGCAGGTA TGACCCCGAAG GG[gap]ACAAT ACAGGGGAGCA GGTGGCTGT	G	gap	Asp	Thr (9141)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P23458 TYROSINE-PROTEIN KINASE JAK1 (EC 2.7.1.112) (JANUS KINASE 1) (JAK-1) - HOMO SAPIENS (HUMAN), 1142 aa.	0	1 (1p31.3)

6971	cg43988890	150	GACATGGAGCC CGAGGCCGGCG CCG[G/gap]CGCC GGCCCGGGCC TCTTCGGCTG	G	gap	Arg	Ala (9142)	FRAMES HIFT	kinase	Human Gene SWISSNEW-ID:P15056 B- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (P94) - HOMO SAPIENS (HUMAN), 765 aa.  cds:SWISSPROT-ID:P15056 B-RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (P94) - HOMO SAPIENS (HUMAN), 765 aa.	0	7 (7q34)
6972	cg43257904	505	GGCGGGGGCCT AAGGCACAAGG CGG[G/gap]CTGC GCTGAGTAGGCA GGCAGGGCAA	G	gap	Ala	Ala (9143)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0	X (Xp11.4)
6973	cg43257904	807	TGTAAGGCAGTG AGCCAGTCATAA G[C/gap]TCGTAG AGCACAAACCCCG TAGGCAT	C	gap	Glu	Asp (9144)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P10398 A- RAF PROTO-ONCOGENE SERINE/THREONINE-PROTEIN KINASE (EC 2.7.1.-) (ONCOGENE PKS2) - HOMO SAPIENS (HUMAN), 606 aa.	0	X (Xp11.4)
6974	cg43016269	1920	GCAAAAGGAGCTA GAAGAGGGAGATT A[C/gap]CTTACG GAAAAGTGTGGA ATCAGCA	C	gap	Thr	Thr (9145)	FRAMES HIFT	kinase	Human Gene SPTREMBL-ID:Q28021 RHO-ASSOCIATED KINASE - BOS TAURUS (BOVINE), 1388 aa.	0	
6975	cg43263359	1179	AGATGGGGCCC CGCAGCCGGCG AGA[G/gap]CTCG GCAAGTCGTCCA CCTCGTCCT	G	gap	Ser	Ser (9146)	FRAMES HIFT	kinase	Human Gene SPTREMBL-ID:Q13476 KINASE SUPPRESSOR OF RAS-1 (KSR1) - HOMO SAPIENS (HUMAN), 635 aa (fragment).	0	
6976	cg43263359	1239	CTGCCCTCTGACT TGCCAGCCCTCTG G[C/gap]TCCTCA GCCTCCGCTTCG TGAGCTT	C	gap	Glu	Asp (9147)	FRAMES HIFT	kinase	Human Gene SPTREMBL-ID:Q13476 KINASE SUPPRESSOR OF RAS-1 (KSR1) - HOMO SAPIENS (HUMAN), 635 aa (fragment).	0	

6977	cg43947749	1457	CTCATCCCTCCT CACTTGAGGTCC C[C/gap]AGCGGG CACTACCACCCT CACCCCG	C	gap	Pro	Gln (9148)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.6E-267	19
6978	cg43947749	1457	TCATCCCTCCTC ACTTGAGGTCCC C[gap]CJAGCGGG CACTACCACCCT CACCCCG	gap	C	Pro	Pro (9149)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.6E-267	19
6979	cg43947749	1461	TCCCTCCTCACT TGAGGTCCCGAG C[G/gap]GGCACT ACCACCTCACC CCGTCTT	G	gap	Gly	Ala (9150)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.6E-267	19
6980	cg43947749	1463	CTCTCTCACTTG AGGTCCCCAGC GG[G/gap]CACTA CCACCTCACC CGTCTCTCA	G	gap	Gly	Ala (9151)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P49840 GLYCOGEN SYNTHASE KINASE-3 ALPHA (EC 2.7.1.37) (GSK-3 ALPHA) - HOMO SAPIENS (HUMAN), 483 aa.	5.6E-267	19
6981	cg43947829	910	TGTTCAAGTACT TCTCTGAGCATT G[G/gap]CCTCTG GCTGGGATTATG CTCAAC	G	gap	Pro	Gln (9152)	FRAMES HIFT	kinase	Human Gene TREMBLNEW- ID:G2979628 AURORA RELATED KINASE 1 - HOMO SAPIENS (HUMAN), 403 aa.	1.5E-217	
6982	cg38438124	1248	GAGAGCGATGG CACCCACCCGGT GG[G/gap]AACCC CCCCAGATAGCC CCGGGAAT	G	gap	Gly	Glu (9153)	FRAMES HIFT	kinase	Human Gene SWISSNEW-ID:O70172 PHOSPHATIDYLINOSITOL-4- PHOSPHATE 5-KINASE TYPE II ALPHA (EC 2.7.1.68) (PIP5KII-ALPHA) (1- PHOSPHATIDYLINOSITOL-4- PHOSPHATE KINASE) (PTDINS(4)P-5- KINASE B ISOFORM) (DIPHOSPHOINOSITIDE KINASE) - MUS MUSCULUS (MOUSE), 405 aa.	2.8E-216	10

6983	cg43917871	1455	ATTGGCGCTGCT GACGGGCGTAC TG[C/gap]CCCCCT GGCATGCTAGAT GAACCCCAT	C	gap	Gly	Ala (9154)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:P19138 CASEIN KINASE II, ALPHA CHAIN (CK II) (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 391 aa.	2E-215	11 (20p13)
6984	cg44131752	1284	TGCCCCCTGCCCA CCAGGTACTGG GG[G/gap]CCTGT GGCAGCAAGATA GGGGGAGA	G	gap	Pro	Leu (9155)	FRAMES HIFT	kinase	Human Gene SPTREMBL-ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	7.8E-173	16
6985	cg44000392	347	CGGCATGGAGA AGGACGGCCTG TGC[gap]C]GCGC TGACCAGCAGTA CGAATGCGT	gap	C	Arg	Pro (9156)	FRAMES HIFT	kinase	Human Gene SWISSPROT-ID:Q00534 CELL DIVISION PROTEIN KINASE 6 (EC 2.7.1.-) (KINASE PLSTIRE) - HOMO SAPIENS (HUMAN), 326 aa.	4.1E-172	7
6986	cg43257282	1015	ATGGTGTCGGA GGCCGGGCTGC GC[C/gap]TGCTG CACTTCCTGTTT ATGTACGA	C	gap	Leu	Cys (9157)	FRAMES HIFT	kinase	Human Gene Homologous to SPTREMBL-ID:Q15130 CDC2-RELATED KINASE - HOMO SAPIENS (HUMAN), 316 aa.	2.9E-147	16
6987	cg44016530	578	TGTAGTCTCTTT GGTGATCTCATC TTG[gap]CTTTTCT GCTCGAGTGATG ACAGCC	G	gap	Ala	Glu (9158)	FRAMES HIFT	kinase	Human Gene Homologous to SPTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment).	1.7E-129	12
6988	cg44016530	583	TCTCTTTGGTGA TCTCATCTGCTT TTT[gap]CTGCTC GAGTGATGACAG CCTTGAA	T	gap	Arg	Arg (9159)	FRAMES HIFT	kinase	Human Gene Homologous to SPTREMBL-ID:Q92631 PROTEIN KINASE - HOMO SAPIENS (HUMAN), 240 aa (fragment).	1.7E-129	12
6989	cg43022553	502	TGCTGGGGCTG AGAGAGGGCTG CAA[G/gap]CTGC TCGTGCACGGCT TTGAGCTGC	G	gap	Leu	Leu (9160)	FRAMES HIFT	kinase	Human Gene Homologous to SPTREMBL-ID:Q90971 KINASE - GALLUS GALLUS (CHICKEN), 729 aa.	1E-102	

6990	cg43022553	754	CATCCTGGAGCT TGCGGGCCATG GC[C/gap]ACCAC CTCATGGTCAGG AGGGTTGT	C	gap	Val	Val (9161)	FRAMES HIFT	kinase	Human Gene Homologous to SPTREMBL-ID:Q90971 KINASE - GALLUS GALLUS (CHICKEN), 729 aa.	1E-102	
6991	cg43952004	2215	GCAGAGGAAATC AAACCCCTGCTT G[G/gap]CCACAG CCCCTAGTGTGT CAGCTAT	G	gap	Ala	Ala (9162)	FRAMES HIFT	kinase	Human Gene Similar to TREMBLNEW- ID:E1263921 KINASE-BINDING PROTEIN 1 - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 645 aa.	6.3E-94	14
6992	cg43986825	270	TTCACCTTCCTC AGGCAGGAGCT GC[C/gap]TGTC GCCTGGCCAACA TCATGAAA	C	gap	Pro	Leu (9163)	FRAMES HIFT	kinase	Human Gene Similar to SWISSPROT- ID:Q15119 [PYRUVATE DEHYDROGENASE(LIPOAMIDE)] KINASE ISOZYME 2 PRECURSOR (EC 2.7.1.99) (PYRUVATE DEHYDROGENASE KINASE ISOFORM 2) - HOMO SAPIENS (HUMAN), 407 aa. lpcis:SPTREMBL-ID:Q15119 PYRUVATE DEHYDROGENASE KINASE - HOMO SAPIENS (HUMAN), 407 aa.	3.2E-89	17
6993	cg43917718	694	AAAGGTGGGT GGAATGCTGGCT CG[G/gap]CCCTG CCAGTCACTGGG TGGCAGCA	G	gap	Pro	Arg (9164)	FRAMES HIFT	kinase	Human Gene Similar to SPTREMBL- ID:Q15599 TYROSINE KINASE ACTIVATOR PROTEIN 1 (TKA-1) - HOMO SAPIENS (HUMAN), 450 aa.	1.4E-79	17
6994	cg41501865	381	GCCAAGGGCGC GCTGCTGGGA CCA[G/gap]CGGC CTCAAGCGCCG CTTCAGCCGC	G	gap	Ser	Thr (9165)	FRAMES HIFT	kinase	Human Gene Similar to TREMBLNEW- ID:D1025880 ZIP-KINASE - HOMO SAPIENS (HUMAN), 454 aa.	2.7E-76	
6995	cg43923082	257	AGGAGACGGGT GCTTTGGCTGCG GC[C/gap]AAAGT CATTGAAACCAA GAGTGAGG	C	gap	Lys	Lys (9166)	FRAMES HIFT	kinase	Human Gene Similar to SPTREMBL- ID:O08815 PROTEIN KINASE - RATTUS NORVEGICUS (RAT), 1206 aa.	9.4E-58	

6996	cg44021449	3311	TTGCTGCTGCAG CAAGGGCTACTG C[C/gap]ACACAG TAGCTGTTAGCC CACAGGC	C	gap	Pro	His (9167)	FRAMES HIFT	kinaserec eptor	Human Gene SWISSPROT-ID:Q06418 TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROSINE-PROTEIN KINASE DTK) - HOMO SAPIENS (HUMAN), 890 aa.	0	15
6997	cg43322545	1486	GTACCCCTGGAG GCCTGGCGCCC AG[G/gap]GGAAG CACAGCCAGTCC ACCAGCTG	G	gap	Gly	Gly (9168)	FRAMES HIFT	kinaserec eptor	Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.lpcis:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)
6998	cg43322545	1487	TACCCCTGGAGG CCTGGCGCCCA GG[G/gap]GAAGC ACAGCCAGTCCA CCAGCTGG	G	gap	Glu	Lys (9169)	FRAMES HIFT	kinaserec eptor	Human Gene SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.lpcis:SWISSPROT-ID:P30530 TYROSINE-PROTEIN KINASE RECEPTOR UFO PRECURSOR (EC 2.7.1.112) (AXL ONCOGENE) - HOMO SAPIENS (HUMAN), 887 aa.	0	19 (19q13.1)
6999	cg43991478	544	CACAGGGACATT TGTCGGGCCGT GG[C/gap]AGCCT CTCCCCCTCGTTC CAGCAACT	C	gap	Leu	Leu (9170)	FRAMES HIFT	kinaserec eptor	Human Gene SWISSPROT-ID:P29597 NON-RECEPTOR TYROSINE-PROTEIN KINASE TYK2 (EC 2.7.1.112) - HOMO SAPIENS (HUMAN), 1187 aa.	0	



7000	cg43998555	1379	GGTCCGCGCCT GGCTGGAAGCC AAG[G/gap]CCTT CAGCCCGCGGA TCGTGGAGAA	G	gap	Ala	Pro (9171)	FRAMES HIFT	kinasereceptor	Human Gene Similar to SWISSPROT- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8 - HOMO SAPIENS (HUMAN), 822 aa.   pcis:SPTREMBL- ID:Q12929 EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE - HOMO SAPIENS (HUMAN), 822 aa.	1.2E-99	11
7001	cg43942537	2552	TTCTTAATTGTTT TGGCCCTTTGGC IC/gap]AAATAAG AGTGATAGATTTT GTTTCA	C	gap	Gly	Ala (9172)	FRAMES HIFT	kinesin	Human Gene SWISSNEW-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.   pcis:SWISSPROT-ID:P33176 KINESIN HEAVY CHAIN (UBIQUITOUS KINESIN HEAVY CHAIN) (UKHC) - HOMO SAPIENS (HUMAN), 963 aa.	0	10
7002	cg43987378	830	GAGCTGGAAGA GCGGCTGAGCA CGC[gap]CJAGGA GGGCTTGGTGC AAGAGCTTCA	gap	C	Gln	Pro (9173)	FRAMES HIFT	kinesin	Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment).	1.5E-254	6
7003	cg43987378	931	TAGAGGAGAAG GAGAGGAGGCT GCA[G/gap]ACAT CAGAAAGCAGCC CTGTCAAGCA	G	gap	Thr	His (9174)	FRAMES HIFT	kinesin	Human Gene SPTREMBL-ID:Q14834 KINESIN-RELATED PROTEIN - HOMO SAPIENS (HUMAN), 519 aa (fragment).	1.5E-254	6
7004	cg43953676	552	CTGTGTGCAGAC CGGGGTGACCG GG[G/gap]TCACC AAGTCCTGTCAC CTGTGCCGA	G	gap	Val	Ser (9175)	FRAMES HIFT	laminin	Human Gene SWISSPROT-ID:P11047 LAMININ GAMMA-1 CHAIN PRECURSOR (LAMININ B2 CHAIN) - HOMO SAPIENS (HUMAN), 1609 aa.	0 1 (1q31)	

7005	cg43983535	1209	CTGTTGCAAAAT CAGCATGATTGA TTGgapJCGAGCC ATGTAAAAAAGC AAGCCGG	G	gap	Arg (9176)	Arg	FRAMES HIFT	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
7006	cg43983535	338	GCAAAATTAAAC TCCAGTGGCTTG C[C]gapJTGTC TTTGGTGAGCTT CAGGGAT	C	gap	Gln (9177)	Gln	FRAMES HIFT	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
7007	cg43983535	722	GAAGAACTCCAG TCGTTGTAGTTG Tgap/CJGCGGAA TTCAAAATTCTACA AGAAAGG	gap	C	Asp (9178)	Thr	FRAMES HIFT	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
7008	cg43983535	726	GAAGTCCAGTCG TTGTAGTTGTGC G[G]gapJAAATCA AATTCTACAAGA AGGTCCA	G	gap	Phe (9179)	Phe	FRAMES HIFT	laminin	Human Gene SWISSPROT-ID:P24043 LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY CHAIN) - HOMO SAPIENS (HUMAN), 3110 aa.	0	6 (6q22)
7009	cg43296393	1540	GGCCTACCTGG CTGCCCTCACCC AGgap/CJTCCGC GCTCTGGTCTAC TACGCCCA	gap	C	Ala (9180)	Val	FRAMES HIFT	lipase	Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa.	0	
7010	cg43296393	1620	TACTCTCTTTGA GGGCGACGAGG G[G]gapJCTCACC GCCGACTTCCTC CGGGAGT	G	gap	Ser (9181)	Leu	FRAMES HIFT	lipase	Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa.	0	
7011	cg43296393	1636	CGACGAGGGGC TCACCGCCGACT TC[C]gapJTCCGG GAGTATGTCACG CTGCATAA	C	gap	Ser (9182)	Leu	FRAMES HIFT	lipase	Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa.	0	

7012	cg43296393	2183	AACGGAGCCTG GAGCTGTGGCC GCG[ <del>gap</del> /C]CCCC AGCAGGCACCC CGCTCGCGGT	gap	C	Arg (9183)	Arg (9183)	FRAMES HIPT	lipase	Human Gene SWISSPROT-ID:Q05469 HORMONE SENSITIVE LIPASE (EC 3.1.1.-) (HSL) - HOMO SAPIENS (HUMAN), 775 aa.	0	0
7013	cg43921881	455	GGGGAGCTGG ACCTGGCGGG GAG[C/ <del>gap</del> ]CCCC TCAGCTGAGGAC TCGACATTG	C	gap	Ala	Leu (9184)	FRAMES HIPT	MHC	Human Gene Similar to SWISSPROT- ID:P46379 LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3) - HOMO SAPIENS (HUMAN), 1132 aa.	2.6E-63	14
7014	cg43921881	512	GACGGAGCCAC GGATGAGGCCT GCC[C/ <del>gap</del> ]AGGA CCAGGGGGAAG GTGGCCTCTG	C	gap	Gly	Gly (9185)	FRAMES HIPT	MHC	Human Gene Similar to SWISSPROT- ID:P46379 LARGE PROLINE-RICH PROTEIN BAT3 (HLA-B-ASSOCIATED TRANSCRIPT 3) - HOMO SAPIENS (HUMAN), 1132 aa.	2.6E-63	14
7015	cg43957213	580	GTGGGGTTCCC ACCCAAGTTCAA G[ <del>gap</del> /G]AGGAGG AGCAGACATCTG TGCTACT	gap	G	Leu	Pro (9186)	FRAMES HIPT	misc_cha nnel	Human Gene SWISSNEW-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa. ipcds:SWISSPROT-ID:P37088 AMILORIDE-SENSITIVE SODIUM CHANNEL ALPHA-SUBUNIT (LUNG NA+ CHANNEL ALPHA SUBUNIT) (ALPHA ENAC) (NONVOLTAGE-GATED SODIUM CHANNEL 1 ALPHA SUBUNIT) (SCNEA) (ALPHA NACH) - HOMO SAPIENS (HUMAN), 669 aa. ipcds:TREMBLNEW-ID:E308262 AMILORIDE-SENSITIVE EPITHELIAL SODIUM CHANNEL ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 669 aa.	0	1 (1p36.1)

7016	cg43924981	481	CCACCGCGTGC CCTTCCACCGTG TG[G/gap]ACACC ATCTCCGTCAAT GGCTCTGT	G	gap	Asp	Thr (9187)	FRAMES HIFT	misc_cha nnel	Human Gene Homologous to SPTREMBL-ID:P97840 URATE TRANSPORTER/CHANNEL - RATTUS NORVEGICUS (RAT), 322 aa.	2.4E-130	
7017	cg43309398	825	TGGAGAAATGGGA GATTGTGAGTGC A[gap/A]CAGGGA GCAAAGGAAACA GAACCGA	gap	A	Gln	Thr (9188)	FRAMES HIFT	misc_cha nnel	Human Gene Similar to SPTREMBL- ID:P91197 SIMILAR TO LIGAND-GATED IONIC CHANNEL PROTEIN - CAENORHABDITIS ELEGANS, 461 aa.	2.1E-67	15 (15q24)
7018	cg43991048	6715	TTGCGAGGGTC GAGCAATTGCT GG[G/gap]TTTCT GCCTCTGCGTTT CCCATAAT	G	gap	Thr	Thr (9189)	FRAMES HIFT	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	0	17
7019	cg30421838	2225	CTGGAGGAGGA GCCGCGGCTTG TCC[C/gap]GCCG GGGCGGCAGC AGGAGGCGTC	C	gap	Ala	Pro (9190)	FRAMES HIFT	nucl_rec pt	Human Gene SWISSNEW-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa.[pcls:SWISSPROT-ID:P06401 PROGESTERONE RECEPTOR (PR) - HOMO SAPIENS (HUMAN), 933 aa.	0	11 (11q22)
7020	cg43249083	2410	CAAGCTGCTGCT CAAGCTGCCCG AC[C/gap]TGCGG ACCCTGAACAAC ATGCATTG	C	gap	Leu	Cys (9191)	FRAMES HIFT	nucl_rec pt	Human Gene SWISSPROT-ID:P20393 V- ERBA RELATED PROTEIN EAR-1 - HOMO SAPIENS (HUMAN), 614 aa.	0	17 (17q11.2)
7021	cg43949886	1962	TATGACATGATG GAGGGCCGCGT GG[G/gap]CAGAG CCATCTCCTCAG CCAGCATC	G	gap	Gly	Ala (9192)	FRAMES HIFT	nucl_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.4E-167	

7022	cg43949886	2149	GGGAGGCCAAG CTCCTAAAGCGG GA[G/gap]GGCAC GCCTCCGCCCC CACCGCCCT	G	gap	Gly	Ala (9193)	FRAMES HIFT	nuc_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.4E-167	
7023	cg43949886	2207	CCTGACCGAGG CCTACAAGACGC AG[G/gap]CCCTG GGCCCCCTGAA GCTGAAGCC	G	gap	Ala	Pro (9194)	FRAMES HIFT	nuc_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.4E-167	
7024	cg43949886	2308	ATGAGATCCCCG GCGAGGAGCTG CG[G/gap]CACAC GCCCCGAGCTGC CCCTGGCCCC	G	gap	His	Thr (9195)	FRAMES HIFT	nuc_rec pt	Human Gene SPTREMBL-ID:Q60974 NUCLEAR RECEPTOR CO- REPRESSOR - MUS MUSCULUS (MOUSE), 2453 aa.	2.4E-167	
7025	cg44128653	1705	ATGAGTGCCCTG CCGTCCCGCCA GC[C/gap]TCCGG AGCTCTCGTCCA GATACTTG	C	gap	Gly	Ala (9196)	FRAMES HIFT	nuclease	Human Gene SWISSNEW-ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa. ID:O00115 DEOXYRIBONUCLEASE II PRECURSOR (EC 3.1.22.1) (DNASE II) (ACID DNASE) (LYSOSOMAL DNASE II) (R31240_2) - HOMO SAPIENS (HUMAN), 360 aa.	1.4E-203	19
7026	cg43947341	285	GCTCTTACTTC TGAGGGCCCCAG GC[C/gap]TGGGC ATAAGGCCAGAT CTTCTCTT	C	gap	Gly	Ala (9197)	FRAMES HIFT	nuclease	Human Gene Homologous to SWISSPROT-ID:P07992 DNA EXCISION REPAIR PROTEIN ERCC-1 - HOMO SAPIENS (HUMAN), 297 aa.	1.1E-115	

7027	cg43969123	2515	CATCGGCAAGAA CCACGTGGCAGT G[C/gap]CCACAC ACTTCTCAAGG TGCTGAT	C	gap	Pro	Pro (9198)	FRAMES HIFT	nuclease	Human Gene Similar to SWISSPROT- ID:P38447 ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G) - BOS TAURUS (BOVINE), 299 aa.	1.2E-65	9
7028	cg43969123	2517	TCGGCAAGAAC ACGTGGCAGT CC[C/gap]ACACA CTTCTCAAGT GCTGATCC	C	gap	Thr	His (9199)	FRAMES HIFT	nuclease	Human Gene Similar to SWISSPROT- ID:P38447 ENDONUCLEASE G PRECURSOR (EC 3.1.30.-) (ENDO G) - BOS TAURUS (BOVINE), 299 aa.	1.2E-65	9
7029	cg43242829	570	GCGTGCTCAGCT GGCTTCGTGGAC G[G/gap]CACAGC CCTGGCGGACC TCAGCCAT	G	gap	Gly	Ala (9200)	FRAMES HIFT	nuclease	Human Gene Similar to SWISSPROT- ID:Q17533 RIBONUCLEASE PH-LIKE PROTEIN B0564.1 - CAENORHABDITIS ELEGANS, 312 aa.	2E-50	
7030	cg43951535	1528	ATCTGGTGGTGA ACTACAGCGAGT A[G/gap]CTTTTA GCCCTTTGCTTG GGCAAAC	G	gap	Ala	Leu (9201)	FRAMES HIFT	nuclease nhib	Human Gene SPTREMBL-ID:Q13181 RNASE L INHIBITOR - HOMO SAPIENS (HUMAN), 599 aa.	2.5e-315	4 (4q31)
7031	cg43918816	591	GGGACCCCATC CCCATCTCGAGG AG[G/gap]CCCCG CCCCATTGTCTT CCTCCGCC	G	gap	Pro	Leu (9202)	FRAMES HIFT	oncogen e	Human Gene SPTREMBL-ID:Q61210 LSC (LSC) ONCOGENE - MUS MUSCULUS (MOUSE), 919 aa.	0	19
7032	cg44012756	5289	TGCTGCTGTCCC GCAAGCGCCGG CG[G/gap]CAGCA TGGCCAGCTCTG GTTCCCTG	G	gap	Gln	Ser (9203)	FRAMES HIFT	oncogen e	Human Gene SWISSPROT-ID:P31695 NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 4 PRECURSOR (TRANSFORMING PROTEIN INT-3) - MUS MUSCULUS (MOUSE), 1964 aa.	0	
7033	cg42732993	592	CACTGGATTAA GCAGAGTTCAAA A[G/gap]CCCTTC AGCGGCCAGTA GCATCTGA	G	gap	Ala	Pro (9204)	FRAMES HIFT	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q13692 BCR/ABL FUSION PROTEIN - HOMO SAPIENS (HUMAN), 284 aa (fragment).	6E-150	

7034	cg43918770	4789	AGAGGATCTGGA CAGCCAAGGAG AC[G/gap]GCAGC AGCCAGCCTGAT ACGATTTCC	G	gap	Gly	Ala (9205)	FRAMES HIFT	oncogen e	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.6E-140	5
7035	cg43918770	4790	GAGGATCTGGAC AGCCAAGGAGA CG[G/gap]CAGCA GCCAGCCTGATA CGATTTCC	G	gap	Gly	Ala (9206)	FRAMES HIFT	oncogen e	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.6E-140	5
7036	cg43918770	4821	GCCAGCCTGATA CGATTTCATCG C[G/gap]TCACGG ACGTCCTCAGAAC ACGCTGG	C	gap	Ser	His (9207)	FRAMES HIFT	oncogen e	Human Gene Homologous to SPTREMBL-ID:P91339 SIMILARITY TO HUMAN PROTO-ONCOGENE DBL - CAENORHABDITIS ELEGANS, 1548 aa.	1.6E-140	5
7037	cg43297056	996	AGACTTCGGAC TTTCTTGATGGG G[gap]/CTCCGCC GCAGCCAGGC TTCTCTCTT	gap	C	Thr	Ser (9208)	FRAMES HIFT	oncogen e	Human Gene Homologous to SPTREMBL-ID:Q28080 PROTOONCOGENE C-MYB - BOS TAURUS (BOVINE), 555 aa.	1.9E-103 (20q13.1)	20
7038	cg43292762	1145	AGACTACTGTAT CAGGACCCGAG AG[G/gap]CAGGC TCCCTGGGTACA GCAGGCCG	G	gap	Ala	Gln (9209)	FRAMES HIFT	oncogen e	Human Gene Similar to SWISSPROT- ID:P17553 WNT-3 PROTO-ONCOGENE PROTEIN PRECURSOR - MUS MUSCULUS (MOUSE), 355 aa.	3E-84 7 (7q31)	15
7039	cg43307658	1767	AGACTTCCTCCC CAACCGGCCAC GC[C/gap]ACACC TGGAGTGGCA CAGCTGCCA	C	gap	His	Thr (9210)	FRAMES HIFT	oxidase	Human Gene SPTREMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0	15

7040	cg43307658	1853	ACGACCTACTGG ATGCAGCCACAG G[C/gap]AAGAAG GTGGCCGAGGG CCACAAGG	C	gap	Lys	Arg (9211)	FRAMES HIFT	oxidase	Human Gene SPTRMBL-ID:Q08397 PROTEIN-LYSINE OXIDASE HOMOLOG PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE HOMOLOG) (LYSYL OXIDASE-LIKE PROTEIN) - HOMO SAPIENS (HUMAN), 574 aa.	0	15
7041	cg44028217	584	CCATGGAGTAGA TCTGCAGGCGGT Algap/G[CTGCGC TTGTGGCCCCAG GGGTTCT	gap	G	Tyr	Leu (9212)	FRAMES HIFT	oxidase	Human Gene SWISSPROT-ID:P19801 AMILORIDE-SENSITIVE AMINE OXIDASE (COPPER-CONTAINING) PRECURSOR (EC 1.4.3.6) (DIAMINE OXIDASE) (DAO) (AMILORIDE-BINDING PROTEIN) (ABP) (HISTAMINASE) - HOMO SAPIENS (HUMAN), 751 aa.	0	7 (7q31)
7042	cg43969851	1187	CAGAGGCCCCAC ATCTCCAGCTGC AA[G/gap]CTGGG CCCCCAGGTGTC ACTGGACC	G	gap	Leu	Trp (9213)	FRAMES HIFT	oxidase	Human Gene TREMBLNEW- ID:G1890108 LYSYL OXIDASE- RELATED PROTEIN - HOMO SAPIENS (HUMAN), 774 aa.	0	
7043	cg43972840	929	AGACAAAGGTGC CCTGGAGGGCA GC[A/gap]GCTGT CCCTCCGAACA GCTATGGC	A	gap	Ser	Ala (9214)	FRAMES HIFT	oxyge nase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168	16 (16p13.3 )
7044	cg43972840	953	CAGCTGTCCCTT CCGAACAGCTAT G[G/gap]CTGTGC TGAGGAAGCCCA GCCTCCA	G	gap	Ala	Leu (9215)	FRAMES HIFT	oxyge nase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168	16 (16p13.3 )
7045	cg43972840	1002	CAGTTCATCCTG GCCGCTGGTGT GG[C/gap]CCTAG CTGCTGGACTCT TGGCCTGG	C	gap	Ala	Ala (9216)	FRAMES HIFT	oxyge nase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168	16 (16p13.3 )



7046	cg43972840	753	AAGACCAAAGAG AGGATCGTGA GG[A/gap]GGCCA ACAAGGCTTTTG AGTATAAC	A	gap	Glu	Gly (9217)	FRAMES HIFT	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME-OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168	16 (16p13.3)
7047	cg43972840	913	TCTACGCTGCTG AACAAGACAAAG GTT[gap]GCCCTG GAGGGCAGCAG CTGTCCCT	T	gap	Ala	Pro (9218)	FRAMES HIFT	oxygenase	Human Gene SWISSPROT-ID:P30519 HEME OXYGENASE 2 (EC 1.14.99.3) (HO-2) - HOMO SAPIENS (HUMAN), 316 aa.	4.6E-168	16 (16p13.3)
7048	cg44010395	718	GGGAGCGGGTG TTGAGTGGGG CTT[C/gap]CCTC TGGAGTCTCCA CGGGGGCAG	C	gap	Gly	Gly (9219)	FRAMES HIFT	oxygenase	Human Gene SWISSNEW-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.lpcis:SWISSPROT-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.	5.2E-151	22 (22q12)
7049	cg44010395	772	CTTGCACTTTGT TGCTGGCCCGCT G[G/gap]CGAAGC CCTGGTGCCCGT GAGGGGC	G	gap	Arg	Arg (9220)	FRAMES HIFT	oxygenase	Human Gene SWISSNEW-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.lpcis:SWISSPROT-ID:P09601 HEME OXYGENASE 1 (EC 1.14.99.3) (HO-1) - HOMO SAPIENS (HUMAN), 288 aa.	5.2E-151	22 (22q12)
7050	cg43918857	776	GCGCCCTCATCG AGTGGATCCGCA G[G/gap]AACAAAG TTGTGCTTTCT GGAAATC	G	gap	Asn	Thr (9221)	FRAMES HIFT	peptidase	Human Gene Similar to SPTRMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	3.4E-96	17
7051	cg43254736	692	CATCTGGGGCTG TGGTGATGTCGT G[G/gap]CGAATG CCTTTGACTGAG ATCCGGG	G	gap	Arg	Arg (9222)	FRAMES HIFT	peptidase	Human Gene Similar to SPTRMBL- ID:P91359 SIMILARITY TO THE M14 PEPTIDASE FAMILY - CAENORHABDITIS ELEGANS, 985 aa.	1.1E-67	

7052	cg42691989	846	CGAAGCCACATT CTCAATCAGCAC G[G/gap]CCCTGC CCCGGAACGTAT TGAAATC	G	gap	Ala (9223)	Ala	FRAMES HIFT	peroxidase	Human Gene Homologous to SWISSPROT-ID:P18283 GLUTATHIONE PEROXIDASE-GASTROINTESTINAL (EC 1.11.1.9) (GSHPX-GI) (GLUTATHIONE PEROXIDASE- RELATED PROTEIN 2) (GPRP) - HOMO SAPIENS (HUMAN), 190 aa.	8.9E-101	14 (14q24.1)
7053	cg40084915	4336	CTCAGCAAAAGC CAGGCCCTTTGGG G[G/gap]CCCTCA TGGGCTCTGCG CATTGGT	G	gap	Ala (9224)	Ala	FRAMES HIFT	phosphatase	Human Gene SPTREMBL-ID:O00197 RECEPTOR PROTEIN TYROSINE PHOSPHATASE HPTP-J PRECURSOR - HOMO SAPIENS (HUMAN), 1436 aa.	0	1
7054	cg42548845	2808	TGCGAGAACTGC TGAAAAATTCAG C[A/gap]AAAAAAT CATTGGATGAG AATATT	A	gap	Gln (9225)	Gln	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	0	
7055	cg42548845	2814	AACTGCTGAAAA ATTCAGCAAAAA A[A/gap]TCATTG GATGAGAAATAT CTAGCT	A	gap	Ile (9226)	Asn	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P32019 TYPE II INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 942 aa (fragment).	0	
7056	cg43139469	885	TGGATAGCGACA ATCAATGACATA A[A/gap]ACTTCTC AATCAGACCCCTG GAACCT	A	gap	Phe (9227)	Phe	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa.	7E-259	5 (5q31)
7057	cg43139469	886	GGATAGCGACAA TCAATGACATAA A[A/gap]CTTCTCA ATCAGACCCCTGG AACTTC	A	gap	Phe (9228)	Phe	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P30307 M PHASE INDUCER PHOSPHATASE 3 (EC 3.1.3.48) - HOMO SAPIENS (HUMAN), 473 aa.	7E-259	5 (5q31)

7058	cg43988365	2487	ACCATTTGCACT CGGGGAAGTAG TC[C/gap]TGCGG AAACTTCTCCTT CTCCAGCA	C	gap	Gln (9229)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:Q14642 TYPE I INOSITOL-1,4,5- TRISPHOSPHATE 5-PHOSPHATASE (EC 3.1.3.56) (5PTASE) - HOMO SAPIENS (HUMAN), 412 aa.lpcis:SPTREMBL-ID:Q14642 INOSITOL 1,4,5-TRIPHOSPHATE 5- PHOSPHATASE - HOMO SAPIENS (HUMAN), 412 aa.	2.6E-227	10
7059	cg43307302	949	TGGAAGAAGACTT TCTAAGGAAGAC T[gap/T]ACCTCCT GCGTTTGATCAT TCACCA	gap	T	Leu (9230)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P17706 T- CELL PROTEIN-TYROSINE PHOSPHATASE (EC 3.1.3.48) (TCPTP) - HOMO SAPIENS (HUMAN), 415 aa.	8.7E-218 (18p11.3)	18
7060	cg42921141	90	CCTCCTCCTGGC CAGGGCAGCAA GC[C/gap]TTAGC CTTGCTTCTTG TTTCTGCT	C	gap	Leu (9231)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:P15309 PROSTATIC ACID PHOSPHATASE PRECURSOR (EC 3.1.3.2) - HOMO SAPIENS (HUMAN), 386 aa.	6.8E-213 3 (3q21)	10
7061	cg43269274	1194	GAGACTGTTGAG TGGTAGGCAC CG[G/gap]TGCCA GCACCGAGCA GGGAATGTG	G	gap	Pro (9232)	FRAMES HIFT	phosphatase	Human Gene SWISSPROT-ID:Q16890 DUAL SPECIFICITY PROTEIN PHOSPHATASE 5 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE HVH3) - HOMO SAPIENS (HUMAN), 384 aa.	3.2E-151	10
7062	cg43272594	663	GTCCAGTTCTTC CTGGTGGCCTTT G[C/gap]CCTCTA CGTGGGCTACAC CCGCGTG	C	gap	Ala (9233)	FRAMES HIFT	phosphatase	Human Gene Similar to SPTREMBL- ID:Q61469 PHOSPHATIDIC ACID PHOSPHATASE - MUS MUSCULUS (MOUSE), 283 aa.	1.4E-79	19

7063	cg43985274	612	AAGGCCAAGTTC TGTGAGGCCCC CG[G/gap]CAGCT GCGTGGCTGTG CACTGCGTG	G	gap	Gly	Ala (9234)	FRAMES HIFT	phosphatase	Human Gene Similar to SPTREMBL-ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa. ipcds:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa. ipcds:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa.	7.8E-70	
7064	cg43985274	650	TGTGCACTGCGT GGCGGGCCCTGG GC[C/gap]GGGCT CCAGTCCTTTGTG GCGCTGGC	C	gap	Arg	Gly (9235)	FRAMES HIFT	phosphatase	Human Gene Similar to SPTREMBL-ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa. ipcds:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa. ipcds:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa.	7.8E-70	
7065	cg43985274	675	CGGGCTCCAGT CCTTGTCGCGCT GG[C/gap]CCTTA TTGAGAGCGGG ATGAAGTAC	C	gap	Ala	Ala (9236)	FRAMES HIFT	phosphatase	Human Gene Similar to SPTREMBL-ID:O00648 PROTEIN TYROSINE PHOSPHATASE PTPCAAX1 - HOMO SAPIENS (HUMAN), 173 aa. ipcds:SPTREMBL-ID:Q63739 TYROSINE PHOSPHATASE - RATTUS NORVEGICUS (RAT), AND MUS MUSCULUS (MOUSE), 173 aa. ipcds:TREMBLNEW-ID:G2961199 TYROSINE PHOSPHATASE - HOMO SAPIENS (HUMAN), 173 aa.	7.8E-70	
7066	cg43948077	1428	GGGGCAAGGTTT GGGTATGGCATG G[G/gap]CAAGCC ACCGATGAGTGC TGTCCTCA	G	gap	Pro	Pro (9237)	FRAMES HIFT	phosphatase inhib	Human Gene Homologous to SPTREMBL-ID:Q28147 NIPP-1, NUCLEAR INHIBITOR OF PROTEIN PHOSPHATASE-1 - BOS TAURUS (BOVINE), 351 aa.	2.1E-146	1

7067	cg44005370	384	GACAGCCGGAG CGCCCGGCAAT GGC[G/gap]GCCT CGACGGCCTCG CACC GGCCCA	G	gap	Ala	Pro (9238)	FRAMES HIFT	phosphat aseinhib	Human Gene Homologous to SWISSPROT-ID:P41236 PROTEIN PHOSPHATASE INHIBITOR 2 (IPP-2) - HOMO SAPIENS (HUMAN), 204 aa.	1.5E-105	
7068	cg43301213	490	CAAGGCTGGC ACCTCTGGACA GC[A/gap]AAAA AAACTGCAGAA GCATCCCT	A	gap	Lys	Lys (9239)	FRAMES HIFT	phosphat aseinhib	Human Gene Similar to SWISSPROT- ID:Q13522 PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (I-1) - HOMO SAPIENS (HUMAN), 171 aa.	7.8E-70	12
7069	cg43301213	498	GGACCTCTGG GACAGCAAAAA AA[A/gap]CTGCA GAATGCATCCCT AAAACTCA	A	gap	Asn	Thr (9240)	FRAMES HIFT	phosphat aseinhib	Human Gene Similar to SWISSPROT- ID:Q13522 PROTEIN PHOSPHATASE INHIBITOR 1 (IPP-1) (I-1) - HOMO SAPIENS (HUMAN), 171 aa.	7.8E-70	12
7070	cg43988162	295	ATGAAGTAGCTC ACCAGCCGCTG CG[G/gap]CCTCT GCTGGTACTCGC TGAGCACA	G	gap	Pro	Arg (9241)	FRAMES HIFT	phosphor ylase	Human Gene SWISSPROT-ID:Q16831 URIDINE PHOSPHORYLASE (EC 2.4.2.3) (UDRPASE) - HOMO SAPIENS (HUMAN), 310 aa.	1.8E-164	7
7071	cg43988162	449	AGGACTCCATCT CGATATTGCGGA C[G/gap]CCGGCT GCATAGGCTGCC TCCAGAT	G	gap	Gly	Gly (9242)	FRAMES HIFT	phosphor ylase	Human Gene SWISSPROT-ID:Q16831 URIDINE PHOSPHORYLASE (EC 2.4.2.3) (UDRPASE) - HOMO SAPIENS (HUMAN), 310 aa.	1.8E-164	7
7072	cg43998195	1251	GAACCTGCCCTG CATCATCACACA G[G/gap]CCCTGC CATTGAGGAACC CAAACAC	G	gap	Ala	Ala (9243)	FRAMES HIFT	phosphor ylase	Human Gene SWISSPROT-ID:P00491 PURINE NUCLEOSIDE PHOSPHORYLASE (EC 2.4.2.1) (INOSINE PHOSPHORYLASE) (PNP) - HOMO SAPIENS (HUMAN), 289 aa.	2.4E-155	

7073	cg44022214	144	GTCCAGGGGGT CCGAAGCGCCG CAG[G/gap]AGCT GCTCCTGGTCTT CCAGGTCCT	G	gap	Leu	Leu (9244)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa. pcds:SWISSPROT- ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.	0	19 (19q13.3)
7074	cg44022214	281	ACTGCGTCCAGA GGCGCGAGAAG CG[gap]/CTCCTC CAGGGCATTGAG ATGGGATA	gap	C	Arg	Ala (9245)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa. pcds:SWISSPROT- ID:P28340 DNA POLYMERASE DELTA CATALYTIC CHAIN (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 1107 aa.	0	19 (19q13.3)
7075	cg43923788	547	CCTTTGCTGAA TTCATTAGTGAT G[C/gap]TTTCAG CAAGTGGTGGC CTTGGTAA	C	gap	Ser	Thr (9246)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P56282 DNA POLYMERASE EPSILON SUBUNIT B (EC 2.7.7.7) (DNA POLYMERASE II SUBUNIT B) - HOMO SAPIENS (HUMAN), 527 aa. pcds:TREMBLNEW- ID:G2832260 DNA POLYMERASE EPSILON SMALL SUBUNIT - HOMO SAPIENS (HUMAN), 527 aa.	1.2E-288	
7076	cg4398632	236	CTTTTGTGAGTC AGGGGCCCCAGC CC[gap]/CJAGGCC TCCCAGGTCATC GTCCTCTG	gap	C	Leu	Leu (9247)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa. pcds:SWISSPROT-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.	6E-237	7

7077	cg43988632	295	CCCAGAAAGCT GATGGCTGGC AGG[C/gap]CAGG CTGCGCAGGTTT ACAAGGCAG	C	gap	Ala	Pro (9248)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.lpcis:SWISSPROT-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.	6E-237	7
7078	cg43988632	296	CCGAGAAGCTGA TGGGCTGGCAG GC[C/gap]AGGCT GCGCAGGTTTAC AAGGCAGG	C	gap	Leu	Leu (9249)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.lpcis:SWISSPROT-ID:P49005 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 469 aa.	6E-237	7
7079	cg43988623	1667	CCTGCCCTTGTA ACCTGCGCAGC CT[G/gap]GCCTG CCAGCCCATCAG CTTCTCGG	G	gap	Ala	Pro (9250)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.lpcis:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.	7E-199	
7080	cg43988623	529	GCGCAGCTTTAG CCGGCAGTATGC C[C/gap]ACATTTA TGCCACCCGCCT CATCCA	C	gap	His	Thr (9251)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.lpcis:SWISSPROT- ID:P49004 DNA POLYMERASE DELTA SMALL SUBUNIT (EC 2.7.7.7) - BOS TAURUS (BOVINE), 469 aa.	7E-199	
7081	cg43988632	579	GAACACACACAGT AATACTGATCTTT [gap/T]GGGTATC AACCTGATATCA ATTCTT	gap	T	Lys	Lys (9252)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.lpcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)

7082	cg43993893	586	CACAGTAATACT GATCTTTGGTA TTC/gapAACCTG ATATCAATTCTTC TGTGTG	gap	Leu	Leu (9253)	FRAMES HIFT	polymera se	Human Gene SWISSNEW-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.lpcis:SWISSPROT-ID:P06746 DNA POLYMERASE BETA (EC 2.7.7.7) - HOMO SAPIENS (HUMAN), 334 aa.	5E-178	8 (8p11.2)
7083	cg43333426	1585	CAGCCACCTGGAC CCTGGAGCGCAT GTC/gapJAGGCTT CCCTCCCGCTG GACAACAT	gap	Gln	Arg (9254)	FRAMES HIFT	potassiu m_chann el	Human Gene SWISSNEW-ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.lpcis:SWISSPROT- ID:P48050 INWARD RECTIFIER POTASSIUM CHANNEL 4 (POTASSIUM CHANNEL, INWARDLY RECTIFYING, SUBFAMILY J, MEMBER 4) (HIPPOCAMPAL INWARD RECTIFIER) (HIR) (HRK1) (HIRK2) (KIR2.3) - HOMO SAPIENS (HUMAN), 445 aa.	4.4E-241	
7084	cg43008113	670	CGCATCACCGTG CAGGTCACCCGC A[G/gap]GCCGGT CCTCTACTTCCA CATCCGC	gap	Arg	Ser (9255)	FRAMES HIFT	potassiu m_chann el	Human Gene SPTREMBL-ID:O00180 POTASSIUM CHANNEL KCNO1 - HOMO SAPIENS (HUMAN), 336 aa.lpcis:TREMBLNEW-ID:G281120 TWO P DOMAIN POTASSIUM CHANNEL SUBUNIT - HOMO SAPIENS (HUMAN), 336 aa.	1.8E-180	1



7085	cg44131493	1304	GAAGAGTACTGC ATGGCCGTGTGT GIG[gap]CAGCGC CATGTCCCAAG TTTACTC	G	gap	Gly	Ala (9256)	FRAMES HIFT	protease	Human Gene SWISSNEW-ID:P05067 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II) (PN-II) (APP1) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)] - HOMO SAPIENS (HUMAN), 770 aa. Jcds:SWISSPROT-ID:P05067 ALZHEIMER'S DISEASE AMYLOID A4 PROTEIN PRECURSOR (PROTEASE NEXIN-II) (PN-II) (APP1) [CONTAINS: BETA-AMYLOID PROTEIN (BETA-APP)] - HOMO SAPIENS (HUMAN), 770 aa.	0	21
7086	cg43916732	1058	GCCCAAAGCAGT GCCGCCGGACA GG[C/gap]ACCTT GCAGAGCAACTT CTGTGCCA	C	gap	Thr	Pro (9257)	FRAMES HIFT	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.2E-247 (7q21.3)	7 (7q21.3)
7087	cg43916732	773	GAGCCGTGAGC GACGACTCCCG GAG[G/gap]CTGG GGAAGTTCTGCG GCGACGCAG	G	gap	Leu	Trp (9258)	FRAMES HIFT	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.2E-247 (7q21.3)	7 (7q21.3)
7088	cg43916732	914	ACAAGACCCTGC CGCGGGGCACT GC[C/gap]AAAGA AGGGCAAGGC CCGGCCCCA	C	gap	Lys	Lys (9259)	FRAMES HIFT	protease	Human Gene SPTREMBL-ID:Q15113 PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN PRECURSOR - HOMO SAPIENS (HUMAN), 449 aa.	1.2E-247 (7q21.3)	7 (7q21.3)
7089	cg42538037	1038	TCTGCCATGGAT GAAAACTCAGAG A[gap/A]GAAAAG GAAGAGGGCCA TCAAACTC	gap	A	Arg	Lys (9260)	FRAMES HIFT	protease	Human Gene SWISSPROT-ID:P55085 PROTEINASE ACTIVATED RECEPTOR 2 PRECURSOR (PAR-2) - HOMO SAPIENS (HUMAN), 397 aa.	2.6E-207	5

7090	cg43921678	459	CTGGCTTCCATG GATTGAGGCCTC T[G/gap]GCCGGA GCTGCCTGGTCC CAGAGTG	gap	Gln	Arg (9281)	FRAMES HIFT	protease	Human Gene SPTREMBL-ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	8.2E-185	15
7091	cg43921678	460	TGGCTTCCATGG ATTGAGGCCTCT G[G/gap]CCGGAG CTGCCTGGTCCC AGAGTGG	gap	Gly	Gly (9262)	FRAMES HIFT	protease	Human Gene SPTREMBL-ID:Q14868 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	8.2E-185	15
7092	cg43306871	642	ATCTGGGTGTAG ACAGCTGGATGC T[G/gap]GGCAGA GCCACAGGGGT AAACACCC	gap	Gln	Ser (9263)	FRAMES HIFT	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. Jpdis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.1E-153	19
7093	cg43306871	644	CTGGGTGTAGAC AGCTGGATGCTG G[G/gap]CAGAGC CACAGGGGTAA CACCCCA	gap	Ala	Ala (9264)	FRAMES HIFT	protease	Human Gene SWISSNEW-ID:O43240 PROTEASE SERINE-LIKE 1 PRECURSOR (EC 3.4.21.-) (NORMAL EPITHELIAL CELL-SPECIFIC 1) - HOMO SAPIENS (HUMAN), 276 aa. Jpdis:TREMBLNEW-ID:G2558912 SERINE PROTEASE-LIKE PROTEASE - HOMO SAPIENS (HUMAN), 276 aa.	3.1E-153	19
7094	cg43310246	2053	CTGGAGCTGGG ATTGTGCGGCAG CG[C/gap]CCCCG AGAAGGGGTG CTGAAGGAG	gap	Ala	Ala (9265)	FRAMES HIFT	protease	Human Gene Homologous to SWISSPROT-ID:P21662 NEUROENDOCRINE CONVERTASE 1 PRECURSOR (EC 3.4.21.93) (NEC 1) (PC1) (PROHORMONE CONVERTASE 1) (PROPROTEIN CONVERTASE 1) (PC3) (FURIN HOMOLOG) (PROPEPTIDE PROCESSING PROTEASE) - MUS MUSCULUS (MOUSE), AND MUS COCKI, 753 aa.	1.1E-141 (20p11.2)	20

7095	cg43930253	923	GAAAGACTGGCT AACTACACCGGA G[G/gap]CATCTA TGCCGAATACCA GGACACC	G	gap	Gly	Ala (9266)	FRAMES HIFT	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.9E-102	20
7096	cg43930253	383	GACGGGCTGGC TCCGCTGGGGC GCA[G/gap]CACA TACCCCGGCCT CATGAGTAC	G	gap	Ser	Thr (9267)	FRAMES HIFT	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.9E-102	20
7097	cg43930253	644	GGTAACGCTGG CTCCTGTGAAGG GG[G/gap]TAATG ACCTGTCCGTGT GGGACTAC	G	gap	Gly	Val (9268)	FRAMES HIFT	protease	Human Gene Homologous to SPTREMBL-ID:Q27125 CATHEPSIN B- LIKE PROTEASE - URECHIS CAUPO (INNKEEPER WORM) (SPOONWORM), 294 aa.	2.9E-102	20
7098	cg44032168	1468	TTCTGGTGGGC CTGGTGAGCTG GG[G/gap]TGAGG GCTGTGGGCTC CTTCACAAC	G	gap	Gly	Val (9269)	FRAMES HIFT	protease	Human Gene Similar to SWISSPROT- ID:P25155 COAGULATION FACTOR X PRECURSOR (EC 3.4.21.6) (STUART FACTOR) (VIRUS ACTIVATING PROTEASE) (VAP) - GALLUS GALLUS (CHICKEN), 475 aa.	2.4E-82 2 (2q13)	
7099	cg43921680	187	CTACGCCAGAC TTCAGCCCTGCC G[G/gap]AGCTGC TGCCGCCAAGA AAGCGGG	G	gap	Glu	Ser (9270)	FRAMES HIFT	protease	Human Gene Similar to SPTREMBL- ID:Q14888 EFFECTOR CELL PROTEASE RECEPTOR 1 - HOMO SAPIENS (HUMAN), 337 aa (fragment).	4.6E-77	15
7100	cg43511784	115	CTCGTGGGGCAT CTCCTGCTGGC A[G/gap]GCCTGT GCTGCCCTGGTCC CTGCTCTC	G	gap	Gly	Ala (9271)	FRAMES HIFT	protease nhib	Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1- ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa.	9.2E-212	
7101	cg43511784	116	TCGTGGGGCATC CTCCTGCTGGCA G[G/gap]CCTGTG CTGCCCTGGTCCC TGCTCTCC	G	gap	Gly	Ala (9272)	FRAMES HIFT	protease nhib	Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1- ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa.	9.2E-212	

7102	cg43511784	126	TCCTCCTGCTGG CAGGCCTGTGCT G[C/gap]CTGGTC CCTGTCTCCCTG GCTGAGG	C	gap	Leu	Trp (9273)	FRAMES HIFT	proteasei nhib	Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1-ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa.	9.2E-212	
7103	cg43511784	272	GCCTTCAGCCTA TACCGCCAGCTG G[C/gap]ACACCA GTCCAACAGCAC CAATATC	C	gap	Ala	Asp (9274)	FRAMES HIFT	proteasei nhib	Human Gene SWISSPROT-ID:P01009 ALPHA-1-ANTITRYPSIN PRECURSOR (ALPHA-1 PROTEASE INHIBITOR) (ALPHA-1-ANTIPROTEINASE) - HOMO SAPIENS (HUMAN), 418 aa.	9.2E-212	
7104	cg43268468	1212	CGCTCCACGG AGAGGCCGAG AGG[G/gap]CCGT GGCCACACTGA GAGGAGACAG	G	gap	Ala	Ala (9275)	FRAMES HIFT	proteasei nhib	Human Gene TREMBLNEW-ID:G299561 EPC-1-SERINE PROTEASE INHIBITOR HOMOLOG - HOMO SAPIENS, 359 aa.	2.6E-188 (17p13.3)	
7105	cg43059041	1118	GACACGATTAAC AGGTGGTCCGC AG[G/gap]CCTGA CCAGAGCCAG GTGGACCTG	G	gap	Gly	Ala (9276)	FRAMES HIFT	proteasei nhib	Human Gene Similar to SWISSPROT- ID:P17475 ALPHA-1-ANTIPROTEINASE PRECURSOR (ALPHA-1-ANTITRYPSIN) (ALPHA-1- PROTEINASE INHIBITOR) - RATTUS NORVEGICUS (RAT), 411 aa.	4.4E-83 (14q32.1)	
7106	cg43969711	1380	CAATTCATCCCA ATGAGCTTCACA G[G/gap]CAAGGC CTCAGTGAGGAA CTCCTGT	G	gap	Pro	Leu (9277)	FRAMES HIFT	reductas e	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.9E-208 2 (2p25)	
7107	cg43969711	1599	AATATCGACGCA AAAGAACCGGAA A[A/gap]GAAAT GCCTTCCACTGC AGCAAAG	A	gap	Phe	Phe (9278)	FRAMES HIFT	reductas e	Human Gene SWISSPROT-ID:P31350 RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) - HOMO SAPIENS (HUMAN), 389 aa.	1.9E-208 2 (2p25)	
7108	cg43941472	659	CCCGCACCAAGA CGGGAGTGGGG TA[C/gap]CCCCA GCTGAGTGCCGT CATTGAGT	C	gap	Pro	Pro (9279)	FRAMES HIFT	reductas e	Human Gene SWISSPROT-ID:P36959 GMP REDUCTASE (EC 1.6.6.8) (GUANOSINE 5'-MONOPHOSPHATE OXIDOREDUCTASE) - HOMO SAPIENS (HUMAN), 345 aa.	7.4E-184 X (Xq28)	

7109	cg43982619	411	GATGTGCTCTTC CTGGCTGTGAAG C[C/gap]ACACAT CATCCCCCTTCAT CCTGGAT	C	gap	Pro	His (9280)	FRAMES HIFT	reductas e	Human Gene SWISSPROT-ID:P32322 PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE) - HOMO SAPIENS (HUMAN), 319 aa.	4.2E-158	17
7110	cg43288949	965	CCTCATCCGCAC GGAGCCGGCTC GG[C/gap]CAACA CCAAACCACACC ACGCCAAA	C	gap	Gly	Ala (9281)	FRAMES HIFT	reductas e	Human Gene SWISSNEW-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.lpcis:SWISSPROT-ID:P53004 BILVERDIN REDUCTASE A PRECURSOR (EC 1.3.1.24) (BILVERDIN-IX ALPHA- REDUCTASE) - HOMO SAPIENS (HUMAN), 296 aa.	1.3E-152	7
7111	cg43948290	866	AATCATGGAGTG GTGTGGCTATGC C[C/gap]TGGCCA GCTGGTCTGTCC AAGGCGC	C	gap	Leu	Trp (9282)	FRAMES HIFT	reductas e	Human Gene Homologous to SWISSPROT-ID:P18405 3-OXO-5- ALPHA-STEROID 4-DEHYDROGENASE 1 (EC 1.3.99.5) (STEROID 5-ALPHA- REDUCTASE 1) (SR TYPE 1) - HOMO SAPIENS (HUMAN), 259 aa.	2.9E-141 5 (5p15)	
7112	cg43921583	275	AGTGCCATTCCT TGGGGCATTCT G[C/gap]CACTGC AGCCCTCAGGC CTGCTGCA	C	gap	Ala	Ala (9283)	FRAMES HIFT	reductas e	Human Gene Homologous to SWISSNEW-ID:P30048 MITOCHONDRIAL THIOREDOXIN- DEPENDENT PEROXIDE REDUCTASE PRECURSOR (ANTIOXIDANT PROTEIN 1) (AOP-1) (MER5 PROTEIN HOMOLOG) (HBC189) - HOMO SAPIENS (HUMAN), 256 aa.lpcis:SWISSPROT-ID:P30048 MITOCHONDRIAL THIOREDOXIN- DEPENDENT PEROXIDE REDUCTASE PRECURSOR (ANTIOXIDANT PROTEIN 1) (AOP-1) (MER5 PROTEIN HOMOLOG) (HBC189) - HOMO SAPIENS (HUMAN), 256 aa.	1.2E-135	10

7113	cg43918176	911	CCACAAGTCGCT CCGCCGTGGCC AG[G/gap]CCCAG GCCCGAGGCTC CTCCGGTTA	G	gap	Gly	Gly (9284)	FRAMES HIFT	reductas e	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2E-133	X
7114	cg43918176	917	GTCGCTCCGCC GTGGCCAGGCC CAG[G/gap]CCCG AGGCTCCTCCG GTTATTACCG	G	gap	Gly	Gly (9285)	FRAMES HIFT	reductas e	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2E-133	X
7115	cg43918176	928	GTGGCCAGGCC CAGGCCCGAGG CTC[C/gap]TCCG GTTATTACCGC ACCAGGCC	C	gap	Gly	Glu (9286)	FRAMES HIFT	reductas e	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2E-133	X

7116	cg43918176	943	CCCGAGGCTCCT CCGGTTATTACC G[C/gap]CACCAG GCCCTTCACGCT CCGACAC	C	gap	Ala	Arg (9287)	FRAMES HIFT	reductas e	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2E-133	X
7117	cg43918176	450	ATCCCGAGCAAT GGGCAGTGTTCAT G[C/gap]CCACTA TTCCCCCTTGG AAGCAGA	C	gap	Gly	Ala (9288)	FRAMES HIFT	reductas e	Human Gene Homologous to SWISSPROT-ID:Q99714 3- HYDROXYACYL-COA DEHYDROGENASE TYPE II (EC 1.1.1.35) (ENDOPLASMIC RETICULUM- ASSOCIATED AMYLOID BETA- PEPTIDE BINDING PROTEIN) (SHORT- CHAIN TYPE DEHYDROGENASE/REDUCTASE XH98G2) - HOMO SAPIENS (HUMAN), 261 aa.	2E-133	X
7118	cg43927549	728	GCGCTCCTTTCC GTAACCCACGGGA G[G/gap]CACGGC CGAGATGTACAC GAAGACA	G	gap	Gly	Ala (9289)	FRAMES HIFT	reductas e	Human Gene Homologous to SWISSPROT-ID:P16083 NAD(P)H DEHYDROGENASE (QUINONE) 2 (EC 1.6.99.2) (QUINONE REDUCTASE) (DT- DIAPHORASE) (AZOREDUCTASE) (PHYLLLOQUINONE REDUCTASE) (MENADIONE REDUCTASE) - HOMO SAPIENS (HUMAN), 231 aa.	1.6E-124 6 (6pter)	
7119	cg43332845	364	GACGTCTCTGTTT CTGGCTGTGAAG C[C/gap]ACATAT CATCCCCCTTCAT CCTGGAT	C	gap	Pro	His (9290)	FRAMES HIFT	reductas e	Human Gene Similar to SWISSPROT- ID:P32322 PYRROLINE-5- CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5CR) (P5C REDUCTASE) - HOMO SAPIENS (HUMAN), 319 aa.	4.6E-65	1

7120	cg43936109	1407	AGAGGCCGGCG GGGGGAGCAGA GTC[C/gap]JTGGC GGCTTGGAACT CCGGCCTAG	C	gap	Arg (9291)	Arg (9291)	FRAMES HIFT	ribosomal prot	Human Gene SWISSPROT-ID:P49406 PUTATIVE 60S RIBOSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 280 aa.	2.5E-151	2
7121	cg43930758	566	TCGAATGACCAC TGCTGGATGTAC CTT/gapJTITTTCT GAGCTCTGTTT GCCTTT	T	gap	Lys	Arg (9292)	FRAMES HIFT	ribosomal prot	Human Gene Similar to SWISSNEW- ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND SUS SCROFA (PIG), 140 aa.lpcis:SWISSPROT-ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 140 aa.	2.3E-70	17
7122	cg43930758	722	GTTGTCAGCACA ATTGATTACAGC TTC/gap]CTACCG GAAGACCCCAAG GAAATCCG	C	gap	Gly	Glu (9293)	FRAMES HIFT	ribosomal prot	Human Gene Similar to SWISSNEW- ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND SUS SCROFA (PIG), 140 aa.lpcis:SWISSPROT-ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 140 aa.	2.3E-70	17
7123	cg43930758	723	TTGTCAGCACA TTGATTACAGCT C[C/gap]TACCGG AAGACCCCAAGGA AATCCGG	C	gap	Gly	Glu (9294)	FRAMES HIFT	ribosomal prot	Human Gene Similar to SWISSNEW- ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND SUS SCROFA (PIG), 140 aa.lpcis:SWISSPROT-ID:P23131 60S RIBOSOMAL PROTEIN L23 (L17) - HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT), 140 aa.	2.3E-70	17
7124	cg43255045	5827	AATCCCAAGAAG GGAAGGGCCAT GG[G/gap]CGGCT TCTGGAGCCCG GCACTCATC	G	gap	Arg	Gly (9295)	FRAMES HIFT	struct	Human Gene SWISSPROT-ID:Q07283 TRICHOHYALIN - HOMO SAPIENS (HUMAN), 1898 aa.	0	1



7125	cg43927378	6235	AAGGGAAGGC CCGGCCCCCG AGC[C/gap]GCTC AGCTCCAAGCCG CCCCTGCC	C	gap	Arg	Ala (9296)	FRAMES HIFT	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
7126	cg43927378	6288	GAAGCCGCTTCT GCAGAGCTTCAC G[C/gap]TCCCGC ACCAGCCCGCG CCCCCGCA	C	gap	Ser	Pro (9297)	FRAMES HIFT	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
7127	cg43927378	715	CGCGTGAACCA GTGCATCGTGTA TC[T/gap]CGGT GAGAGCGGCTC CGGCAAGAC	T	gap	Ser	Arg (9298)	FRAMES HIFT	struct	Human Gene SPTREMBL-ID:Q13459 MYOSIN-IXB - HOMO SAPIENS (HUMAN), 2022 aa.	0	2
7128	cg43944016	2870	GGCTTGGCATTG CCCATGGGCTTC A[A/gap]GGGTCT CGGCAGGCTTG GCGTTGCC	A	gap	Leu	End (9299)	FRAMES HIFT	struct	Human Gene SWISSPROT-ID:Q15746 MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) (CONTAINS: TELOKIN) - HOMO SAPIENS (HUMAN), 1913 aa.	0	3
7128	cg43944016	642	CAAGGAAAGCTT GGGACACATCTT C[T/gap]TCAGATT CTAGTTTTTCTG CATTGA	T	gap	Glu	Glu (9300)	FRAMES HIFT	struct	Human Gene SWISSPROT-ID:Q15746 MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) (CONTAINS: TELOKIN) - HOMO SAPIENS (HUMAN), 1913 aa.	0	3
7130	cg43944016	643	AAGGAAAGCTTG GGACACATCTTC TT[T/gap]CAGATT TAGTTTTTCTGC ATTGAG	T	gap	Glu	Glu (9301)	FRAMES HIFT	struct	Human Gene SWISSPROT-ID:Q15746 MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) (CONTAINS: TELOKIN) - HOMO SAPIENS (HUMAN), 1913 aa.	0	3

7131	cg43996806	3139	AACGCTCCCTCC CATATGGCACCG C[C/gap]ATGGAA AAAGCTCAGCTC AAGCCTC	C	gap	Met	Trp (9302)	FRAMES HIFT	struct	Human Gene SWISSNEW-ID:P08648 FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-F) (INTEGRIN ALPHA-5) (VLA-5) (CD49E) - HOMO SAPIENS (HUMAN), 1049 aa.lpcis:SWISSPROT-ID:P08648 FIBRONECTIN RECEPTOR ALPHA SUBUNIT PRECURSOR (INTEGRIN ALPHA-F) (INTEGRIN ALPHA-5) (VLA-5) (CD49E) - HOMO SAPIENS (HUMAN), 1049 aa.	0	12 (12q11)
7132	cg44033566	2968	GTGGACTCAGCC CTCCGAGTGCAC A[C/gap]ACTATG CGTAGATTGCGA GGAGACC	C	gap	Thr	Asn (9303)	FRAMES HIFT	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.lpcis:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0	14 (14q22)
7133	cg44033566	2972	CTCAGCCCTCCG AGTGCACACACT A[gap/C]TGCCTA GATTGCGAGGA GACCAGCA	gap	C	Cys	Leu (9304)	FRAMES HIFT	struct	Human Gene SWISSNEW-ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.lpcis:SWISSPROT- ID:P11277 SPECTRIN BETA CHAIN, ERYTHROCYTE - HOMO SAPIENS (HUMAN), 2137 aa.	0	14 (14q22)
7134	cg42693827	2323	TGTGAACGTCAG AGTCTTGGACAC G[G/gap]CCAGGC CCAGTCCTCAAC CTGCGGC	G	gap	Ala	Pro (9305)	FRAMES HIFT	struct	Human Gene SPTREMBL-ID:Q10466 TITIN, HEART ISOFORM N2-B (EC 2.7.1.-) (CONNECTIN) - HOMO SAPIENS (HUMAN), 26926 aa.	0	2 (2q24.3)
7135	cg44001078	2033	AAGTTGAGCTTG GCCGAGAGCGA AC[C/gap]AAGGG CGTAGCCGTCAG GCACAAAC	C	gap	Gly	Val (9306)	FRAMES HIFT	struct	Human Gene TREMBLNEW- ID:G2820823 CARDIAC MYOSIN BINDING PROTEIN-C - HOMO SAPIENS (HUMAN), 1274 aa.	0	

7136	cg43916919	297	TGCATGCGCGA GATGAAGCCCTC GG[C/gap]CACCT GCAGGGCTGCC TGCCGCTCC	C	gap	Ala	Pro (9307)	FRAMES HIFT	sstruct	Human Gene SWISSNEW-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.[pcls:SWISSPROT-ID:P40121 MACROPHAGE CAPPING PROTEIN (ACTIN-REGULATORY PROTEIN CAP- G) - HOMO SAPIENS (HUMAN), 348 aa.	4.3E-188	2 (2cen)
7137	cg43304066	2303	TCAGTCCCAGTA ACCGGGCCTGG GG[ap/C]ACCTC CAGCTCCAGCC GATAGGACA	gap	C	Val	Val (9308)	FRAMES HIFT	sstruct	Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.2E-186	2
7138	cg43304066	2325	GGGGACCTCCA GCTCCAGCCGAT AG[G/gap]ACAGG TTCTCAGGGTG CACACGCA	G	gap	Ser	Ser (9309)	FRAMES HIFT	sstruct	Human Gene SPTREMBL-ID:O00379 DELTA-CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	2.2E-186	2
7139	cg43918346	684	TGCAGTCAGAAG AGACTCGTGTGT G[G/gap]CACCGC CGGGATGGAAA GTGGCAGA	G	gap	His	Thr (9310)	FRAMES HIFT	sstruct	Human Gene Homologous to SWISSPROT-ID:P15791 CALCIUM/CALMODULIN-DEPENDENT PROTEIN KINASE TYPE II DELTA CHAIN (CAM- KINASE II DELTA CHAIN) (EC 2.7.1.123) (CAMK-II, DELTA SUBUNIT) - RATTUS NORVEGICUS (RAT), 533 aa.	2.4E-130	
7140	cg43980282	3863	CCTGGGCAGCA CCTCCGGGACT GAC[ap/C]ITCG GCAGTGGCTGG GGGACTGCTT	gap	C	Thr	Thr (9311)	FRAMES HIFT	sstruct	Human Gene Homologous to SPTREMBL-ID:O00379 DELTA- CATENIN - HOMO SAPIENS (HUMAN), 792 aa.	3.9E-113	22

7141	cg43981852	662	CCGCAGTGAGATG GAGGATCGGT CG[gap]CATCC CGCCCGCTCAC CCACTCCTC	gap	Ala (9312)	Ala	FRAMES HIFT	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.8E-113	
7142	cg43981852	812	GCGCTCATGCAG TTGTAGAACCG G[gap]CGATCT CGCACTTGCTGA CCTCCAG	gap	Ala (9313)	Ala	FRAMES HIFT	struct	Human Gene Homologous to SWISSPROT-ID:Q92176 CORONIN- LIKE PROTEIN P57 - BOS TAURUS (BOVINE), 461 aa.	7.8E-113	
7143	cg42887734	249	CTGAAGAGCCTG ATGCTGGCCAAG G[C/gap]CAAGGA ATGCTGGGAGCA GGAGCAC	gap	Ala (9314)	Ala	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.6E-94	1 (1q31.3)
7144	cg42887734	250	TGAAGAGCCTGA TGCTGGCCAAG GC[C/gap]AAGGA ATGCTGGGAGCA GGAGCAC	gap	Arg (9315)	Lys	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.6E-94	1 (1q31.3)
7145	cg42887734	313	CTGAGAAAGTGC GCTACCTGGCAG A[G/gap]CGCATC CCCACGCTGCA GACCCGTG	gap	Ala (9316)	Arg	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.6E-94	1 (1q31.3)
7146	cg42887734	538	GTCGAGTCCGTG TCTCGGCTGACG C[C/gap]ATGCTC CGGGCCCTGCT GGGCTCCA	gap	Cys (9317)	Met	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P19237 TROPONIN I, SLOW SKELETAL MUSCLE (TROPONIN I, SLOW-TWITCH ISOFORM) - HOMO SAPIENS (HUMAN), 186 aa.	2.6E-94	1 (1q31.3)
7147	cg42896604	695	ACTCCTCATTCT TCACATTGAGGC G[G/gap]CCCATG GCTGCGAAGGT GTCCCGAA	gap	Gly (9318)	Gly	FRAMES HIFT	struct	Human Gene Similar to SPTREMBL- ID:Q14843 MYOSIN LIGHT CHAIN 2 - HOMO SAPIENS (HUMAN), 170 aa.	8.6E-87	12 (12q23)

7148	cg42898003	516	CTCGTCCGTCAC GTGCTCCCGG AG[G/gap]CCCTG AAAATCTCAGCC AGCTCCTC	G	gap	Ala (9319)	Ala (9319)	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.5E-80	20 (20q12)
7149	cg42898003	539	AGGCCCTGAAA TCTCAGCCAGCT CIC/gap]TCCGG TCGATGTAGCCG TCTGCAT	C	gap	Glu (9320)	Glu (9320)	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P02585 TROPONIN C, SKELETAL MUSCLE - HOMO SAPIENS (HUMAN), 159 aa.	1.5E-80	20 (20q12)
7150	cg43962741	1591	TATTGGCGTAAT GCTCTGAAAGAC GIC/gap]CCCCGG CCGTGGCTGCC CAGACGTA	C	gap	Gly (9321)	Ala (9321)	FRAMES HIFT	struct	Human Gene Similar to SWISSNEW- ID:P35080 PROFILIN II - HOMO SAPIENS (HUMAN), 139 aa. lpcis:SWISSPROT-ID:P35080 PROFILIN II - HOMO SAPIENS (HUMAN), 139 aa.	6.6E-73	3 (3q25.1)
7151	cg44014373	749	CAGTTCGTGGAT GTCACCTTGCT GIC/gap]TCTGCA CAGTGGCTGGA CTGGCTGC	C	gap	Ser	Thr (9322)	FRAMES HIFT	struct	Human Gene Similar to SPTREMBL- ID:Q07426 KERATIN - CARASSIUS AURATUS (GOLDFISH), 455 aa.	6.1E-70	17
7152	cg43936426	729	TCAAGTAGTTTC CATCCAGCCGCA GIC/gap]TAGCGC AGGTGTGGCAC GTTCTCCA	G	gap	Tyr (9323)	Tyr (9323)	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P50608 FIBROMODULIN PRECURSOR (FM) - MUS MUSCULUS (MOUSE), 376 aa.	5.6E-67	1 (1q32)
7153	cg43927885	422	GTGCAGATGCAC TCCAGGCCGGG GC[C/gap]TCCCA GTTTGAAACAAG CGCAGCCA	C	gap	Ser	Pro (9324)	FRAMES HIFT	struct	Human Gene Similar to SWISSPROT- ID:P19065 SYNAPTOBREVIN 2 (VESICLE ASSOCIATED MEMBRANE PROTEIN 2) (VAMP-2) - HOMO SAPIENS (HUMAN), AND BOS TAURUS (BOVINE), 115 aa.	1.2E-55	17
7154	cg43961860	1112	AATGCTGCTTTT CCCCACATTTGG G[A/gap]AACCAA TTACTCCAACCC GAATGGC	A	gap	Phe	Ser (9325)	FRAMES HIFT	struct	Human Gene Similar to SPTREMBL- ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.5E-51	

7155	cg43961860	1137	AAACCAATTACT CCAACCGGAATG G[C/gap]TTTGCT GCAAGTTTCCTG AAAACCT	C	gap	Ala	Pro (9326)	FRAMES HIFT	struct	Human Gene Similar to SPTREMBL- ID:Q94703 MYOSIN-RELATED PROTEIN - PHYSARUM POLYCEPHALUM (SLIME MOLD), 341 aa (fragment).	3.5E-51	
7156	cg43248320	2488	TTTGATTACAGAA GTGGCGCCCG GC[G/gap]GGCAG CAGCCCTCTTGC CCAAAGCC	G	gap	Arg	Arg (9327)	FRAMES HIFT	sulfotran sferase	Human Gene SWISSPROT-ID:P52848 HEPARAN SULFATE N- DEACETYLASEN- SULFOTRANSFERASE (EC 2.8.2.-) (N- HSST) (N-HEPARAN SULFATE SULFOTRANSFERASE) (GLUCOSAMINYL N- DEACETYLASEN- SULFOTRANSFERASE) - HOMO SAPIENS (HUMAN), 882 aa.	0	5 (5q32)
7157	cg44005661	2103	TTTTCCACACCA GAAGTTGGGG TG[G/gap]CCGAG CCCACCTCAATGA AAGGATGG	G	gap	Pro	His (9328)	FRAMES HIFT	sulfotran sferase	Human Gene SPTREMBL-ID:O00338 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 296 aa. lpcds:TREMBLNEW-ID:G2828824 SULFOTRANSFERASE - HOMO SAPIENS (HUMAN), 296 aa.	5.4E-165	
7158	cg43972499	256	ATATCTAAGTGT GCTGCCCCCGTA G[G/gap]AGGCAC TGGAAATTCCTTG CCCAGCA	G	gap	Pro	Leu (9329)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa.	0	2
7159	cg43972499	588	GTCATGTAGAGC ACATCAGTGTCA G[G/gap]CAGCGC CTCCTCAATGCT CTCGAAT	G	gap	Pro	Leu (9330)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P27708 CAD PROTEIN (CONTAINS: GLUTAMINE-DEPENDENT CARBAMOYL-PHOSPHATE SYNTHASE (EC 6.3.5.5), ASPARTATE CARBAMOYLTRANSFERASE (EC 2.1.3.2), DIHYDROOROTASE (EC 3.5.2.3)) - HOMO SAPIENS (HUMAN), 2225 aa.	0	2

7160	cg40388639	1224	TGGCTCACTCCC CCATGCCAACGG C[C/gap]TGGCCC CCAGGCCCCCA GGCCAGGA	C	gap	Leu	Trp (9331)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
7161	cg40388639	1232	TCCCCCATGCCA ACGGCCTGGCC CC[C/gap]AGGCC CCCAGGCCAGG ACCCCGCGA	C	gap	Arg	Gly (9332)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
7162	cg40388639	1245	CGGCCTGGCCC CCAGGCCCCCA GGC[C/gap]AGGA CCCCGCGAAGA AAGCAACCAG	C	gap	Gln	Arg (9333)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P29475 NITRIC-OXIDE SYNTHASE, BRAIN (EC 1.14.13.39) (NOS, TYPE I) (NEURONAL NOS) (NNOS) - HOMO SAPIENS (HUMAN), 1434 aa.	0	12 (12q24.2)
7163	cg43987111	2284	GCATGCTTTCTA TGTCCTCCACGG T[gap/T]CCACCA AGCTCAATAACA CACACTT	gap	T	Thr	Asn (9334)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P17812 CTP SYNTHASE (EC 6.3.4.2) (UTP-- AMMONIA LIGASE) (CTP SYNTHETASE) - HOMO SAPIENS (HUMAN), 591 aa.	0	18 (1p34.1)
7164	cg43981333	403	GTCACATCCAC CAGGCCCCCGG CA[G/gap]CAGGG TAGATGGGAGAG AGGGAGAG	G	gap	Ala	Val (9335)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P18858 DNA LIGASE I (EC 6.5.1.1) (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (ATP)) - HOMO SAPIENS (HUMAN), 919 aa.	0	19 (19q13.2)

7165	cg43948262	649	GCA TTT TTT CCA T T A CCAC TTT TGGAC A/gap]AAGGGGC CAGAAAGAATTC TCATGA	gap	Phe	Leu (9336)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P22102 PHOSPHORIBOSYLAMINE--GLYCINE LIGASE (EC 6.3.4.13) (GARS) (GLYCINAMIDE RIBONUCLEOTIDE SYNTHETASE) (PHOSPHORIBOSYLGLYCINAMIDE SYNTHETASE) / PHOSPHORIBOSYLFORMYLGLYCINA MIDINE CYCLO-LIGASE (EC 6.3.3.1) (AIRS) (PHOSPHORIBOSYL- AMINOIMIDAZOLE SYNTHETASE) (AIR SYNTHASE) / PHOSPHORIBOSYLGLYCINAMIDE FORMYLTRANSFERASE (EC 2.1.2.2) (GART) (GAR TRANSFORMYLASE) (5'- PHOSPHORIBOSYLGLYCINAMIDE TRANSFORMYLASE) - HOMO SAPIENS (HUMAN), 1010 aa	0	21 (21q22.1)
7166	cg43918681	911	CCACATCACACA G GCTCTTCCAGTG G[G/gap]CACACC GCCCATCCATT GAATGGA	gap	Cys	Cys (9337)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P13196 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA- AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa.	0	3 (3p21.1)
7167	cg43918681	750	GATGTACCCCTCC G AACACAACCAAA G[G/gap]CTTTGC CAAGTGTTCCAG AAATGAT	gap	Ala	Ala (9338)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P13196 5- AMINOLEVULINIC ACID SYNTHASE MITOCHONDRIAL PRECURSOR, NONSPECIFIC (EC 2.3.1.37) (DELTA- AMINOLEVULINATE SYNTHASE) (DELTA-ALA SYNTHETASE) (ALAS-H) - HOMO SAPIENS (HUMAN), 640 aa.	0	3 (3p21.1)
7168	cg43976335	475	GCCCTCACACAG C GGTATGGGTGT C[C/gap]AGGACT GCCACTCCCGCT GCCACAC	gap	Leu	Leu (9339)	FRAMES HIFT	synthase	Human Gene SWISSPROT-ID:P48637 GLUTATHIONE SYNTHETASE (EC 6.3.2.3) (GLUTATHIONE SYNTHASE) (GSH SYNTHETASE) (GSH-S) - HOMO SAPIENS (HUMAN), 474 aa.	5.3E-240	20 (20q11.2)



7169	cg43959826	605	CATGGGGCTGG AGAGCCTTCCTG ATG[ <i>gap</i> ]CCAGT GGCCAGGGCTT GTGGCGTGG	G	<i>gap</i>	Gly	Gly (9340)	FRAMES HIFT	synthase	Human Gene Homologous to SWISSPROT-ID:P10746 UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75) (UROS) (UROPORPHYRINOGEN- III COSYNTHETASE) (HYDROXYMETHYLBILANE HYDROLYASE (CYCLIZING)) (UROIIIS) HOMO SAPIENS (HUMAN), 265 aa.	7E-140	10 (10q25.2)
7170	cg43959826	692	CGGCCAGCGCG CGAGCCGTAGT GGG[G <i>gap</i> ]CCGA TGGCTGCAAACT TAATTTGAT	G	<i>gap</i>	Gly	Gly (9341)	FRAMES HIFT	synthase	Human Gene Homologous to SWISSPROT-ID:P10746 UROPORPHYRINOGEN-III SYNTHASE (EC 4.2.1.75) (UROS) (UROPORPHYRINOGEN- III COSYNTHETASE) (HYDROXYMETHYLBILANE HYDROLYASE (CYCLIZING)) (UROIIIS) HOMO SAPIENS (HUMAN), 265 aa.	7E-140	10 (10q25.2)
7171	cg43933088	500	CAAGGCTGGCTT GGTGGATGACTT TIG[ <i>gap</i> ]AGAAGA AGTTTAATGCGC TGAAGGT	G	<i>gap</i>	Glu	Arg (9342)	FRAMES HIFT	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.9E-75	12
7172	cg43933088	502	AGGCTGGCTTG GTGGATGACTTT GA[G <i>gap</i> ]AAGAA GTTTAATGCGCT GAAGGTT	G	<i>gap</i>	Lys	Arg (9343)	FRAMES HIFT	synthase	Human Gene Similar to SWISSPROT- ID:P13620 ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34) - BOS TAURUS (BOVINE), 160 aa.	1.9E-75	12
7173	cg43983588	109	CAAGCCCCACCCC TCACCTGGCCTT G[C <i>gap</i> ]CCTGGG CAGCCACAGCCT CCATGGC	C	<i>gap</i>	Gly	Ala (9344)	FRAMES HIFT	synthase	Human Gene Similar to SWISSPROT- ID:P07952 BISPHOSPHOGLYCERATE MUTASE (EC 5.4.2.4) (2,3- BISPHOSPHOGLYCERATE MUTASE, ERYTHROCYTE) (2,3- BISPHOSPHOGLYCERATE SYNTHASE) (BPGM) (EC 5.4.2.1) (EC 3.1.3.13) (BPG-DEPENDENT PGAM) - ORYCTOLAGUS CUNICULUS (RABBIT), 258 aa.	9.3E-74	

7174	cg43963566	577	TTCTGCCCTTGTT GAGGCCTGTGA GG[C/gap]CCCCG TAATGCCGCTCA TTGAGGCG	C	gap	Gly	Ala (9345)	FRAMES HIFT	synthase	Human Gene Similar to SWISSPROT- ID:P07952 BISPHOSPHOGLYCERATE MUTASE (EC 5.4.2.4) (2,3- BISPHOSPHOGLYCERATE MUTASE, ERYTHROCYTE) (2,3- BISPHOSPHOGLYCERATE SYNTHASE) (BPGM) (EC 5.4.2.1) (EC 3.1.3.13) (BPG-DEPENDENT PGAM) - ORYCTOLAGUS CUNICULUS (RABBIT), 258 aa.	9.3E-74	
7175	cg44017251	1064	CTGTGGGTGAG GGCTGGGGCAG CGG[C/gap]TGCC GCATCCAGCAGT GCCCCGGGCA	C	gap	Cys	Ala (9346)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7176	cg44017251	1118	AGACAGCTGAGT ACCAGTCATTGT G[C/gap]CCTCAC GGCCGGGGCTA CCTGGCGC	C	gap	Pro	Leu (9347)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7177	cg44017251	1120	ACAGCTGAGTAC CAGTCATTGTGC C[C/gap]TCACGG CCGGGGCTACC TGGCGCCC	C	gap	Pro	Leu (9348)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7178	cg44017251	1161	CCTGGCGCCCCA GTGGAGACCTGA GC[C/gap]TCCGG AGAGACGTGGA CGAATGTCA	C	gap	Leu	Ser (9349)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	

7179	cg44017251	1521	CAGCCACCCCTCG GCTGGACCGTCA G[G/gap]CCACCT ACACAGAGTGCT GCTGCCT	G	gap	Ala	Pro (9350)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7180	cg44017251	887	CTGCTAGCCCCG TTCTGCCCCGCA G[G/gap]CCACCT CCGCCACCCCT GCCCCGCC	G	gap	Pro	His (9351)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7181	cg44017251	937	CGACCCAGCACA CCTAGGCAGG CC[C/gap]TGTGG GGAGTGGGCG CGGGAGTGC	C	gap	Pro	Leu (9352)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:O00508 LATENT TGF-BETA BINDING PROTEIN- 4 - HOMO SAPIENS (HUMAN), 1587 aa.	6.5e-315	
7182	cg43931248	1787	TGGAAGTGGATC CACGAGCCCAA GG[G/gap]CTACC ATGCCAACTTCT GCCTCGGG	G	gap	Gly	Ala (9353)	FRAMES HIFT	tgf	Human Gene SWISSPROT-ID:P01137 TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR (TGF-BETA 1) - HOMO SAPIENS (HUMAN), 390 aa.	9.7E-214	19
7183	cg43980446	10250	CTTCACGTTCCC AGCCTCCAAAT G[gap]/GJCGTCCG CCCCATGGCTCG TG TAGGA	gap	G	Arg	Arg (9354)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166 (15q21.1)	15
7184	cg43980446	2708	AGGTGAAGCTTC CAGGAGTGTCT G[G/gap]CAAAATG CCCTAGACCCG CACAGAT	G	gap	Cys	Cys (9355)	FRAMES HIFT	tgf	Human Gene SPTREMBL-ID:Q28019 LATENT TGF-BETA BINDING PROTEIN- 2 - BOS TAURUS (BOVINE), 1963 aa.	1.3E-166 (15q21.1)	15

7185	cg43272560	829	ACAGGAGGTGC ATGTCCTGAATC TC[ <i>gap</i> ]GCACT GCAGGCCAGGG GCTGGCCAG	C	<i>gap</i>	Arg	Ala (9356)	FRAMES HIFT	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
7186	cg43272560	837	TGCATGTCCTGA ATCTCCGCACTG C[ <i>A</i> <i>gap</i> ]GGCCAG GGGCTGGCCAG CTACAGAG	A	<i>gap</i>	Arg	Gly (9357)	FRAMES HIFT	tgfrecept or	Human Gene SWISSPROT-ID:Q03167 TGF-BETA RECEPTOR TYPE III PRECURSOR (TGFR-3) (BETAGLYCAN) - HOMO SAPIENS (HUMAN), 849 aa.	0	1 (1p33)
7187	cg43982633	1191	TGATTTTGTGGT TATGTGGCTGGA A[ <i>G</i> <i>gap</i> ]CACCGA GACCTTCITTTT CATAATT	G	<i>gap</i>	Ala	Val (9358)	FRAMES HIFT	tgfrecept or	Human Gene SWISSPROT-ID:P56159 GDNF RECEPTOR ALPHA PRECURSOR (GDNFR-ALPHA) (TGF- BETA RELATED NEUROTROPHIC FACTOR RECEPTOR 1) - HOMO SAPIENS (HUMAN), 464 aa.	1.5E-254	
7188	cg43918322	1060	GTCGTGACCAAG ACGCTACGGAG GT[ <i>gap</i> ]CJCCCAG GGGATCGCCG CGGTCGCCA	<i>gap</i>	C	Asp	Gly (9359)	FRAMES HIFT	thioester ase	Human Gene Similar to SPTREMBL- ID:Q19781 SIMILAR TO ACYL-COA THIOESTERASE. NCBI Gi: 1213545 - CAENORHABDITIS ELEGANS, 343 aa.	1.1E-53	20
7189	cg36988276	790	GCATTCAATGGA ACCCAACCTAGAT G[C <i>gap</i> ]AGTGAA TCTAAGCGATAA TAATAAT	C	<i>gap</i>	Ala	Glu (9360)	FRAMES HIFT	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)
7190	cg36988276	792	TTCATGGAACC CAACTAGATGCA G[ <i>gap</i> ]CJTGAAATC TAAGCGATAATA ATAATTT	<i>gap</i>	C	Val	Ala (9361)	FRAMES HIFT	tm7	Human Gene SWISSPROT-ID:P23945 FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (FSH-R) (FOLLITROPIN RECEPTOR) - HOMO SAPIENS (HUMAN), 695 aa.	0	2 (2p21)

7181	cg43300806	1000	CCAAGGCCAGC CGCAGCTCTGAG AA[G/gap]TCGCT GGCGTGTCTCAA GACCGTAA	G	gap	Ser	Arg (9362)	FRAMES HIFT	tm7	Human Gene SWISSPROT-ID:P21453 PROBABLE G PROTEIN-COUPLED RECEPTOR EDG-1 - HOMO SAPIENS (HUMAN), 381 aa. pcls:TREMBLNEW- ID:G2868608 G PROTEIN-COUPLED RECEPTOR - HOMO SAPIENS (HUMAN), 381 aa (fragment).	9.4E-200	22 (22q13)
7192	cg43967090	1249	TTTCTTAAGCAC TTTTCAGAGCGA G[G/gap]CCGAGC CCAGTCTAAGT CCGAGTC	G	gap	Ala	Pro (9363)	FRAMES HIFT	tm7	Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa.	5.1E-195	2
7193	cg43967090	923	CAGATTCGGAGG ATCATGGCTGCG G[C/gap]CAAAAC CAAGCAGCACTG GACGAGG	C	gap	Ala	Ala (9364)	FRAMES HIFT	tm7	Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa.	5.1E-195	2
7194	cg43967090	924	AGATTCGGAGGA TCATGGCTGCGG C[C/gap]AAACCC AAGCAGCACTGG ACGAGGT	C	gap	Lys	Asn (9365)	FRAMES HIFT	tm7	Human Gene SWISSNEW-ID:O43194 PUTATIVE G PROTEIN-COUPLED RECEPTOR GPR39 - HOMO SAPIENS (HUMAN), 453 aa.	5.1E-195	2
7195	cg42908704	924	CGCGGGAGGAG GTCAGCAGGACA AG[gap/A]GTGCG GGGCGCGCAAG GATAGCAAG	gap	A	Arg	Arg (9366)	FRAMES HIFT	tm7	Human Gene SWISSPROT-ID:P46663 B1 BRADYKININ RECEPTOR (BK-1 RECEPTOR) - HOMO SAPIENS (HUMAN), 353 aa.	7E-188	14 (14q32.1)
7196	cg43040271	1239	TACGTGAACAAG AGGACGCCCCCG GC[G/gap]CGCCG CTGCGCTCATCT CGCTCACT	G	gap	Arg	Pro (9367)	FRAMES HIFT	tm7	Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa. pcls:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.9E-74	

7197	cg43040271	1243	TGAACAAGAGGAGC CGCCCCGGCGC GC[C/gap]GCTGC GCTCATCTCGCT CACTTGGC	C	gap	Ala	Leu (9368)	FRAMES HIFT	tm7	Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.   pcis:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.9E-74	
7198	cg43040271	1245	AACAAGAGGAGC CCCCGGCGCGC CG[C/gap]TGCGC TCATCTCGCTCA CTTGGCTT	C	gap	Ala	Val (9369)	FRAMES HIFT	tm7	Human Gene Similar to SWISSPROT- ID:Q25322 TYRAMINE/OCTOPAMINE RECEPTOR 2 (TYR-LOC 2) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.   pcis:SPTREMBL-ID:Q25322 GCR2 (G PROTEIN-COUPLED RECEPTOR) - LOCUSTA MIGRATORIA (MIGRATORY LOCUST), 484 aa.	2.9E-74	
7199	cg43962131	2093	GTGGCCACACTG CGCCTGGAAG GC[C/gap]TGCGG AGGACGTTTCTG CAGGCCGA	C	gap	Arg	Ser (9370)	FRAMES HIFT	tnfrecept or	Human Gene SPTREMBL-ID:Q12933 TUMOR NECROSIS FACTOR TYPE 2 RECEPTOR ASSOCIATED PROTEIN 3 - HOMO SAPIENS (HUMAN), 501 aa.	9.2E-257	9
7200	cg42700065	108	TGAAGGAGCGCT TCCTACCGTTAG G[G/gap]AACTCT GGGACAGAGC GCCCCGGC	G	gap	Asn	Thr (9371)	FRAMES HIFT	tnfrecept or	Human Gene TREMBLNEW- ID:G2957264 TNF RELATED TRAIL RECEPTOR - HOMO SAPIENS (HUMAN), 299 aa.	2.3E-164	8
7201	cg43988937	768	TTCTGGCTCGTC CTTGCCCCCTTG G[G/gap]AGCCAA GAGACCCCTTCC CTTCTT	G	gap	Ser	Ser (9372)	FRAMES HIFT	traffic	Human Gene SPTREMBL-ID:Q99408 PUTATIVE NUCLEOLAR TRAFFICKING PHOSPHOPROTEIN - HOMO SAPIENS (HUMAN), 1410 aa.	0.5 (5q32)	

7202	cg43934374	2836	AGGTTTCATCTA GAGGCAGAACAA G[C/gap]AGTACT AATGAAGATGAG GATTTGA	C	gap	Ser	Val (9373)	FRAMES HIFT	transcript factor	Human Gene SWISSNEW-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa.jpds:SWISSPROT-ID:Q99081 TRANSCRIPTION FACTOR HTF4 (TRANSCRIPTION FACTOR 12) (E-BOX- BINDING PROTEIN) (HEB) - HOMO SAPIENS (HUMAN), 682 aa	0	15 (15q21)
7203	cg43321351	2475	CAGGGCCTCCG GAGGGCCCGC TGG[G/gap]CAGG CCTTCTGAATCT TGTGCTGAA	G	gap	Ala	Ala (9374)	FRAMES HIFT	transcript factor	Human Gene SPTRMBL-ID:O00146 P120E4F TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 783 aa.	1E-290	
7204	cg43321351	538	CAGTGGCCCTCGC TGATGGCCGAG GC[C/gap]AGCGT CATGGCCACCTG CTCIGTCA	C	gap	Leu	Leu (9375)	FRAMES HIFT	transcript factor	Human Gene SPTRMBL-ID:O00146 P120E4F TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 783 aa.	1E-290	
7205	cg42896335	318	GCTCGGGGCC CCAGCAAGTCCC CC[G/gap]GTCGT CCCCGCAGGCC GCCTTCACC	G	gap	Arg	Arg (9376)	FRAMES HIFT	transcript factor	Human Gene TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	2.1E-285	12
7206	cg43947862	505	TGATATGATAGC TATCATTGGTTT C[gap/CTGCTTT CATTGTGTCCAG AATAAAA	gap	C	Glu	Gly (9377)	FRAMES HIFT	transcript factor	Human Gene TREMBLNEW-ID:G545525 LBP-1C=TRANSCRIPTION FACTOR ALPHA-GLOBIN CP2 HOMOLOG {[ALTERNATIVELY SPLICED]} - HOMO SAPIENS, 502 aa.	3.7E-276	12
7207	cg43917801	840	ACGGAAGCGCT GCTGGCCGGCG AGA[gap/G]CTCG GACTCGGGCGC CGGCCTCGAG	gap	G	Asp	Glu (9378)	FRAMES HIFT	transcript factor	Human Gene SWISSNEW-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.jpds:SWISSPROT-ID:Q06945 TRANSCRIPTION FACTOR SOX-4 - HOMO SAPIENS (HUMAN), 474 aa.	1.3E-249	6 (6p22.3)

7208	cg43920700	1283	TGCTTGCTGGAG TCAGACCAGGGA G[C/gap]CCCCGG GCCACAGCATCA GCCCTGC	C	gap	Pro	Pro (9379)	FRAMES HIFT	transcript factor	Human Gene SWISSPROT-ID:Q14938 NUCLEAR FACTOR 1X (NF1-X) (NF-1X) (CCAAT-BOX BINDING TRANSCRIPTION FACTOR) (CTF) (TGGA-BINDING PROTEIN) - HOMO SAPIENS (HUMAN), 441 aa.	2.1E-243	19 (19p13.3)
7209	cg21646034	870	TCCAAATCTTCA GAAACTCCAGTA G[T/gap]GGCCAC AGAAGAAAGTAGT TACTGCA	T	gap	Val	Gly (9380)	FRAMES HIFT	transcript factor	Human Gene SWISSPROT-ID:Q06545 GA BINDING PROTEIN BETA-2 CHAIN (GABP-BETA-2 SUBUNIT) (TRANSCRIPTION FACTOR E4TF1-47) (GAPBP2) - HOMO SAPIENS (HUMAN), 347 aa.	9E-179	15
7210	cg43950592	97	CGCAGCAAACTT CGGGGGCGCGC GG[C/gap]GGCAA CTCCACCCGCG CGGGCGCGC	C	gap	Gly	Ala (9381)	FRAMES HIFT	transcript factor	Human Gene SWISSPROT-ID:P48431 TRANSCRIPTION FACTOR SOX-2 - HOMO SAPIENS (HUMAN), 317 aa.	4.7E-173	3 (3q26.3)
7211	cg43929348	739	GATGAAGGCCA GGGATAAATTC AA[G/gap]AGTTG CTTCGGACACT TCCCTTC	G	gap	Leu	Leu (9382)	FRAMES HIFT	transcript factor	Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa.	6.5E-169	2
7212	cg43929348	746	CCAGGGATAAAT TTCAGAGATTGC T[gap/C]TTCGGA CACTCCCTTTC TGCTCTT	gap	C	Lys	Arg (9383)	FRAMES HIFT	transcript factor	Human Gene SPTREMBL-ID:Q15630 TRANSCRIPTION FACTOR - HOMO SAPIENS (HUMAN), 324 aa.	6.5E-169	2
7213	cg43935763	742	CAGGCAGACACT TTCAGTTTCTTTT T[gap]CTTGGCT TTCAGCACTGGA GGCAGA	T	gap	Lys	Lys (9384)	FRAMES HIFT	transcript factor	Human Gene SPTREMBL-ID:Q13889 BASIC TRANSCRIPTION FACTOR 2, 35 KD SUBUNIT - HOMO SAPIENS (HUMAN), 303 aa.	1E-161	
7214	cg43982109	1793	GTCGACTTCCAC AGCCGGTGCAC AG[C/gap]TCTGC TCCAGACCTTCC CAGGGCAC	C	gap	Glu	Asp (9385)	FRAMES HIFT	transcript factor	Human Gene Homologous to SWISSPROT-ID:Q00059 MITOCHONDRIAL TRANSCRIPTION FACTOR 1 PRECURSOR (MTTF1) - HOMO SAPIENS (HUMAN), 246 aa.	5.6E-131	10 (7p)



7215	cg44028769	482	GGTGCTCACAAA CCACCGTCCGCA G[G]gap]AGGCAA ACTTCAGGGACA GCACGCA	G	gap	Ser	Ser (9386)	FRAMES HIFT	transcript factor	Human Gene Homologous to SWISSPROT-ID:O02482 TRANSCRIPTION FACTOR UNC-37 - CAENORHABDITIS ELEGANS, 612 aa.	4.6E-119	1
7216	cg43918209	1675	AGCGACAGCTG CAGACTCCGGTG CA[G]gap]CCGCA GGCCACCCGCG TGCATGCGG	G	gap	Leu	Cys (9387)	FRAMES HIFT	transcript factor	Human Gene Homologous to SPTREMBL-ID:Q03827 TRANSCRIPTION FACTOR ETR101 - HOMO SAPIENS (HUMAN), 223 aa.	2.7E-115	19
7217	cg43287584	707	TCCGCTGGCAAC AGTGCTCCCAAT A[gap]A]GCCCCA TGGCCATGCTGC ACATTGG	gap	A	Ser	Lys (9388)	FRAMES HIFT	transcript factor	Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa.	2.6E-90	
7218	cg43287584	785	TGTCATTGACAA CATTATGCGTCT G[G]gap]ACGATG TCCTTGGCTACA TCAATCC	G	gap	Asp	Thr (9389)	FRAMES HIFT	transcript factor	Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa.	2.6E-90	
7219	cg43287584	793	CAACATTATGCG TCTGGACGATGT C[gap]T]CTTGGC TACATCAATCCT GAAATGC	gap	T	Leu	Ser (9390)	FRAMES HIFT	transcript factor	Human Gene Similar to TREMBLNEW- ID:E1172965 TRANSCRIPTION FACTOR TFE3 - HOMO SAPIENS (HUMAN), 575 aa.	2.6E-90	
7220	cg43917302	1588	ACCAGGCGGTG CACACTGGCAGC CG[C]gap]CCCCA CGCCTGGCGCG TCTGCGCCCC	C	gap	Pro	Pro (9391)	FRAMES HIFT	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.   pcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.9E-68	7

7221	cg43917302	1572	GGCGGTGCACA CTGGCAGCCGC CCC[C/gap]ACGC CTGCGCGGTCTG CGCCCGCAG	C	gap	His	Thr (9392)	FRAMES HIFT	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.   pcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.9E-68	7
7222	cg43917302	1590	CGGCCCCACG CTGCGCCGTCT GC[G/gap]CCCGC AGCTTCAGCTCC AAAAACCAA	G	gap	Ala	Pro (9393)	FRAMES HIFT	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.   pcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.9E-68	7
7223	cg43917302	1652	ACGAGGCGATCC ACACAGGCTCCC GC[gap]CCCTTC TCCTGCCCGCAG TGCGGAA	C	gap	Pro	Pro (9394)	FRAMES HIFT	transcript factor	Human Gene Similar to SWISSNEW- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.   pcis:SWISSPROT- ID:Q61751 RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17) - MUS MUSCULUS (MOUSE), 572 aa.	3.9E-68	7
7224	cg29214653	587	CGGGGACGGTT CTCTGCTAGCTC CCT[gap]AACTG CTTCTGGCCAGG AGTCCAGT	T	gap	Leu	Gln (9395)	FRAMES HIFT	transcript factor	Human Gene Similar to SWISSPROT- ID:P50548 ETS-DOMAIN TRANSCRIPTION FACTOR ERF - HOMO SAPIENS (HUMAN), 548 aa.	4.9E-68	1
7225	cg43917396	2229	CATGCGTTGGG CATCTCAGGGTC G[G/gap]CCTTGC CCGCCACCATCC AGCGCGA	G	gap	Ala	Ala (9396)	FRAMES HIFT	transcript factor	Human Gene Similar to TREMBLNEW- ID:G2920821 TRANSCRIPTION FACTOR T-BOX 5 - HOMO SAPIENS (HUMAN), 518 aa.	6.9E-68	

7226	cg43944978	1414	AACAGGCCCGC AGATGCCCGCAG GTC[C/gap]TTTCG GCACCGTCTCCA GGGCCATCT	C	gap	Lys	Lys (9397)	FRAMES HIFT	transcript factor	Human Gene Similar to SPTREMBL- ID:Q16550 TRANSCRIPTION FACTOR SUPT4H - HOMO SAPIENS (HUMAN), 117 aa.	3.4E-60	17
7227	cg43946772	3282	CATGAACGGTA CTTTTAGTTTTT [T/gap]CACATAA CTCTCTAAAGGC CTTTTC	T	gap	Lys	Lys (9398)	FRAMES HIFT	transferase	Human Gene SPTREMBL-ID:Q29121 UDP-GALNAC:POLYPEPTIDE ALFA-1,0 N-ACETYL GALACTOSAMINYL TRANSFERASE - SUS SCROFA (PIG), 559 aa.	0	18
7228	cg43935558	3108	ACAGTATGCACA AAACATGGGCCT G[C/gap]CCCAGA ACCGTATCATTT TTTCACC	C	gap	Pro	Pro (9399)	FRAMES HIFT	transferase	Human Gene SWISSPROT-ID:P56558 UDP-N-ACETYLGLUCOSAMINE-- PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERAS E 110 KD SUBUNIT (EC 2.4.1.-) (O- GLCNAC TRANSFERASE P110 SUBUNIT) - RATTUS NORVEGICUS (RAT), 1036 aa.[pcds:TREMBLNEW- ID:G1931579 O-GLCNAC TRANSFERASE, P110 SUBUNIT - RATTUS NORVEGICUS (RAT), 1036 aa.	0	
7229	cg43918882	1905	ACCAAAAGAGGG CCCAAGCCCCG GC[C/gap]GCGGT GCTGGGCTCCAT GTTCTCTCC	C	gap	Ala	Ala (9400)	FRAMES HIFT	transferase	Human Gene SWISSPROT-ID:P39656 DOLICHYL- DIPHOSPHOOLIGOSACCHARIDE-- PROTEIN GLYCOSYLTRANSFERASE 48 KD SUBUNIT PRECURSOR (EC 2.4.1.119) (OLIGOSACCHARYL TRANSFERASE 48 KD SUBUNIT) (DDOST 48 KD SUBUNIT) (KIAA0115) (HA0543) - HOMO SAPIENS (HUMAN), 456 aa.	5.3E-245	1

7230	cg2537639	258	CACCTAGGAAGG ATGTCCTCGTG T[G/gap]ACCCCT TGGCTGGCTCCC ATTGTCT	gap	Thr	Pro (9401)	FRAMES HIPT	transfe se	Human Gene SWISSPROT-ID:P18442 FUCOSYLGLYCOPROTEIN ALPHA-N- ACETYLGALACTOSAMINYLTRANSFER ASE (EC 2.4.1.40) (HISTO-BLOOD GROUP A TRANSFERASE) (A TRANSFERASE) / FUCOSYLGLYCOPROTEIN 3-ALPHA- GALACTOSYLTRANSFERASE (EC 2.4.1.37) (HISTO-BLOOD GROUP B TRANSFERASE) (B TRANSFERASE) (NAGAT) - HOMO SAPIENS (HUMAN), 354 aa.	6.5E-192	9 (9q34)
7231	cg43258046	1453	GCCACAGCCTGT GCACCTGCTGCC C[C/gap]TGACCG GGATACAGCATC TCAACAT	gap	Leu	Cys (9402)	FRAMES HIPT	transfe se	Human Gene Homologous to TREMBLINW-ID:G2673964 LECITHIN:CHOLESTEROL ACYL TRANSFERASE - AKODON TORQUES, 294 aa (fragment).	3.2E-146	16 (16q22.1)
7232	cg43949162	1194	CTCCGTTGGGA TAGTGGAGCTTG G[G/gap]CCTTGC TGCCATGATAGC TTTTCAG	gap	Pro	Pro (9403)	FRAMES HIPT	transfe se	Human Gene Homologous to TREMBLINW-ID:G2738933 GLUTATHIONE TRANSFERASE (EC 2.5.1.18) - HOMO SAPIENS (HUMAN), 222 aa.	1.3E-115	6
7233	cg43933127	1862	CTGGATCTGTGA TACTTGCTGTGT G[A/gap]CTGCCG TCTGGAGCTGTT CATTITG	gap	Val	Ala (9404)	FRAMES HIPT	transport	Human Gene SWISSPROT-ID:P41541 GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP) - BOS TAURUS (BOVINE), 961 aa.	0	4
7234	cg40351913	1680	TCCAGCAGATGA CCGGGCAGCGG CC[C/gap]AGCCT GTACTGGCGGCT GTGCTGGA	gap	Ser	Ala (9405)	FRAMES HIPT	transport	Human Gene SWISSPROT-ID:Q01959 SODIUM-DEPENDENT DOPAMINE TRANSPORTER (DA TRANSPORTER) (DAT) - HOMO SAPIENS (HUMAN), 620 aa.	0	5 (5p15.3)
7235	cg43993573	252	GACGTCAGAATG ATTCCTTGCAGA G[C/gap]CGCGCT GACCTTTGCCCG ATGCTCTG	gap	Ala	Ala (9406)	FRAMES HIPT	transport	Human Gene SWISSPROT-ID:P52569 LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2) - HOMO SAPIENS (HUMAN), 658 aa.	0	8 (8p22)

7236	cg44011204	1168	CAGGATGAAACG GCTGATGTGCTT G[G/gap]CCACGC CATTATTCTCCT CCACGCA	G	gap	Ala (9407)	Ala	FRAMES HIFT	transport	Human Gene SWISSNEW-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B(0) (ATB(0)) - HOMO SAPIENS (HUMAN), 541 aa.   pcis:SWISSPROT-ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.   pcis:SPTREMBL- ID:Q15758 NEUTRAL AMINO ACID TRANSPORTER B - HOMO SAPIENS (HUMAN), 541 aa.	6.9E-197	
7237	cg44025532	678	CTGTGCACGCG GCTGGCCATCAT GG[gap]GTTGAAC GGTCGCCCTGCG GTGCCCTGGG	gap	G	Gly (9408)	Val	FRAMES HIFT	transport	Human Gene SWISSPROT-ID:P41234 ATP-BINDING CASSETTE TRANSPORTER 2 - MUS MUSCULUS (MOUSE), 1472 aa (fragment).	6.8E-174	
7238	cg43945806	307	AAACTCTGGTCT GGAAGAATCAGT C[A/gap]CCTGAG CAAGGCTTCCGG AAGTAGA	A	gap	Gly (9409)	Gly	FRAMES HIFT	transport	Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, QDB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa.	2.2E-145	6
7239	cg43945806	432	AGATCTGAGGCG AGTGCCTTCCGG G[G/gap]TACCCA ATAGGCAATTGC TGTGTAG	G	gap	Pro (9410)	Pro	FRAMES HIFT	transport	Human Gene Homologous to SPTREMBL-ID:Q31604 DMA, DMB, HLA- Z1, IPP2, LMP2, TAP1, LMP7, TAP2, DOB, QDB2 AND RING8, 9, 13 AND 14 GENES - HOMO SAPIENS (HUMAN), 261 aa.	2.2E-145	6
7240	cg43928832	1562	CGGTGCGGACA TGGCAACAGCC GCA[G/gap]CACC GGGTGCTGTAGA ACCGGTCAC	G	gap	Cys (9411)	Cys	FRAMES HIFT	transport	Human Gene Homologous to SWISSPROT-ID:Q15012 GOLGI 4- TRANSMEMBRANE SPANNING TRANSPORTER MTP (KIAA0108) - HOMO SAPIENS (HUMAN), 233 aa.	2E-126	2
7241	cg43061328	262	CTGCAACAGGAA AACATTGTTCC C[C/gap]AGATGC TGGAGATGCAA GTAAGGC	C	gap	Trp (9412)	Trp	FRAMES HIFT	transport	Human Gene Homologous to TREMBLNEW-ID:E315451 PUTATIVE INTEGRAL MEMBRANE TRANSPORT PROTEIN - RATTUS NORVEGICUS (RAT), 552 aa.	5.6E-125	

7242	cg43331724	414	GTGCCCCTGGAC TTGCAGACCGTG A[G/gap]GACAGT ATTGGCTGTGT TGGGAAG	G	gap	Arg (9413)	Arg	FRAMES HIFT	transport	Human Gene Similar to SPTREMBL- ID:Q61185 KIDNEY-SPECIFIC TRANSPORT PROTEIN - MUS MUSCULUS (MOUSE), 545 aa.	1.2E-55	
7243	cg43990999	427	TTCTTATCCCA GCTATGGTGTG G[G/gap]CACTGC CTTCTTCATCAAT TTCATA	G	gap	Gly (9414)	Gly	FRAMES HIFT	transport	Human Gene Similar to SWISSPROT- ID:P32802 ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LATE ENDOCYTIC INTERMEDIATE COMPONENT) - SACCCHAROMYCES CEREVISIAE (BAKER'S YEAST), 667 aa.	7.5E-55	10
7244	cg43986426	1241	TAAGCAGTGCAA GGTGCTTGAGC C[C/gap]TATGGT GGCCATGCTGG GTGCAGTA	C	gap	Tyr (9415)	Met	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
7245	cg43986426	1251	AAGGTGCTTGA GCCCTATGGTGG C[C/gap]ATGCTG GGTGCACTAGCT GCCCAGG	C	gap	His (9416)	Met	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
7246	cg43986426	1261	GAGCCCTATGGT GGCCATGCTGG GT[G/gap]CAGTA GCTGCCCAGGA AGTCTGAA	G	gap	Cys (9417)	Ser	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
7247	cg43986426	2004	TAGCACAGCCGA GCACAGCCCTGCA G[T/gap]TGGGCC CGGCATGAGTTT GAAGAAC	T	gap	Trp (9418)	Gly	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1

7248	cg439886426	2361	ACCTCCTCTACG TACTGGCAGCTG C[C/gap]AACCTG TATGCCAGATG CATGGGC	C	gap	Asn	Thr (9419)	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
7249	cg439886426	2761	AGCAGCTGTGG CAGGCCTGTTGG GC[C/gap]TGGAG CTGTATAAGGTG GTGAGTGG	C	gap	Leu	Trp (9420)	FRAMES HIFT	ubiquitin	Human Gene SWISSPROT-ID:P41226 UBIQUITIN-ACTIVATING ENZYME E1 HOMOLOG (D8) - HOMO SAPIENS (HUMAN), 1011 aa.	0	1
7250	cg43291895	702	TCATCCGGAAGC AGGTCCTGGGG AC[C/gap]AAGGT GGACGCGGAGC GTGACGGCG	C	gap	Lys	Arg (9421)	FRAMES HIFT	ubiquitin	Human Gene Homologous to SWISSPROT-ID:P49427 UBIQUITIN- CONJUGATING ENZYME E2-32 KD COMPLEMENTING (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2- CDC34) - HOMO SAPIENS (HUMAN), 236 aa.	3.5E-129	
7251	cg44923887	2517	AGAGTATTCTTC AGCTAGGTCAGC C[C/gap]GAAGCG GGTGCTCAGGCT GGGGGTC	C	gap	Arg	Arg (9422)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51986 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4E-82	22
7252	cg44923887	2870	CTCAAGCTCCT TCATCAGCCTCC T[G/gap]CTGGCC GCCATCTTGAT TTGGTGC	G	gap	Ser	Arg (9423)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSPROT- ID:P51986 UBIQUITIN-CONJUGATING ENZYME E2-18 KD UBCH7 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (UBCM4) (E2-F1) (L-UBC) - HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE), 154 aa.	4E-82	22

7253	cg43939935	2099	GCAATGACCACA TGAAATAACGG G[C/gap]GTTGCT CTCATCTGGTTC GGCTTTG	gap	Ala	Pro (9424)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN- CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.pcds:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152.aa.	7.7E-79	12
7254	cg43939935	2173	CAAACGCTGGGT TTCCTTGATGAT C[C/gap]TGCGGG GCAGCCCGGCC ATCTTGTC	gap	Arg	Arg (9425)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSNEW- ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN- CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152 aa.pcds:SWISSPROT-ID:Q16781 UBIQUITIN-CONJUGATING ENZYME E2-17 KD (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) - HOMO SAPIENS (HUMAN), 152.aa.	7.7E-79	12
7255	cg43974851	1430	GTGGGGGAGTT GAGCAGGTGCC GCA[G/gap]GATG ATGGAGCGGTC CATGATGGTG	gap	Leu	Cys (9426)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1E-70	1
7256	cg43974851	1431	TGGGGGAGTTG AGCAGGTGCCG CAG[G/gap]ATGA TGGAGCGGTCC ATGATGGTGC	gap	Ile	Ile (9427)	FRAMES HIFT	ubiquitin	Human Gene Similar to SWISSPROT- ID:P54860 UBIQUITIN FUSION DEGRADATION PROTEIN 2 (UB FUSION PROTEIN 2) - SACCHAROMYCES CEREVISIAE (BAKER'S YEAST), 961 aa.	1E-70	1



7257	cg43921289	1307	CAGCTGGCAGC CAAGGAGGCGA AAG[C/gap]TTCG AGACCTGGAGG ACTCACTGGC	C	gap	Leu	Phe (9428)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
7258	cg43921289	1794	GGAGATGATCCC TTGCTGACTTAC C[G/gap]GTTCCC ACCAAAGTTCAC CCTGAAG	G	gap	Arg	Arg (9429)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
7259	cg43921289	1795	GAGATGATCCCT TGCTGACTTACC G[G/gap]TTCCTCA CCAAAGTTCACC CTGAAGG	G	gap	Phe	Ser (9430)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
7260	cg43921289	1856	GGTGACGATCTG GGCTGCAGGAG CT[G/gap]GGGCC ACCCACAGCCCC CCTACCGA	G	gap	Gly	Gly (9431)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
7261	cg43921289	2045	TGGAGATGACCT GCTCCATCACCA C[C/gap]ACGTGA GTGGTAGCCGC CGCTGAGG	C	gap	His	Thr (9432)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02545 LAMIN A (70 KD LAMIN) - Homo sapiens (Human), 664 aa.	0	1
7262	cg43928067	2129	GTAGGACACTGC TGGAGCTGAGTG G[C/gap]TTCACA GCGGCAATGACA GCAGCGT	C	gap	Lys	Asn (9433)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTRMBL-ACC:O75152 KIAA0863 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
7263	cg43928067	4145	GTGCGCTTTGGT ACATGTGGAATA G[gap/A]AAAAAA AATAGCAGTCTT CTCCTTG	gap	A	Phe	Phe (9434)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTRMBL-ACC:O75152 KIAA0863 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1

7264	cg43929067	4153	TGGTACATGTGG AATAGAAAAAAA Algap/ATAGCAG TCTTCTCCTTGA TTAGGCA	gap	A	Phe	Phe (9435)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q75152 KIAA0663 PROTEIN - HOMO SAPIENS (HUMAN), 810 aa.	0	1
7265	cg43989426	2748	GACCAAGTCTCA TTAGGCCAAGGC C[C/gap]ACAACT GCTCCTATCACC ATCTCCT	C	gap	Thr	Gln (9436)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15463 PTPL1-ASSOCIATED RHOGAP - HOMO SAPIENS (HUMAN), 1261 aa.	0	1
7266	cg43924236	986	GCTTCAAGCTG CATACGGTGCC C[C/gap]AGTGGG GAGCGAGTCC ACGGACAA	C	gap	Leu	Leu (9437)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16632 TFIIC2 SUBUNIT - HOMO SAPIENS (HUMAN), 911 aa.	0	2
7267	cg43925699	1687	CCCGGGCCACTT CCTGGCCACCG CA[G/gap]GCCCC TCGCCCATGGCC GCTGGCCT	G	gap	Gly	Ala (9438)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q03989 MODULATOR RECOGNITION FACTOR I - HOMO SAPIENS (HUMAN), 614 aa (fragment).	0	2
7268	cg44927137	1868	AGAGGAGTCTGA TGATGAAATAGC Algap/AJGATAAG GATTCTGAAGAT AATTGGG	gap	A	Asp	Arg (9439)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	2
7269	cg44927137	1880	TGATGAAATAGC AGATAAGGATTG T[gap/T]GAAGAT AATTGGGATGAA GATGAGG	gap	T	Glu	End (9440)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15061 ORF, PARTIAL CDS - HOMO SAPIENS (HUMAN), 686 aa (fragment).	0	2
7270	cg43918935	306	AGGGACAGACG CACCGATCGCC GGA[G/gap]GGAC AGACACACGACC ACGGGGCGC	G	gap	Gly	Gly (9441)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3

7271	cg43918935	308	GGACAGACGCA CCGATCGCCGG AGG[G/gap]ACAG ACACACGACCAC GCGGCGCCA	G	gap	Thr	Gln (9442)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
7272	cg43918935	337	GACACAGACCA CGCGGCGCCAC CG[C/gap]CCACG CCTCCACCCACC GGCGCCCA	C	gap	Ala	Ala (9443)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
7273	cg43918935	415	TGGCACAAACTT TCCTCCCGGGAC G[G/gap]AACACG CTGCCTCAGGGA GCCCGCG	G	gap	Gly	Glu (9444)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
7274	cg43918935	443	CACGCTGCCTCA GGAGCCCGCG AC[C/gap]GCGCC TTCTCCTCGCC GGTCCCAT	C	gap	Ala	Arg (9445)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14699 HYPOTHETICAL PROTEIN KIAA0084 (HA2022) - Homo sapiens (Human), 648 aa (fragment).	0	3
7275	cg43939697	414	AGATCCGCATGA AGGAGCTGGAG CG[G/gap]CACAG AAGGAGGTAGAA GAGAGACC	G	gap	Ala	His (9446)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75766 TRIP PROTEIN - HOMO SAPIENS (HUMAN), 784 aa.	0	3
7276	cg43940975	1352	CATCACCAGCTT CATCCGTTAGTG G[G/gap]CCTCGC CCTCTGAAAAC TGCCCTT	G	gap	Ala	Ala (9447)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE-TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3

7277	cg43940975	381	ACAGAGCAGTCC ACTAATGCTGCA T[C/gap]CACCAC GTGTAGTGATGC CAGGTTC	C	gap	Asp	Met (9448)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE-TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
7278	cg43940975	382	CAGAGCAGTCCA CTAATGCTGCAT C[C/gap]ACCACG TG TAGTGATGCC AGTTCA	C	gap	Val	Val (9449)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P47897 GLUTAMINYL-TRNA SYNTHETASE (EC 6.1.1.18) (GLUTAMINE-TRNA LIGASE) (GLNRS) - Homo sapiens (Human), 775 aa.	0	3
7279	cg44917921	3496	CCAGCCCCCAAA ACCAGCCTGGA GG[C/gap]ACTCA CTTCACAGGGTC CTGCCACA	C	gap	Ala	Asp (9450)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75162 KIAA0675 PROTEIN - HOMO SAPIENS (HUMAN), 1208 aa.	0	3
7280	cg43930961	1504	ATCTTTAACTCA TTTTTTTTTTT[ gap]AAAAGGAGG ACATTGTAACA AGTG	T	gap	Lys	Lys (9451)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA20772 KIAA0313 PROTEIN - HOMO SAPIENS (HUMAN), 1499 aa.	0	4
7281	cg43935402	1165	AGCAACTCTTAC AGAGGGCAAAA A[gap/A]GGGGC TCAAAAGAAAT TGAAAA	gap	A	Lys	Lys (9452)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4
7282	cg43935402	412	ATCGGCACCAAC CTGCGCCGGTTC C[G/gap]GGCCGT GTTTGGGGAGA GCGGCGGG	G	gap	Arg	Arg (9453)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03164 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4

7283	cg43935402	973	ACAGAAAGGATA AAGACCCCTTCG G[G/gap]TCTCCT CATTAAATTCTGA ACTGGAA	G	gap	Gly	Val (9454)	FRAMES HIPT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q03184 ZINC FINGER PROTEIN HRX (ALL-1) (TRITHORAX-LIKE PROTEIN) - Homo sapiens (Human), 3969 aa.	0	4
7284	cg43924112	1967	TGTTGTTCAAGA AACTAAAAACTG G[C/gap]TTTGCT GCACCTTGATCA GCTGTAG	C	gap	Lys	Asn (9455)	FRAMES HIPT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49790 NUCLEAR PORE COMPLEX PROTEIN NUP153 (NUCLEOPORIN NUP153) (153 KD NUCLEOPORIN) - Homo sapiens (Human), 1475 aa.	0	6
7285	cg43925091	228	ACCCCAAGTCTA GGGCTACCGGA AG[G/gap]TAGAG AAGCTCTGGTG GCAGTGCA	G	gap	Thr	Thr (9456)	FRAMES HIPT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14999 HYPOTHETICAL PROTEIN KIAA0076 (HA0936) - Homo sapiens (Human), 1698 aa.	0	6
7286	cg43929503	1035	GCTGCGGGGTC GCAGGCTTTGCC GG[gap/C]CTTCC ACGCAGGAGCA GACCCACG	gap	C	Ala	Gly (9457)	FRAMES HIPT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)- METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6
7287	cg43929503	1349	CCAGTGCCGAG GCTCCATTCCGC AC[C/gap]TCCGG CAGGTCGGACAT CGTGTCTC	C	gap	Glu	Glu (9458)	FRAMES HIPT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26358 DNA (CYTOSINE-5)- METHYLTRANSFERASE (EC 2.1.1.37) (DNA METHYLTRANSFERASE) (DNA METASE) (MCMT) (M.HSAI) - Homo sapiens (Human), 1495 aa.	0	6
7288	cg44036171	2202	TGGAGTGATTCA GCACACAGGCG CA[G/gap]CAGCT GAAGAAATTTAAT GATGATAC	G	gap	Ala	Gln (9459)	FRAMES HIPT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75485 MULTIPLE MEMBRANE SPANNING RECEPTOR TRC8 - HOMO SAPIENS (HUMAN), 664 aa.	0	8

7289	cg43958488	1801	GCAGGTGCTCAT CCTTGGCGGAG GC[C/gap]AACAA ATGTTACATTTT GCTTCCC	C	gap	Leu (9460)	Leu (9460)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBL-NEW- ACC:BAA31649 KIAA0674 PROTEIN - HOMO SAPIENS (HUMAN), 1234 aa (fragment).	0	9
7290	cg43923753	3157	TATGTCACAGAC CTTCTGGGGT G[G/gap]CTGCTG CCTTCTCCTCCT CTGAGTC	G	gap	Ala (9461)	Ala (9461)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
7291	cg43923753	3690	CTTCGCTCTGG GACCTTGGCAGA C[gap/C]TTGAGC CAGAACTATAG ATGTCTA	gap	C	Asn (9462)	Lys (9462)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
7292	cg43923753	3733	GATGCTAAGAG GGAAGAGGCATT G[G/gap]CATCCT GCTGTGATGCTC CTGTGCGC	G	gap	Ala (9463)	Ala (9463)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15030 MRNA (KIAA0035) FOR ORF (RAT 140KD NUCLEOLAR PHOSPHOPROTEIN HOMOLOGUE), PARTIAL CDS - HOMO SAPIENS (HUMAN), 707 aa (fragment).	0	10
7293	cg43925880	769	CACCTTGCAGCT CAGGAGCCGGG CC[C/gap]TTCCG GCTCATAACCGT GGACATGT	C	gap	Lys (9464)	Lys (9464)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q13435 SPLICEOSOME ASSOCIATED PROTEIN 145 (SAP 145) (SF3B150) - Homo sapiens (Human), 872 aa.	0	11
7294	cg43966967	1484	GGGCGTCGGGC GGGACAGTGGA AGA[G/gap]AGAG GGACTTTGCCTA CGTAGCTCG	G	gap	Glu (9465)	Arg (9465)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa.	0	11

7295	cg43986987	1486	GCGTCGGGCGG GACAGTGGAAGA GA[G/gap]AGGGA CTTGCCCTACGT AGCTCGTG	G	gap	Arg	Gly (9466)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa.	0	11
7296	cg43986987	1490	CGGGCGGGACA GTGGAAGAGAG AGG[G/gap]ACTT TGCCTACGTAGC TCGTGATAA	G	gap	Asp	Thr (9467)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00213 STAT-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 710 aa.	0	11
7297	cg43334182	5146	AGGGGCTGTCT GCTGTATTCCT GC[T/gap]GCACA CTTGAGGGTGGA TATACCCC	T	gap	Gln	Arg (9468)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15052 KIAA0344 - HOMO SAPIENS (HUMAN), 1246 aa.	0	12
7298	cg43916884	993	AAAACCTTCCTG GCCAAAGCTAG G[C/gap]CCGTGG GCACCAGTCGCA CATTCTCT	C	gap	Gly	Ala (9469)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
7299	cg43916884	287	GAGACACAGTG GGAGGCTGAGG CC[C/gap]TTGG GGGTATCATTCT GTTTCTGGA	C	gap	Lys	Lys (9470)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P46087 PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION- ASSOCIATED NUCLEOLAR PROTEIN P120) - Homo sapiens (Human), 855 aa.	0	12
7300	cg43932838	324	TGCCTCCATCCA CCGGGGCTATG GC[C/gap]GCAGA AGAGGTATTGCA GACGGTGG	C	gap	Ala	Gln (9471)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43892 BICAUDAL-D - HOMO SAPIENS (HUMAN), 975 aa.	0	12

7301	cg44918447	608	AAATCTTTTCAGG CTATGGCTTTTT [gap]/TGTCTCTT GGCCTTATATCC TGGACG	gap	T	Gln (9472)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75691 DRIM PROTEIN - HOMO SAPIENS (HUMAN), 2785 aa.	0	12
7302	cg43961443	539	CGCCGCCCTCGT CCAGGTCCAGCA GC[C/gap]TCCGG TTGACCTCCAGT GTCATGCA	C	gap	Arg (9473)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14393 GROWTH-ARREST-SPECIFIC PROTEIN - HOMO SAPIENS (HUMAN), 678 aa.	0	13
7303	cg43968223	774	GCTGCCTGGCA GTGCAGATGAGC CG[G/gap]CTGAT GCCCTCAATGCA CTGGCTCT	G	gap	Ser (9474)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60342 KIAA0602 PROTEIN - HOMO SAPIENS (HUMAN), 962 aa (fragment).	0	14
7304	cg44022133	3698	GAGAGGGACAG GGAGAGAGAGA GAG[gap]/AAAGG GAGCGGGACAG GGGGGACCGA	gap	A	Arg (9475)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75158 KIAA0670 PROTEIN - HOMO SAPIENS (HUMAN), 1280 aa (fragment).	0	14
7305	cg43055918	485	AGGGGGCCTGG GCTTTGGAGGG GCC[C/gap]GCAG AGCGCTGGCATA GGACATGGC	C	gap	Arg (9476)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P42694 HYPOTHETICAL PROTEIN KIAA0054 - Homo sapiens (Human), 1942 aa.	0	17
7306	cg43949150	887	AGATGAACCTTCT TAAGCACATTCT T[G/gap]GGAAGG ATGTAGGTGTAG CCAGTCT	G	gap	Pro (9477)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75965 SPLICING FACTOR PRP8 - HOMO SAPIENS (HUMAN), 2335 aa.	0	17
7307	cg44023800	352	GCCTGGACGCT CAGCCACTCACT CT[gap]/CTCCGC CATTGCTGAGGC TGCACCCC	gap	C	Glu (9478)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14521 GIANT LARVAE HOMOLOGUE - HOMO SAPIENS (HUMAN), 1015 aa.	0	17



7308	cg44001797	3902	GCTATCTTCCTG AAAGGCTGCATA G[C/gap]CTTCAG TCCTCTTTTCCTT TTCTT	C	gap	Gly	Ala (9479)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15311 RLIP76 PROTEIN - HOMO SAPIENS (HUMAN), 655 aa.	0	18
7309	cg43917942	1322	GGGGTCCAGG CATGCCCCCGG GGG[G/gap]CCGA GGCCGAGGAAG AGGCCAAGGC	G	gap	Gly	Ala (9480)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7310	cg43917942	1491	TAGAGATCTCC GGCAGCTGCCA CC[C/gap]AACGG GGACCCCAACTT CAAGTTGT	C	gap	Asn	Thr (9481)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7311	cg43917942	1498	CTCCCGGCAGCT GCCACCCCAACG GG[G/gap]ACCCC AACTTCAAGTTG TTTCATCAT	G	gap	Asp	Thr (9482)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7312	cg43917942	1616	TGCCCAGTTGGA CCAGGCCCCAGG TG[G/gap]CCCAG GCCCTGCTGGC CCAATGGGG	G	gap	Gly	Ala (9483)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7313	cg43917942	1641	GCCCAGGCCCT GCTGGCCCAATG GG[G/gap]CCCTT CAATCCTGGGCC CTTCAACC	G	gap	Pro	Pro (9484)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19

7314	cg43917942	1892	CCCGGCCCGCGC ACCGGCCCGCTG CGG[C/gap]CCCA CCGGCTCAGGG TGAGCCCCCT	C	gap	Ala	Ala (9485)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7315	cg43917942	1912	TGCGGCCCGCAC CGGCTCAGGGT GAG[C/gap]CCCC TCAGCCCCCACC CACCGGCCA	C	gap	Pro	Pro (9486)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7316	cg43917942	1916	GCCCCACCGGC TCAGGGTGAGC CC[C/gap]TCAG CCCCCACCACC GGCCAGTCG	C	gap	Pro	Leu (9487)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7317	cg43917942	2077	GAAGCAAGCGC AAGTGCCACC GGA[G/gap]GGG GTCCAGGAGCTC CCCCAGGCTC	G	gap	Gly	Gly (9488)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00301 KSRP - HOMO SAPIENS (HUMAN), 711 aa.	0	19
7318	cg43917942	820	GGAGTGGGTATT CTGGTAGCCTGC T[G/gap]GGCTTG GCGCCACCTGG TGGTAGCT	G	gap	Pro	Gln (9489)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00267 SUPT5H PROTEIN - HOMO SAPIENS (HUMAN), 1087 aa.	0	19
7319	cg43917942	1308	CTCTGGGCTGG GGCTGAGGATTG CG[G/gap]CCCTG GGCAGCTTCTC CTTCCCA	G	gap	Pro	Arg (9490)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0	19

7320	cg43981657	335	CCTGAGGCGTG CCCAGGCTCTG GCC[C/gap]GGGC AGCAGGGGTGA GGCAGGGGGCT	C	gap	Arg (9491)	Arg (9491)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0	19
7321	cg43981657	443	CTGCTCCCAGG GGCCCTGGCGG GCG[G/gap]CCTG GGCCGGCCCTG CCCAGACAGC	G	gap	Ala (9492)	Ala (9492)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0	19
7322	cg43981657	568	GAGTAGGGGTTT CTGGGCGCTTGA G[C/gap]CGCCTT TGCAGTCGGAG GGGCAGCC	C	gap	Arg (9493)	Arg (9493)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75807 APOPTOSIS ASSOCIATED PROTEIN - HOMO SAPIENS (HUMAN), 674 aa.	0	19
7323	cg43981657	1070	GGCAAGCTCATC GCTCTGTTTCTG G[G/gap]CTTCGC TCTTGGCGGCAT CGAGCTG	G	gap	Ala (9494)	Ala (9494)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
7324	cg43981657	701	CTTCAGAAAGCTC CTGCAGTCTCGT G[G/gap]CGGCGC GCCCCAGGTCA CTTGTTAA	G	gap	Ala (9495)	Ala (9495)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
7325	cg43981657	708	GCTCCTGCAGTC TCGTGGCGGCG CG[C/gap]CCCAG GTCACCTTGTTAA CTTCTTCT	C	gap	Gly (9496)	Gly (9496)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75300 ES/130 - HOMO SAPIENS (HUMAN), 977 aa.	0	20
7326	cg43921598	1826	ACAAGGACTGG GAGCGGCACCA CCG[C/gap]CTCT GTGGTCAGAACC TGCATGGCC	C	gap	Leu (9497)	Ser (9497)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43439 MTG8-LIKE PROTEIN (MTG8 RELATED PROTEIN) (EHT) - HOMO SAPIENS (HUMAN), 604 aa.	0	20

7327	cg43919155	1307	GTAAGAAAGAG AAGACAGAGA GG[G/gap]CAGCA GCCTGAAGAAGA AGTGTG	G	gap	Gly	Ala (9498)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14241 ELONGIN A - HOMO SAPIENS (HUMAN), 772 aa.	0	1 (1p36.1)
7328	cg43988854	893	CAATGCTTGAC AATAGCAAAAA A[gap]/AJTAAATCT CCCTTTTGAAG CTTTAT	gap	A	Asn	Lys (9499)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P46013 ANTIGEN KI-67 - Homo sapiens (Human), 3256 aa.	0	10 (10q25)
7329	cg43973740	1103	GATTGCTATTTT TAGAGCTTTTTT T[gap]AGGCATCT CATTACCCCTCT GCCTC	T	gap	Leu	Leu (9500)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q61123 MATERNAL EMBRYONIC MESSAGE 3 (MEM3) - MUS MUSCULUS (MOUSE), 754 aa.	0	16 (12q12)
7330	cg44928323	4878	TTGAGGAATTTA TGACTAGGCATC A[gap]/TJGGTACA TGAAAAAGAAAGA ATTCAAG	gap	T	Gln	His (9501)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P97526 NEUROFIBROMIN - RATTUS NORVEGICUS (RAT), 2820 aa.	0	17 (17q11.2)
7331	cg43948022	921	CTGTCACGGTGT CCCCAGCCCCC CA[G/gap]GTGGC TGCGCACTGCAT CCTCAGTG	G	gap	Leu	Trp (9502)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa.	0	3 (3p21.33)
7332	cg43948022	922	GTCACGGTGTCC CCAGCCCCCA GG[gap]/GJTGCT GCGCACTGCATC CTCAGTGT	gap	G	His	His (9503)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa.	0	3 (3p21.33)
7333	cg43948022	703	GGGGCACAAC AAGGTCAACTGA GG[G/gap]CCCCG GGCTGGCCAATA GCGGCCAA	G	gap	Gly	Gly (9504)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa.	0	3 (3p21.33)

7334	cg43948022	713	CAAGGTCAACTG AGGCCCCCGG CT[G/gap]GCCAA TAGCGGCCCAAG GTAAAGCC	G	gap	Pro	Gln (9505)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P16278 BETA-GALACTOSIDASE PRECURSOR (EC 3.2.1.23) (LACTASE) (ACID BETA- GALACTOSIDASE) - Homo sapiens (Human), 677 aa.	0	3 (3p21.33)
7335	cg43955232	838	AGCAGCAGCAG CAGCAGCAGCA GCA[G/gap]CACC TCAGCAGGGCTC CGGGGCTCA	G	gap	His	Thr (9506)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P54253 ATAXIN-1 (SPINOCEREBELLAR ATAXIA TYPE 1 PROTEIN) - Homo sapiens (Human), 816 aa.	0	6 (6p23)
7336	cg42907760	1681	CATCCCCCTCAC CTTCGGCGGAC CG[G/gap]CGGCG CCAGCTTCGTGC CCCTGGAG	G	gap	Arg	Gly (9507)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15464 SHB MRNA - HOMO SAPIENS (HUMAN), 596 aa.	0	9 (9p12)
7337	cg43311566	1080	CCAACCTCCACC CTGACGGCCGC GC[C/gap]ATGGC CACCAGTTTGC ACACTTGA	C	gap	Met	Tyr (9508)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment).	0	X
7338	cg43311566	856	CAAGGATGTACT GCGCACTGACC GG[G/gap]CCCAC CCCTACTATGCG GGGCCTGA	G	gap	Ala	Pro (9509)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14830 DNA SEGMENT, JOHNS HOPKINS UNIVERSITY 4 (MG81) - HOMO SAPIENS (HUMAN), 651 aa (fragment).	0	X
7339	cg43921793	1032	CTCGCAGGGAG CTGATAGGCTGG AA[G/gap]CTATTT TTGAAGTTTCTT TTTGT	G	gap	Ser	Ser (9510)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X
7340	cg43921793	1318	CTGGGGGTGCATA GTAGTAGCCGGA G[G/gap]TCTCAT CGTACTGGTAGG TAGAGAC	G	gap	Thr	Thr (9511)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X

7341	cg43921793	364	GCCCCGTGCAC CCAGCCGGAG CCC[C/gap]GCAC CCGTGTTGGGC CTCGATAGG	C	gap	Arg (9512)	Arg	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14136 KIAA0122 PROTEIN - HOMO SAPIENS (HUMAN), 1010 aa (fragment).	0	X
7342	cg42682094	289	CATAGTAGAGAA GGGGGGCCCT GG[gap/G]CCTGC TCCAAGCCAGCC TTGCAGCA	gap	G	Gly (9513)	Gly	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14674 KIAA0165 PROTEIN - HOMO SAPIENS (HUMAN), 1795 aa.	0	
7343	cg42682094	3085	GACAGACTGCTG TGAGGACAGGG CT[gap/C]GGCGC AGAGCGAGCAG TCACAGGTG	gap	C	Glu (9514)	Ser	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14674 KIAA0165 PROTEIN - HOMO SAPIENS (HUMAN), 1795 aa.	0	
7344	cg43032555	1098	AGAGCTTGGCC GTCTCTTGGGG TC[C/gap]TTCCG GTCATTACCTC AAAGTGCC	C	gap	Lys (9515)	Lys	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 898 aa.	0	
7345	cg43032555	189	CCACTGGCACCC TTCTGCCCCAGGG G[C/gap]TGACCC TCGGGCCCCCATC CCCAGCA	C	gap	His (9516)	Gln	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q14764 MAJOR VAULT PROTEIN (MVP) (LUNG RESISTANCE-RELATED PROTEIN) - Homo sapiens (Human), 898 aa.	0	
7346	cg43033383	1243	ACAGACTTTATT GTGGGGGGGTT CC[C/gap]ACCTG GGACCCACCTC TTAAATAA	C	gap	Trp (9517)	Trp	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0	

7347	cg43303383	1383	GGGCTGGAGGG GTGAGGCAGG GCC[C/gap]TTGT CACCTGCATGCC CACATCCAC	C	gap	Lys (9518)	Lys (9518)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CA45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0	
7348	cg43303383	1455	AGATGCTCTGGG AGGGGCTAGGG AG[gap/C]CCCCA GGCTAGGGGCA AGATGGCAG	gap	C	Gly (9519)	Gly (9519)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CA45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0	
7349	cg43303383	664	CTGAGGCCGAG TCGCTGCCGCT GC[G/gap]GGCTC TGATTGAGATGG TGGTGGA	G	gap	Pro (9520)	Pro (9520)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CA45385 TRITHORAX HOMOLOGUE 2 - HOMO SAPIENS (HUMAN), 2715 aa.	0	
7350	cg43927175	134	AGCATCTTCTGG AATAGGGCGATG G[C/gap]CTCATC CACCTTCCTGAG CTCTGCT	C	gap	Ala (9521)	Pro (9521)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD21819 G7A - HOMO SAPIENS (HUMAN), 1264 aa.	0	
7351	cg43932090	1755	CCATGTCGGACA CTCCTCCTCCT C[C/gap]TCTAAAT CTCTAGGTCCT CCTGT	C	gap	Glu (9522)	Glu (9522)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:000566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0	
7352	cg43932090	1757	ATGTCGGACACT TCCTCCTCCTCC TTC[gap]TAAATCT TCTAGGTCCTCC TTGICA	C	gap	Glu (9523)	Arg (9523)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:000566 M PHASE PHOSPHOPROTEIN 10 - HOMO SAPIENS (HUMAN), 672 aa (fragment).	0	
7353	cg43940146	354	ATGCCGACATAC TTCAGGGCATCA G[C/gap]CTGGCT GTATCTGTAATC AAAAAAC	C	gap	Ala (9524)	Leu (9524)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15910 ENHANCER OF ZESTE HOMOLOG 2 (ENX-1) - Homo sapiens (Human), 746 aa.	0	

7354	cg43940465	5447	CTGAGGGCTCG GTCATGCTGGT TCIG[gap]TTCGG CTGCTCAGAGAC TTCACCTAA	C	gap	Lys	Lys (9525)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60300 KIAA0553 PROTEIN - HOMO SAPIENS (HUMAN), 1095 aa (fragment).	0	
7355	cg43966585	1546	CAAGCACCTGCG CCTGTCCCTGAA CIG[gap]GCCACG GCCAGTGTACAG TACAGCA	G	gap	Gly	Ala (9526)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	
7356	cg43966585	1547	AAGCACCTGCGC CTGTCCCTGAAC GIG[gap]CCACGG CCAGTGTACAGT ACAGCAT	G	gap	Gly	Ala (9527)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	
7357	cg43966585	1643	CACCCCATCCCA CTGGAGTCAGG GGIG[gap]CTCGG CCGACATCACCC TTCGCAGC	G	gap	Gly	Ala (9528)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	
7358	cg43966585	1701	GGGCCCAGGAC CCCCACCAGAG GCCIG[gap]GGCC CCACGCCCCCT GCCGCGCCCG	G	gap	Gly	Ala (9529)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	
7359	cg43966585	1703	GCCCAGGACCC CCCACCAGAGC CGGIG[gap]CCCC ACGCCCCCTGC CGCGCCCGCG	G	gap	Gly	Ala (9530)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	
7360	cg43966585	867	TCITTCGTGCCG CCAAAGCCTCCA GIG[gap]CCCAAG GTCAGCATCCCA CTGTCAG	G	gap	Pro	Pro (9531)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14492 APS, COMPLETE CDS - HOMO SAPIENS (HUMAN), 632 aa.	0	



7361	cg44003855	393	CTCCTGGGTGGT GCCACCGGAGC CC[C/gap]GGCCC AGCTTCTTCTCC ATCTCCCC	C	gap	Arg	Gly (9532)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P49641 ALPHA-MANNOSIDASE IX (EC 3.2.1.114) (MANNOsyl- OLIGOSACCHARIDE 1,3-1,6-ALPHA- MANNOSIDASE) (MAN IX) - Homo sapiens (Human), 1139 aa.	0	
7382	cg44011100	566	CAAGCTCCTGGG GAGGGGGCCCT GC[C/gap]GCAGG GCTTCCCCCTTC CCTCTCCA	C	gap	Ala	Ala (9533)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15450 P160 - HOMO SAPIENS (HUMAN), 1251 aa.	0	
7363	cg44016445	1446	GGGCTCCCTGC CCCGCTGCAGC CCC[gap]CTTGCT TGGGAGGCACT GGACTTAGGC	gap	C	Arg	Arg (9534)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75427 LEUCIN RICH NEURONAL PROTEIN - HOMO SAPIENS (HUMAN), 832 aa.	0	
7364	cg44024279	1732	ATGCCAACAGGA GGCCATGCTTCA G[C/gap]AGCTTG GTGGTGGATGAA ACATATG	C	gap	Ser	Ala (9535)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobULIN) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	
7365	cg44024278	1850	CTGCAACGATG AAGCAAGAGTTT C[gap]CTTCATTAA CCTTGTGAAGCA AAAGCC	gap	C	Leu	Pro (9536)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobULIN) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	
7366	cg44024279	1941	TTCTCAGGCCTG TTGGAGAAATGC T[G/gap]CCAAGG CCAGGAACAGG AAGTCTGC	G	gap	Cys	Ser (9537)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P02771 ALPHA-FETOPROTEIN PRECURSOR (ALPHA-FETOglobULIN) (ALPHA-1- FETOPROTEIN) - Homo sapiens (Human), 609 aa.	0	

7367	cg44932543	319	TGTTGATCTGTC CCTCCTGGATTT C[C/gap]TGCCGG GTCTCGGCAGG CAGATGGT	C	gap	Gln (9538)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75341 BRCA1-ASSOCIATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 600 aa.	0	
7368	cg43957199	1189	CCGAGGAAATAT CAGGCTGATGG CT[G/gap]GGGCA GGCCCGGAGCT GGTAGTGTG	G	gap	Pro (9539)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q16610 EXTRACELLULAR MATRIX PROTEIN 1 PRECURSOR (SECRETORY COMPONENT P85) - Homo sapiens (Human), 540 aa.	1	1.0e-313
7369	cg44002959	4273	GGCTGCCCTCGTC CGGGGTCTCAG GG[G/gap]CCAGT GGCGGGGGCT TTCAGGGGT	G	gap	Ala (9540)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92513 MYELOBLAST KIAA0239 - HOMO SAPIENS (HUMAN), 571 aa (fragment).	5	1.4e-316
7370	cg43937128	832	CTGGTTTTTCATT CCATTCCTTGCT G/gap]CCTTTGG CTGTATCTCTCC ACGAG	G	gap	Glu (9541)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	X	4.0e-317
7371	cg43937128	504	TGTGAAAGGTGC TTATCTCGTTGT C[C/gap]TTCGGA GTTGCCTGCTGA CTGTTTC	C	gap	Lys (9542)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51654 GLYPICAN-3 PRECURSOR (INTESTINAL PROTEIN OCI-5) (GTR2- 2) (MXR7) - Homo sapiens (Human), 580 aa.	X	4.0e-317
7372	cg44015618	837	AGGACAGAGGA CAGTGAGGGAC AGG[G/gap]CTGG GGCCAAAAGAAAT TAACAGATC	G	gap	Ser (9543)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75148 KIAA0658 PROTEIN - HOMO SAPIENS (HUMAN), 589 aa (fragment).	11	8.7e-312

7373	cg43923376	1635	CCCCAGGCTCTGG GCCCAGAGCAG GG[G/gap]CTGTT GCCGAAAGGCT GTGGAGCAA	gap	Ala	Leu (9544)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P06865 BETA-HEXOSAMINIDASE ALPHA CHAIN PRECURSOR (EC 3.2.1.52) (N- ACETYL- BETA-GLUCOSAMINIDASE) (BETA-N-ACETYLHEXOSAMINIDASE) - Homo sapiens (Human), 529 aa.	9.2E-297	15
7374	cg43981656	1518	AGTCTCTTTCCG A TTTGCCACCAGA A[A/gap]GGGCTT TGTCCTCTGCTC TTCGGAT	gap	Leu	Leu (9545)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAA08974 GUANINE NUCLEOTIDE-EXCHANGE FACTOR - HOMO SAPIENS (HUMAN), 548 aa.	1.6E-292	10
7375	cg44128920	1189	ATGAGAAGACAC C CTCAGATGGGG GA[C/gap]CCCCG CAGCTTGGAGCC CCAGATCG	gap	Pro	Pro (9546)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
7376	cg44128920	1418	GGACACCAAGG C AGAGCTCTGAAG AG[C/gap]CTCCC TCAGAAGAGAGC CAGGACAC	gap	Pro	Leu (9547)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
7377	cg44128920	1520	CATAGGTCAC TG C TGTGGCCATCTA C[C/gap]ACTTTG AAGGTCCAGC GAGGGCAC	gap	His	Thr (9548)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15184 CDC42-INTERACTING PROTEIN 4 - HOMO SAPIENS (HUMAN), 545 aa.	1E-290	19
7378	cg43949262	1272	GGGTCCCCGCTG C AAGCTGCCCCAG GGC[C/gap]TGCG GGTCGCTCTGAA TGCCCTTCA	gap	Gln	Gln (9549)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	

7379	cg43949262	770	CAGCAGGCACC AGGCTGGGCA CCA[G/gap]CTGG GGCTGGGTAC GCCCAGAAGG	G	gap	Leu	Trp (9550)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA7832 KIAA0988 PROTEIN - HOMO SAPIENS (HUMAN), 1192 aa.	9E-290	
7380	cg43931799	2153	GCTGGGGTCT GAACCGCAACCA GG[G/gap]CCTGA ACAGGCTGATGC TGGCTGTG	G	gap	Gly	Ala (9551)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83001 KIAA1049 PROTEIN - HOMO SAPIENS (HUMAN), 550 aa (fragment).	7.6E-289	22
7381	cg44010409	1496	GACGAGCAGAA CTGCGAGTGGT GGG[G/gap]CGGT AGCCAGGCAAG CTGAGCAGGG	G	gap	Arg	Arg (9552)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q14981 NUMA PROTEIN - HOMO SAPIENS (HUMAN), 2101 aa.	2.1E-281	11
7382	cg43930921	1135	CAATCTCAAAGA AGGAGATGGT CC[C/gap]TTGCG GTAAATCTCATT GCCTGGAG	C	gap	Lys	Lys (9553)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
7383	cg43930921	877	CATAGCTGAACT CGATCAGCAGCT TIG[gap]CCGTAG CCCCGGCGCTG GTAGGGAG	G	gap	Gly	Gly (9554)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q92993 60 KD TAT INTERACTIVE PROTEIN - Homo sapiens (Human), 513 aa.	2.4E-280	11
7384	cg44001088	352	GGTCACAACACA GTGACCGGACG AA[G/gap]TTGTT CCAATTGGTTTT CCAATGCA	G	gap	Leu	Phe (9555)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	2.2E-279	X
7385	cg44001088	469	TTTGCTCTTTAT TTTTCGGATAG C/gap]AGTTTGAA TGGCCTTCTTCT GTTTG	C	gap	Ala	Leu (9556)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43428 RALBP1-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	2.2E-279	X

7386	cg44022026	1703	CCCAGGGTGTG CTGGAGCACCAC AC[C/gap]TACGG CGCCCTGCTCTT CCCCTGCTG	C	gap	Tyr	Thr (9557)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43292 HGAA1 - HOMO SAPIENS (HUMAN), 621 aa.	1.2E-278	8
7387	cg43252100	1461	TCTAACATTTTC ATCAGCCTATGG [C/gap]AAGTGGT TTTGTGGATTTT CTAAA	C	gap	Ala	Glu (9558)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA83037 KIAA1085 PROTEIN - HOMO SAPIENS (HUMAN), 584 aa (fragment).	4.9E-278	
7388	cg43922691	188	GGCCGGACTGG AAAGCCGGAGC GGG[G/gap]CCAG GCGGGCCTCCC CAAAAGCCTG	G	gap	Pro	Gln (9559)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
7389	cg43922691	324	GCTCCGGCAGC GGAACCGCTG AGG[C/gap]TGGA GGAGGACAAAC CGGCCGTGGA	C	gap	Leu	Trp (9560)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
7390	cg43922691	353	AGGAGGACAAAC CGGCCGTGGAG CG[G/gap]TGCTT GGAGGAGCTGG TCTTCGGCG	G	gap	Cys	Ala (9561)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34043 CGI-48 PROTEIN - HOMO SAPIENS (HUMAN), 521 aa.	8.5E-278	17
7391	cg43988211	1246	ACCCAAATCGAA TCCATAGGCTGC G[C/gap]CAGGGG CCTGTTATCATG TAATAGG	C	gap	Trp	Cys (9562)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD41476 TRANSCRIPTION FACTOR IIC63 - HOMO SAPIENS (HUMAN), 519 aa.	6.2E-275	
7392	cg43958878	131	GGTGATGGGTTG GTCCTCAGCGGA T[G/gap]CCTTGG TGGATGAGGCTG CTTTTG	G	gap	Gly	Gly (9563)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9

7393	cg43958878	1461	TTTGCCAGGAGT TCGGCCCGGAG TC[C/gap]TGCCG GCGCTGTGGGA TCGGTTGGC	gap	Arg (9564)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
7394	cg43958878	1510	CGGCCCGCATG GGTGAGGGGGC CGG[gap/G]CCTG CGGCTTCCTTGG CTTCGCTG	gap	Pro (9565)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
7395	cg43958878	1530	GCCGGCCCTGCG GCTTCCTTGGCT TT[gap/G]CGCTG CCAGCGCGCAG GGGGTGCAAT	gap	Glu (9566)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
7396	cg43958878	247	AGGGTCTCATCT GCTGCTGGGGAT G[C/gap]CACTGT GGCCCCATCTG GGCTCATG	gap	Ala (9567)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD16405 CELL CYCLE PROTEIN CDC20 - HOMO SAPIENS (HUMAN), 499 aa.	3E-269	9
7397	cg43153237	244	CCAGCCCTGGT GCTGGGGGTGG CCC[C/gap]TGTG CCTGGGTGTGG CCAGCCCCCT	gap	Leu (9568)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60540 HYALURONIDASE - HOMO SAPIENS (HUMAN), 463 aa.	1E-267	
7398	cg43967058	536	CCTTCAGAAGG GCGCGGCGGGC CC[gap/C]GTTGG AACAAATTTTCGT GGATAGGC	gap	Arg (9569)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60788 DJ32F7.1 - HOMO SAPIENS (HUMAN), 506 aa (fragment).	6.5E-264	X

7399	cg43967058	541	CAGAAGGGCGC GGCGGGCCCGT TGG[gap]G/AACA AATTCGTGGAT AGGCTGCCT	gap	G	Asn	Glu (9570)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60788 DJ32F7.1 - HOMO SAPIENS (HUMAN), 506 aa (fragment).	6.5E-264	X
7400	cg43967058	570	AATTCGTGGAT AGGCTGCCTCAG G[gap]/C/JAGTTAG AAATCGTGTGCA AGCGCTT	gap	C	Gly	Gly (9571)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60788 DJ32F7.1 - HOMO SAPIENS (HUMAN), 506 aa (fragment).	6.5E-264	X
7401	cg43980328	1085	CTGAAAGAGATC ATCATCACTGCT G[G/gap]CCTCGC CTAGAGCAGGAA ACAIGGG	G	gap	Ala	Ala (9572)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA25518 KIAA0592 PROTEIN - HOMO SAPIENS (HUMAN), 1353 aa (fragment).	3.7E-262	10
7402	cg43922182	1381	GCTGCTGCTCGA CAGCCCCACGTC G[C/gap]GCACGC CGCCGCCGCC TCCTGCTC	C	gap	Arg	Ala - (9573)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
7403	cg43922182	1570	CCTGCTGGCGC CGGGGGCCCCG TGC[G/gap]CGGC CTGCTCGTCGGC CTCGTGCGC	G	gap	Ala	Arg (9574)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
7404	cg43922182	1858	TCTGAGTCTCCC AGCCTCGACCT G[G/gap]CCGCCG CCTGCCAATCTT CAGCCGC	G	gap	Gly	Ala (9575)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P47974 TIS11D PROTEIN (BUTYRATE RESPONSE FACTOR 2) (EGF- RESPONSE FACTOR 2) (ERF-2) - Homo sapiens (Human), 482 aa.	1.1E-261	2
7405	cg43922648	2335	GCCAGTAATGGA CACCTGTCTGTT G[G/gap]CTTTGC CCAGAGCAGCA GTCCCTTT	G	gap	Ala	Ala (9576)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15054 HYPOTHETICAL PROTEIN KIAA0039 - Homo sapiens (Human), 491 aa (fragment).	3.3E-260	11

7406	cg43980777	1028	CAATCTGGGGTCTG GTGAGCAAGTG GC[gap]/CJTTCIT GGCCCTCCTTTT CATCATTT	gap	C	Ala	Gly (9577)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P23497 NUCLEAR AUTOANTIGEN SP-100 (SPECKLED 100 KD) - Homo sapiens (Human), 688 aa.	6.2E-259	2
7407	cg43929959	195	AAGAAAACATGT CAGGACACAAAT G[gap]/CJTATCC CTGGGACTTACA GGATCGA	gap	C	Cys	Cys (9578)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P78506 DIABETES MELLITUS TYPE I AUTOANTIGEN (ISLET CELL AUTOANTIGEN P69) - HOMO SAPIENS (HUMAN), 483 aa.	2.1E-258	7
7408	cg43254094	1287	CCGGCTCCAGCTC AGGAATGCTGCA G[C/gap]AAGCAC AGTGTGGCCTTG ATCTTCG	C	gap	Gln	Lys (9579)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P78539 SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa.	6.4E-257	X
7409	cg43254094	267	CCGCCTCTGCTG CTGCTGCTGCTG C[gap]/TJGCGTCC CGCCCAGCCCG AGCTTCCC	gap	T	Arg	Leu (9580)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P78539 SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa.	6.4E-257	X
7410	cg43254094	803	CCAACAACTGA CAGTCCGGGTGT C[C/gap]JTGCGAG ACACCCGAAGGA AGAGACA	C	gap	Trp	Gly (9581)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P78539 SUSHI REPEAT-CONTAINING PROTEIN SRPX PRECURSOR - Homo sapiens (Human), 464 aa.	6.4E-257	X
7411	cg43986498	1366	GCTACATCTACC ACAGTGACATCG T[G/gap]CAGTCC CTGCCACCGGAT CTGCGGC	G	gap	Gln	Ser (9582)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.3E-255	19
7412	cg43986498	1519	AGATCGAGCGCA AATTCGACAAGT G[G/gap]CAGGAG CGCCCGCCTGT GAAGCAGG	G	gap	Gln	Arg (9583)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.3E-255	19



7413	cg43986498	1950	CGGCAGAGAAG AAGTGGCTGA GGC[C/gap]AACC AGAAAGTATTTCT CCAGCATGG	C	gap	Asn	Thr (9584)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.3E-255	19
7414	cg43986498	961	GCACGGTCAAG GAGCTGGCAA CAG[C/gap]CTGG ACAAAGTGCAAGA ACAATGAGA	C	gap	Leu	Trp (9585)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43677 HYPOTHETICAL 55.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 499 aa.	1.3E-255	19
7415	cg43978430	1070	TACGACGCCACA TCTCTGCCCGCA G[G/gap]TGCAGA CCCACAGCAAGT GATCAAT	G	gap	Gly	Val (9586)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75879 CYTOCHROME OXIDASE ASSEMBLY FACTOR - HOMO SAPIENS (HUMAN), 557 aa.	2.8E-255	4
7416	cg44034555	470	GCGGAGCTCAT GGCAAGGGCT GGG[C/gap]CAAG GGGCTCCTTCCC GAAGTCCAC	C	gap	Gly	Ala (9587)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.8E-252	1
7417	cg44034555	471	GCGGAGCTCATG GGCAAGGGCTG GGC[C/gap]AAGG GGCTCCTTCCCG AAGTCCACC	C	gap	Gly	Ala (9588)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q13228 SELENIUM-BINDING PROTEIN 1 - Homo sapiens (Human), 472 aa.	3.8E-252	1
7418	cg39711096	893	CCGGAGGAGGCC ACAGTTACTGCC TC[C/gap]AGCTG CAGCAGTGACAT CGCTGACC	C	gap	Ser	Ala (9589)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18428 LIPOPOLYSACCHARIDE-BINDING PROTEIN PRECURSOR (LBP) - Homo sapiens (Human), 481 aa.	1E-251	

7419 cg43254830	1275	CATTCCAAAGCT CTGACCCAGAAC A[G/gap]ATGCGA CAGAGTTTGCTG ACTGCAA	G	gap	Met	Cys (9590)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76821 KIAA0977 PROTEIN - HOMO SAPIENS (HUMAN), 1166 aa.	1.3E-251	2
7420 cg43254830	1323	CAATCCGTTCCG GAGAGGCTGCT GC[C/gap]AAATT GAAAGGGTTAC CATTCCAT	C	gap	Lys	Asn (9591)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76821 KIAA0977 PROTEIN - HOMO SAPIENS (HUMAN), 1166 aa.	1.3E-251	2
7421 cg44910581	2889	CAAACTCTGAAG TGAACATCATGAT C[gap]ATGTAGA ATACCAGATCCT TATACIC	gap	A	Cys	Met (9592)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q16349 H-NUC - HOMO SAPIENS (HUMAN), 824 aa.	5.8E-251	
7422 cg43945969	303	GGAGGCCCTGC GCGCGCTCACG GCG[C/gap]TCTT CAAAGAGCAGC GGAACCGAGA	C	gap	Leu	Ser (9593)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43383 HYPOTHETICAL 53.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 475 aa.	4.1E-246	22
7423 cg43980318	142	CAACGGCGATTG CGGCCGCCCA GG[C/gap]CGCG GCCCGGAGGAA ACCGGGTGAC	G	gap	Ala	Arg (9594)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCLINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
7424 cg43980318	150	ATTGCGGCCGC CCCAGGGCGCG GCC[C/gap]GGAG GAAACCGGGTG ACGGTGGTGC	C	gap	Gly	Glu (9595)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCLINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
7425 cg43980318	231	GGAAGGTGGTG GACCTGCTGGC GCA[G/gap]GACG CCGACATCGTGT GCCGCTGCC	G	gap	Asp	Thr (9596)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCLINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)

7426	cg43980318	232	GAAGGTGGTGG ACCTGCTGGCG CAG[G/gap]ACGC CGACATCGTGTG CCGCTGCCA	G	gap	Asp (9597)	Thr (9597)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
7427	cg43980318	237	TGGTGGACCTGCC TGGCGCAGGAC GC[C/gap]GACAT CGTGTGCCCGCT GCCAGGGAG	C	gap	Asp (9598)	Thr (9598)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
7428	cg43980318	87	GCGTCACTGGA GCCATGGCGTTC GC[C/gap]GAGAC CTACCGGGCGG CATCCTCCC	C	gap	Glu (9599)	Arg (9599)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P30520 ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP-ASPARTATE LIGASE) - Homo sapiens (Human), 455 aa.	1.6E-244	1 (1cen)
7429	cg43984815	358	GTCAGTGCTCAC CCCTGGCTGGG AG[G/gap]CAGAG CCGGACCTTCCT CGTGGAGC	G	gap	Gln (9600)	Arg (9600)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43632 SPINDLE POLE BODY PROTEIN SPC97 HOMOLOG - HOMO SAPIENS (HUMAN), 902 aa.	3E-236	10
7430	cg43984815	729	AGCCTGCTCCAC GACAGGAGCTTC A[G/gap]CTACAC AGGGGACAGCC AGGCGCAG	G	gap	Ser (9601)	Thr (9601)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O43632 SPINDLE POLE BODY PROTEIN SPC97 HOMOLOG - HOMO SAPIENS (HUMAN), 902 aa.	3E-236	10
7431	cg43932322	327	TGGTCCAGCCGT GGAAAGGGCGG CA[G/gap]GCCGAT GCCTCGCCCATC GCGGTCA	gap	G	Cys (9602)	Leu (9602)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88941 GLYCOPROTEIN PROCESSING GLUCOSIDASE I - RATTUS NORVEGICUS (RAT), 834 aa.	6.5E-236	2
7432	cg4330158	1330	GAAGTCGCACAA GACCGCAACCA G[gap]/CJACAGGA CGAGGGGATCC TGCCCTCG	gap	C	Arg (9603)	Ser (9603)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa.	2.1E-235	

7433	cg43330158	1332	AAGTCGCACAAG ACCCGCAACCAG A[C/gap]AGGACG AGGGATCCTG CCCTCGGG	C	gap	Gln	Arg (9604)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa.	2.1E-235	
7434	cg43330158	1333	AGTCGCACAAGA CCCGCAACCAGA C[A/gap]GGACGA GGGATCCTGC CCTCGGGC	A	gap	Gln	Arg (9605)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75462 CYTOKINE-LIKE FACTOR-1 PRECURSOR - HOMO SAPIENS (HUMAN), 422 aa.	2.1E-235	
7435	cg43930174	1376	CAGTGCTGCGG GGCCGCATGGT GCG[G/gap]TACC TGATGCGCTCGC GTGAGATCA	G	gap	Tyr	Thr (9606)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14742 NUCLEOLAR PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	2.4E-234	12
7436	cg43948360	2451	CTCCATGTTGAG GGCCAGTCCTC G[C/gap]TCTGCA GGGAGCCATCT GTGGCJT	C	gap	Ser	Thr (9607)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O88746 TOM1 - MUS MUSCULUS (MOUSE), 492 aa.	5.1E-234	22
7437	cg43952917	1353	TGGGCATTGACA GCAACCTGGGT C[C/gap]TAACGG TTTGGTTAACAC CAGCACG	C	gap	Gly	Glu (9608)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q99611 SELENIDE, WATER KINASE 2 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 2) (SELENIUM DONOR PROTEIN 2) - Homo sapiens (Human), 448 aa.	1.5E-232	
7438	cg43940463	852	GTGCTCTTGGTA GTACTCCAGGAA G[G/gap]CGCGGC CCACACTCTGCG CCACCGG	G	gap	Ala	Ala (9609)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99771 JIP-1 - HOMO SAPIENS (HUMAN), 467 aa.	3.1E-232	

7439	cg43947107	781	CCATGGCGACCC GCTGCCCTCAGCT C[C/gap]TGCCGG CTCACCTCTCTCC TTTGCCA	gap	Gln (9610)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75528 ADA3-LIKE PROTEIN - HOMO SAPIENS (HUMAN), 432 aa.	2.8E-231	3
7440	cg43948144	1163	TAAAAAGGCCAA GTTTCACCACTC T[G/gap]ATTGCC TTTCAACCTGGC TACTTCA	gap	Asp (9611)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74901 KIAA0878 PROTEIN - HOMO SAPIENS (HUMAN), 611 aa.	4.6E-231	5
7441	cg43986279	2340	CCTACCGCTTCC GCGCCCCCGAC TG[G/gap]CTGTG CCGCGTGGTGA AGCACCTGC	gap	Leu (9612)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P37288 VASOPRESSIN V1A RECEPTOR (VASCULAR/HEPATIC-TYPE ARGININE VASOPRESSIN RECEPTOR) (ANTIDIURETIC HORMONE RECEPTOR 1A) (AVPR V1A) - Homo sapiens (Human), 418 aa.	7.5E-231 (12q14)	12
7442	cg43986279	2588	GTCACCAAGGCC C CGCGACTGCTG GG[C/gap]CACCT TCATCCAGCCCT GGGGTTCT	gap	Ala (9613)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P37288 VASOPRESSIN V1A RECEPTOR (VASCULAR/HEPATIC-TYPE ARGININE VASOPRESSIN RECEPTOR) (ANTIDIURETIC HORMONE RECEPTOR 1A) (AVPR V1A) - Homo sapiens (Human), 418 aa.	7.5E-231 (12q14)	12
7443	cg43916785	3222	GATCTGGATGCC C CTCTGCCAGAA G[G/gap]CGCTGC CTGATTCTCTCA AGCTCCT	gap	Arg (9614)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAC97961 S164 - HOMO SAPIENS (HUMAN), 735 aa (fragment).	2.5E-230	14
7444	cg43933074	1088	CAGCTCCACCCCT C GAAGTCGCTGCT G[C/gap]GCCCCC ACTTCTCAACA CGCCTGA	gap	Ala (9615)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa.	3.2E-228	19

7445	cg43933074	115	GTGCAGTTCTAC AAGGTGTGCGTG A[G/gap]CGTGGT GAGCGAGAAGT GCCGJATC	G	gap	Ser	Thr (9616)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa.	3.2E-228	19
7446	cg43933074	967	TCCACCCGGATC CTGGCCATGAAG G[C/gap]CTCGCT CTGCAAGCTGTC GCCCTGC	C	gap	Ala	Ala (9617)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD31087 VITAMIN D RECEPTOR INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 873 aa.	3.2E-228	19
7447	cg43978295	756	TGCCAGGGATGA ATAGCCACTGGG G[C/gap]CCTGGC CATAGCTGGACT GTCTCTT	C	gap	Gly	Gly (9618)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
7448	cg43978295	758	CCAGGGATGAAT AGCCACTGGG CC[C/gap]TGGCC ATAGCTGGACTG TCCTTTC	C	gap	Gly	Gly (9619)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q99519 SIALIDASE PRECURSOR - HOMO SAPIENS (HUMAN), 415 aa.	1.4E-227	6
7449	cg43918561	603	AGAGGACGTGC GCAGCCCCGCG GGG[G/gap]CCCA AGGTCCCCTGGT TCCCAAGAA	G	gap	Pro	Pro (9620)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P04177 TYROSINE 3-MONOOXYGENASE (EC 1.14.16.2) (TYROSINE 3- HYDROXYLASE) (TH) - Rattus norvegicus (Rat), 498 aa.	2.1E-224 (11p15.5)	11
7450	cg43994204	674	CGCACGTCAAGA CTGTCTGCGACG C[A/gap]GCAGAG AAGGGAGTGAG GACCCCTCA	A	gap	Ala	Gln (9621)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60664 CARGO SELECTION PROTEIN TIP47 - HOMO SAPIENS (HUMAN), 434 aa.	5.4E-221	19
7451	cg44032871	637	TGTGGTGGGT CTCCTCGGAGCT GG[G/gap]CCCTT GGCGGGCAGC TGCAGAAAT	G	gap	Pro	Pro (9622)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O43566 REGULATOR OF G-PROTEIN SIGNALING 14 (RGS14) - Homo sapiens (Human), 441 aa (fragment).	1.1E-220	5

7452	cg43980557	741	CAGGCTCTAGAA AGTCATCTGCTG C[C/gap]CCCCAG GTCTTCCAGGGA ATCCTCC	C	gap	Gly	Ala (9623)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q13391 HYPOTHETICAL PROTEIN 384D8_6 - HOMO SAPIENS (HUMAN), 533 aa.	2.7E-220	22
7453	cg43082833	1042	CTGGCCCCAGAA AGGGGCTTTTG C[C/gap]ACCAGC TTCAGAAAAACA TGGCAGC	C	gap	Pro	His (9624)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q93088 BETAIN-HOMOCYSTEINE S- METHYLTRANSFERASE (EC 2.1.1.5) - Homo sapiens (Human), 406 aa.	2.1E-219	5
7454	cg43934903	894	CTGGAGCAAAAC CTCCCTGAAGTC C[C/gap]TGAGGG GCAATGTTCCAG GCAAGGT	C	gap	Gln	Gln (9625)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	3.1E-218	1
7455	cg43251548	233	AGCTTCCTATGG ATCTGCGGGACC G[C/gap]TTCACG GAAATGCGCGA GATGGACC	C	gap	Phe	Ser (9626)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60394 PAC CLONE DJ0872F07 FROM 7Q31, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 408 aa (fragment).	2.7E-217	
7456	cg43251548	274	GAGATGGACCTG CAGGTGCAGAA G[C/gap]AATGGA TCAACTAGAACA AAGAGTC	C	gap	Ala	Glu (9627)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60394 PAC CLONE DJ0872F07 FROM 7Q31, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 408 aa (fragment).	2.7E-217	
7457	cg43990581	262	CAGATCCTCAGC CACCGCTTCAAA G[C/gap]CTGTGC CCCAGCAGGTC CAGTGAGC	C	gap	Ala	Ala (9628)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60851 RAP2 INTERACTING PROTEIN 8 - HOMO SAPIENS (HUMAN), 405 aa.	1.6E-214	17
7458	cg43880581	263	AGATCCTCAGCC ACCGCTTCAAAG C[C/gap]TGTGCC CCAGCAGGTCCA GTGAGCT	C	gap	Cys	Val (9629)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60851 RAP2 INTERACTING PROTEIN 8 - HOMO SAPIENS (HUMAN), 405 aa.	1.6E-214	17

7459	cg43062448	1362	GAATCCATAAAA TGGTGAAGTCCC A[ <i>gap</i> ]/TJGGAGCT CCACAAATGTAG CCAAATT	gap	T	Leu	His (9630)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P22760 ARYLACETAMIDE DEACETYLASE (EC 3.1.1.-) (AADAC) - Homo sapiens (Human), 398 aa.	9.9E-213	3 (3q21.3)
7460	cg43968195	156	TGGAGGAGCTG CTCGCAAAGGCA GA[G/ <i>gap</i> ]/CAGGA CGAGGCAGAGA AGTTGCAAC	G	gap	Gln	Arg (9631)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:Q15050 HYPOTHETICAL PROTEIN KIAA0112 (HA0609) - Homo sapiens (Human), 399 aa (fragment).	2.8E-211	8
7461	cg43332618	619	GTCACAGGGCA CCTCGAAGCTGA AA[G/ <i>gap</i> ]/CTTCG TTGTAATAGGGG TTCAGAGT	G	gap	Ala	Val (9632)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:O00445 SYNAPTOTAGMIN V - Homo sapiens (Human), 386 aa.	5.8E-208	19
7462	cg43932174	464	CACTACTTCTTAT TCCTGGGCTTTA G[ <i>gap</i> ]/CTCTTCGG CTGCATTACGCA GGAAA	G	gap	Leu	End (9633)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P78406 MRNA-ASSOCIATED PROTEIN MRNP 41 (RAE1 PROTEIN HOMOLOG) - Homo sapiens (Human), 368 aa.	4.1E-207	20
7463	cg43995867	1174	GAAGAACTTGTA GAACATTACAAA A[A/ <i>gap</i> ]/GGCACC AATTTTACAAGT GAACAA	A	gap	Lys	Arg (9634)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18333 CYTOPLASMIC PROTEIN NCK - Homo sapiens (Human), 377 aa.	8.5E-207	3 (3q21)
7464	cg43920365	922	TGCTTTGTGAAT GGTGCTGGGCT CG[C/ <i>gap</i> ]/CATGG CTACTTGTGATA TCATTTTC	C	gap	Ala	Ala (9635)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P53590 SUCCINYL-COA LIGASE [GDP- FORMING] BETA-CHAIN, MITOCHONDRIAL PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS- BETA) - <i>Sus scrofa</i> (Pig), 417 aa.	6E-206	3
7465	cg43968205	508	AGGGCCACGGA GACACACTGTAC GT[G/ <i>gap</i> ]/GGGAC CACCCGCAATTC CATCCTGC	G	gap	Gly	Gly (9636)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB46373 HYPOTHETICAL 71.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 653 aa (fragment).	6.9E-206	



7466	cg43999733	1292	GGCCGGCGCT GACACGGCCAG CTC[G/gap]GGCT CGGCCCGAAC TCCTCCCGGA	G	gap	Pro	Pro (9637)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7467	cg43999733	1310	CCAGCTCGGC TCGGCCCCGAA CTC[G/gap]TCCC GGAAGGCTCG CGGGCCTCGG	C	gap	Glu	Glu (9638)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7468	cg43999733	1327	CCGAACCTCTCC CGGAAGGCTCG CC[G/gap]GGCCT CGCCAGCAGC TCCGCGACC	G	gap	Arg	Gly (9639)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7469	cg43999733	464	AGCGGTGGCTCT CCACCATGAGGC G[G/gap]CCAAAG GCTCTGTAGTCG CCACGTC	G	gap	Gly	Gly (9640)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7470	cg43999733	614	GCTCTCCAGTT GTACCTCCCGGA G[G/gap]CTTTCC TTGCCCGAGCGCC CGGGCCA	G	gap	Ser	Ser (9641)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7471	cg43999733	659	GGGCCACTTCTT CACATTGGCGCC G[C/gap]CGCACA GGTACTCGCTG GAGGCCA	C	gap	Arg	Arg (9642)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)

7472	cg43999733	660	GGCCACTTCTC ACATTGGCGCG C[C/gap]GCACAG GGTACTCGCTGG AGGCCAG	C	gap	Arg (9643)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P51570 GALACTOKINASE 1 (EC 2.7.1.6) - Homo sapiens (Human), 392 aa.	8.8E-205	17 (17q24)
7473	cg43302693	632	GCAGCTGGCTC GGCAGGCCGTC AG[G/gap]ACCCA GGAGGTGGCG CAGGGGTCA	G	gap	Pro (9644)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
7474	cg43302693	671	GCGCAGGGGTC ATCCAGGATTG AG[G/gap]CCCTG GCCCCACCTGA GTGACAAATG	G	gap	Pro (9645)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
7475	cg43302693	678	GGTCATCCAGGA TTTGAGGCCCTG G[C/gap]CCCCACC TGAGTGACAAATG ATGTATT	C	gap	Gly (9646)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
7476	cg43302693	681	CATCCAGGATT GAGGCCCTGGC CC[C/gap]ACCTG AGTGACAATGAT GTATTGA	C	gap	Val (9647)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53602 DIPHOSPHOMEVALONATE DECARBOXYLASE (EC 4.1.1.33) (MEVALONATE PYROPHOSPHATE DECARBOXYLASE) - Homo sapiens (Human), 400 aa.	2.7E-204	16
7477	cg43950996	2126	GTAGCTGATCCA GTCCAGAACCTG C[G/gap]TCTTCG ACCAGAACTGGG GCTGTTC	G	gap	Thr (9648)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTRMBL-ACC:P78545 ESE-1B - HOMO SAPIENS (HUMAN), 371 aa.	6.2E-204	1

7478	cg43942842	2011	CATGAGGCCGAA CATGTTCCGCA G[G/gap]CCTTGC TCACCGCAGCCA TCTTGGC	gap	Ala (9649)	Ala (9649)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49903 SELENIDE, WATER DIKINASE 1 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) - Homo sapiens (Human), 383 aa.	1.9E-203	17
7479	cg43942842	2730	GAATGACACAAG TATCCATTCCAA T[G/gap]CCAAGC CTTGGGATAACG GCTCCCA	gap	Gly (9650)	Gly (9650)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P49903 SELENIDE, WATER DIKINASE 1 (EC 2.7.9.3) (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) - Homo sapiens (Human), 383 aa.	1.9E-203	17
7480	cg43959472	990	TGAGGTAGATGA TGACCACATTGT C[C/gap]TCCGGC CCTGATGGCTGC ACCTCGT	gap	Glu (9651)	Glu (9651)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14498 ISLR PRECURSOR - HOMO SAPIENS (HUMAN), 428 aa.	2.4E-203	15
7481	cg43918848	2198	ACGGCCTGTTGG TGACCTCAGCTC C[G/gap]GGCAGG GAATCCGTTGCA GTGCCGG	gap	Pro (9652)	Pro (9652)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
7482	cg43918848	2200	GGCCTGTTGGTG ACCTCAGCTCCG G[G/gap]CAGGGA ATCCGTTGCAGT GCCGGTC	gap	Pro (9653)	Pro (9653)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45756 HYPOTHETICAL 44.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 393 aa.	5.6E-202	2
7483	cg44128902	825	CCTAGGAAAGG GAATACTCTCTA TG[gap]ATTATATG GAGAAGACATGA CACCAC	gap	Val (9654)	Asp (9654)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P18615 RD PROTEIN - Homo sapiens (Human), 380 aa.	1E-201 (1p36.2)	1
7484	cg43940298	804	GTCACCTGAATGA TAGGTGATTATG G[G/gap]CCCCGG GCACCTCCGCTT CTTATGA	gap	Pro (9655)	Pro (9655)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15908 YL-1 PROTEIN - Homo sapiens (Human), 364 aa.	3.7E-197	1

7485	cg44015472	1167	ACTTGGATGTTG TCGGGCGGGCGT TG[gap]CACAG GGCCAGCGCTC ACCGCCAGG	G	gap	Pro	Gln (9656)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)
7486	cg44015472	618	CCTTCCTCTTCT TGGGGTAGCACA G[C/gap]CCTCCG GACTCTCGGGAT TAAGATG	C	gap	Ala	Leu (9657)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)
7487	cg44015472	716	GGTGAAGATGGA GTCCTCAGGGAT G[C/gap]CCACAC CCTGGGCAACCA CTCTGAA	C	gap	Gly	Ala (9658)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBIPROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)

7488	cg44015472	771	TGCAGGAGAGTT TCCCTCAGCTGC G[Gap]CGCCCG CCCGTAGAGCTT GGCAGTA	G	gap	Pro	Arg (9659)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P02760 AMBP PROTEIN PRECURSOR [CONTAINS: ALPHA-1- MICROGLOBULIN (PROTEIN HC) (COMPLEX-FORMING GLYCOPROTEIN HETEROGENEOUS IN CHARGE); INTER-ALPHA- TRYPSIN INHIBITOR LIGHT CHAIN (ITI-LC) (BIKUNIN) (HI- 30)] - Homo sapiens (Human), 352 aa.	8.9E-196	9 (9q32)
7489	cg43287442	765	CTGGGCAGAAAT TTTGTCCTCCAAA A[Gap]ATTCTATTA TGCTGCAAAAGCC GTAAAT	gap	A	Phe	Phe (9660)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD09188 PLACENTA-SPECIFIC ATP-BINDING CASSETTE TRANSPORTER - HOMO SAPIENS (HUMAN), 655 aa.	3.1E-193	4
7490	cg43970111	1377	CCTGGCTGAGTC AGCTGGGGCTG AC[Gap]TCCGG AGTCAGCCATCT TGAGGAAC	C	gap	Gly	Val (9661)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43131 SYLD708613 PROTEIN HOMO SAPIENS (HUMAN), 357 aa.	6.5E-193	14
7491	cg43935935	284	TTAGTCTTACG GCGTCAATAACA A[Gap]TGCTTC AACATCATCAGC TCCAAATC	A	gap	Phe	Leu (9662)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O60735 GA17 PROTEIN - HOMO SAPIENS (HUMAN), 374 aa.	1.7E-192	X
7492	cg43973314	638	ATGATCTGACTA ACTTCACTGATA TT[Gap]CCCCCT GGTGGAGTAGA GGAGAAAG	T	gap	Pro	Pro (9663)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:O75521 DBI-RELATED PROTEIN 1 (DRS-1) - Homo sapiens (Human), 364 aa.	3.6E-192	6
7493	cg43984795	1267	TGTTTCTTTTC AGCTCTTCAAAC[ C[Gap]TCCGGGA AAGATCATCAAA GTCAAT	C	gap	Arg	Ser (9664)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P53980 HYPOTHETICAL PROTEIN KIAA0174 - Homo sapiens (Human), 364 aa.	5.8E-192	16

7494	cg43968431	235	TCGTGCTGCTG CCCTGCGCCG CGC/gap/GCCCGC CCATCCGCTCCT CTCTGCTC	C	gap	Ala	Arg (9665)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
7495	cg43968431	438	CACGCCCTGTAC ATCTTCTTCATG G/gap/GJCCTTGG GAGCCAGGAAC GAGAAGA	gap	G	Ala	Ala (9666)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
7496	cg43968431	500	CCACTTGGGTAA GGAGCCTTTGG GG/gap/GJTCCAC CTGGGCCAGGT AGGTGATGA	gap	G	Asp	Asp (9667)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34047 CGI-52 PROTEIN - HOMO SAPIENS (HUMAN), 359 aa.	1E-191	11
7497	cg43920610	924	CAGGCCACCTGT TTCTTCCAAACA G/C/gap/TTTCAG CAACATGAACCT TCCCAT	C	gap	Ser	Thr (9668)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD22381 QUINONE OXIDOREDUCTASE HOMOLOG-1 - HOMO SAPIENS (HUMAN), 349 aa.	5.9E-191	21
7498	cg4396402	1046	GGAAGAGGAGG AGGAGGAGGAA GATG/gap/AGGA AGAAGAGGACTT ATGTTTTT	G	gap	Ser	Tyr (9669)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7499	cg4396402	1220	TCAACTTCTGGA TCTTCTTCACCC T/gap/G/CACCTG CAACATACTCCT GTGATGG	gap	G	Glu	Ala (9670)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7500	cg4396402	1249	TGCAACATACTC CTGTGATGGATC A/gap/GJTTCG GTCAAGTTTCTC CCCAGTA	gap	G	Lys	Asn (9671)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2

7501	cg43998402	1300	ATTCGTTTCAG TGCAAAACCCACT G[gap/G]TTTCTC ATCTCCGCTATT AGCTCCG	gap	G	Lys	Asn (9672)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7502	cg43998402	1376	TCAGTGGGAACC GAAC TTGCATTG A[gap/C]TTCCAG AAAGACCAACA AAGGACA	gap	C	Ile	Ser (9673)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7503	cg43998402	1427	TTCTCGATCTGT GTTGACATGACC C[C/gap]ATTTGT GACATTTAATGC ACCTCAC	C	gap	Trp	Trp (9674)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7504	cg43998402	599	CTTCTGCTTTGC TCTTCACCAGGA T[gap/G]TTTCGCT GTGCCCCGTTCC TTGTC	gap	G	Asn	Thr (9675)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7505	cg43998402	962	TTTTCTTTCTTT TCTTCCCTTTGTAT gap/G]TTTTTTTT CTTTATTGTTACT CTC	gap	G	Ile	Thr (9676)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q12804 RECEPIN - HOMO SAPIENS (HUMAN), 451 aa.	2.6E-189	2
7506	cg44002198	1629	GAAGGGCCTCG GACTTCAGCGTG AG[G/gap]CCCCGA GGCGCCAGGG GCTGCTGCA	G	gap	Gly	Gly (9677)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7
7507	cg44002198	1665	CCAGGGGCTGC TGCAGCAGGAAC AG[G/gap]CGAGG CCCCGAAACCA GCAGCGAGA	G	gap	Arg	Arg (9678)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7

7508	cg44002198	716	CTGGAGGACTCC TTGGAGCCTGCA G[gap/C]CCCCCTG GTGTCCCAAGGC CCCAGAA	gap	C	Leu	Ala (9679)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45960 WUGSC:H_RG122E10.2B PROTEIN - HOMO SAPIENS (HUMAN), 364 aa.	8.8E-189	7
7509	cg43249389	991	GATTGGGGCCG CCGACTACCAGC CC[A/gap]CTGAG CAGGACATCCTC CGAACCAG	A gap	gap	Thr (9680)	Leu (9680)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P09471 GUANINE NUCLEOTIDE-BINDING PROTEIN G(O), ALPHA SUBUNIT 1 - Homo sapiens (Human), 353 aa.	1.4E-188	15
7510	cg43947129	1222	TTTTTCTAAAGC ATCATCTCCTTT G[gap]GCATTGC CAATGCGGAATG GAATAT	G gap	gap	Ala	Ala (9681)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10858 PROBABLE PHOSPHOERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa.	3E-188	
7511	cg43947129	2137	GACCAGGCCCA AAGTTGACCACC TG[C/gap]CTGGG GGCGTCCATGGT GCGGCGGC	C gap	gap	Arg	Ser (9682)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P10858 PROBABLE PHOSPHOERINE AMINOTRANSFERASE (EC 2.6.1.52) (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP) - Oryctolagus cuniculus (Rabbit), 370 aa.	3E-188	
7512	cg43922383	660	CGATGCCATTGT GGCTAAGGTACA G[C/gap]TCCCCG AGGTTCAACAGG TTCGCA	C gap	gap	Glu	Asp (9683)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15435 YEAST SDS22 HOMOLOG - HOMO SAPIENS (HUMAN), 360 aa.	7.3E-185	2
7513	cg43047610	604	ACACTATCGAGG AGGGCACGATG CC[C/gap]AAGGA GATGTCGGACAT CATCCAGC	C gap	gap	Lys	Arg (9684)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB37839 TRANSDUCIN ALPHA- SUBUNIT - HOMO SAPIENS (HUMAN), 350 aa.	7.3E-185 3 (3p21)	



7514	cg43950786	1309	GCCTGGGCTCTC CCTACCCCACT TG[G/gap]CCATC GGCTCTCCTATC GCGGCGCC	G	gap	Ala (9685)	Ala (9685)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
7515	cg43950796	783	GCTCCTCAGTTT TCAGTCTGGCT G[C/gap]CCCACT GGTCTACTGAC TCTCCAT	C	gap	Gly (9686)	Gly (9686)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB45684 C14ORF3 PROTEIN - HOMO SAPIENS (HUMAN), 338 aa.	2.5E-184	
7516	cg44007066	1553	GCCTCTGGGT TGCGCTCGGCC TG[C/gap]CTGCG GAAGTAGTCTGG CCCCTGT	C	gap	Arg (9687)	Ser (9687)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAB50224 HYPOTHETICAL 41.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 373 aa (fragment).	1.7E-183	
7517	cg44128927	589	GACCCAGCCAG AGGCCTCCCGC GGA[G/gap]CCGG GACTGCAGAGTC GACCTGGGC	G	gap	Ser (9688)	Thr (9688)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD38070 REVERSION-INDUCED LIM PROTEIN - HOMO SAPIENS (HUMAN), 330 aa.	2.8E-183	5
7518	cg43986952	1388	CAAACTGGCACT TGCCCCCGTAG CG[G/gap]CAGCG CCCACTCTCTGA GAAGGTCC	G	gap	Cys (9689)	Cys (9689)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSPROT-ACC:P26651 TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR- INDUCIBLE NUCLEAR PROTEIN NUP475) - Homo sapiens (Human), 326 aa.	2.9E-181 (19q13.1)	19
7519	cg43923337	216	GTGGCAGGGAC GACGCCAGAAAT GG[G/gap]AGCTG ACTGATATGGTG GTGTGGGT	G	gap	Glu (9690)	Ser (9690)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD34081 CGI-86 PROTEIN - HOMO SAPIENS (HUMAN), 339 aa.	3.7E-181	14

7520	cg43299409	279	TCGGCCACCCAC GGCGCTGAGGA CGC[C/gap]ACGG ATGCCCTCCGTG CCTCCATC	C	gap	Thr	Arg (9691)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD31282 DELTA-6 FATTY ACID DESATURASE - HOMO SAPIENS (HUMAN), 445 aa.	7.9E-181	
7521	cg43951707	415	GCAGGCGGCGCT TGGCCGAGCGG GCG[G/gap]CCGG GGGCTGCAGCC CAAGAAGCGT	G	gap	Ala	Pro (9692)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q15814 COFACTOR C - HOMO SAPIENS (HUMAN), 346 aa.	2.7E-178	6
7522	cg43961139	1782	CAAAGGTGTAGA GCTGCTTCCCTT C[G/gap]TGTCGC TTCCCAATGACG GGCATGA	G	gap	His	Gln (9693)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB43360 HYPOTHETICAL 96.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 837 aa.	2.7E-178	22
7523	cg43989747	1720	GCATTACCTGG GAGTCTGGTGC T[G/gap]CACCCT CCGGGTGCAGA TGCCGCTG	G	gap	Gln	Ser (9694)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD03500 G BETA-LIKE PROTEIN GBL - RATTUS NORVEGICUS (RAT), 326 aa.	5.1E-177	16
7524	cg42733649	1058	AGCCTGGAGCTC CTGTTCCCTGAA T[C/gap]CTTCGG CTTCATCACCTA TCAGGGC	C	gap	Ser	Ser (9695)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75493 CARBONIC ANHYDRASE-RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 328 aa.	1.1E-176	
7525	cg42733649	1059	GCCTGGAGCTC CTGTTCCCTGAA TC[C/gap]TTCGG CTTCATCACCTA TCAGGGCT	C	gap	Phe	Ser (9696)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75493 CARBONIC ANHYDRASE-RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 328 aa.	1.1E-176	
7526	cg43268525	820	TGTCACCTCCAC AGTGCCCGCGG GA[G/gap]CTGCC ATCGTCACATAC AAATGCAA	G	gap	Leu	Cys (9697)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76815 KIAA0971 PROTEIN - HOMO SAPIENS (HUMAN), 648 aa.	1.1E-176	

7527	cg44035397	1626	TTTTGGTCTGT GGTTTCAGCCGT G[G/gap]CCTGGG CCTAAGGCTCTG CTCTGGC	G	gap	Pro	His (9698)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45826 C2H2-150 - HOMO SAPIENS (HUMAN), 326 aa.	1.7E-176	7
7528	cg44035397	1632	GTCTGTGGTTTC AGCCGTGGCCT GG[G/gap]CCTAA GGCTCTCCTCTG GCTCCTCA	G	gap	Pro	Pro (9699)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD45826 C2H2-150 - HOMO SAPIENS (HUMAN), 328 aa.	1.7E-176	7
7529	cg43931789	89	CCGAGTCGGCC CAGGGTCCCC GGG[C/gap]CCGG CAGCGTCGCTG GAGCTGTGGC	C	gap	Pro	Arg (9700)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14584 HYPOTHETICAL 67.1 KD PROTEIN - HOMO SAPIENS (HUMAN), 613 aa.	2E-175	16
7530	cg43941890	1330	GGCATCAGGAG AAAGGCTGGGTC TT[G/gap]GGACC TTGTCTCTCCCA GTTGGCCT	G	gap	Gly	Asp (9701)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43024 MNUDC PROTEIN - HOMO SAPIENS (HUMAN), 331 aa.	5.2E-175	
7531	cg43941890	1332	CATCAGGAGAAA GGCTGGGTCTTG G[G/gap]ACCTTG TCCTCCCCAGTT GGCCTAC	G	gap	Gly	Asp (9702)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD43024 MNUDC PROTEIN - HOMO SAPIENS (HUMAN), 331 aa.	5.2E-175	
7532	cg43987532	3773	CACGAGTCGCG CACGGCCTCGC AGA[G/gap]CCAG CGACACGGGA GATGGGCCGG	G	gap	Leu	Ser (9703)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
7533	cg43987532	3983	CCATCTTCTTG AGCCACAGTTGT G[G/gap]CACAGC CGCAGGTCGCG GGGGATGT	G	gap	Cys	Cys (9704)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8

7534	cg43967532	4074	GGAAGCTCACGT AGTCGTACTCGC TTG[ <i>gap</i> ]GCCGAG CCCACGGCCAG AAGCGCCG	G	gap	Ala	Ala (9705)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
7535	cg43967532	4128	CCAGCGCCACG AGCACGCCACG GGC[T/ <i>gap</i> ]GCCC CGCGCGGGCC CCCTCGCTGC	T	gap	Ala	Ala (9706)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14779 SECRETED APOPTOSIS RELATED PROTEIN 2 - HOMO SAPIENS (HUMAN), 314 aa.	2.3E-174	8
7536	cg43941339	1446	GTTTAACTGGTA TGGCACAGGTGA TTG[ <i>gap</i> ]CCTAGG AGGCAAAAGCAA ATCACTG	G	gap	Gly	Gly (9707)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:P10451 OSTEOPONTIN PRECURSOR (BONE SIALOPROTEIN 1) (URINARY STONE PROTEIN) (SECRETED PHOSPHOPROTEIN 1) (SPP-1) (NEPHROPONTIN) (UROPONTIN) - Homo sapiens (Human), 314 aa.	8.2E-170	4 (4q21)
7537	cg44032718	794	GCTTCTGGAACC ACAGGTGGCCG AA[G/ <i>gap</i> ]GGTCT CAAAGGCTCTAA TGGCCTCA	G	gap	Arg	Arg (9708)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O76058 DJ1409.2 (MELANOMA-ASSOCIATED ANTIGEN MAGE LIKE) - HOMO SAPIENS (HUMAN), 606 aa.	5.7E-169	X
7538	cg44034179	1178	TGGGCAGAGCC GTTGGGGCCAC GC[C/ <i>gap</i> ]ATCGC GGACGTCATCCT GGAGGGTC	C	gap	Gly	Ala (9709)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14792 HEPARAN SULFATE 3-O- SULFOTRANSFERASE-1 PRECURSOR HOMO SAPIENS (HUMAN), 307 aa.	1.6E-166	4
7539	cg44034179	1272	GGGAAGGCACT AGCTGGGGCTG GGC[C/ <i>gap</i> ]ACCA GCAGCACCGCG CCCAGGAGCA	C	gap	Val	Val (9710)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O14792 HEPARAN SULFATE 3-O- SULFOTRANSFERASE-1 PRECURSOR HOMO SAPIENS (HUMAN), 307 aa.	1.6E-166	4

7540	cg43928509	1244	CCTGCAGCAGTA ACGGGAGGATG GA[G/gap]GGGCC ACCCCCACATA CAGCGAGG	G	gap	Gly (9711)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O15165 CLONE 22 - HOMO SAPIENS (HUMAN), 306 aa.	4.2E-166	18
7541	cg44003630	1080	ATGGTTGGAATT CGGACCAGATAG A[G/gap]GGCTCG CCCCAGAACATG CCTCTTG	G	gap	Leu (9712)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA76796 KIAA0952 PROTEIN - HOMO SAPIENS (HUMAN), 522 aa.	5.1E-164	
7542	cg44004690	826	GCTGCTGAGGAT GCTGGAGAACG GG[C/gap]AGATG GACCGAGCGGA GCACAAGGG	C	gap	Gln (9713)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:BAA74892 KIAA0869 PROTEIN - HOMO SAPIENS (HUMAN), 888 aa (fragment).	2.5E-161	
7543	cg43929687	425	TGGTGTCAAT TCTCCAGCATGA G[C/gap]TCTGCT GGTCTCTCGT CTGACCTG	C	gap	Glu (9714)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:CAB51351 DJ475B7.2 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 717 aa.	8.5E-160	
7544	cg43315424	341	GCTCAGGAACA CAGCTGACCG GA[G/gap]GCAGT GGCCAGGAGAG GCAGGCTAG	G	gap	Ala (9715)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60525 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA 5 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 538 aa.	8.8E-158	
7545	cg43315424	342	CTCAGGAACAC ACGCTGACCGG AG[G/gap]CAGTG GCCAGGAGAGG CAGGCTAGG	G	gap	Ala (9716)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q60525 GUANINE NUCLEOTIDE-BINDING PROTEIN BETA 5 - MESOCRICETUS AURATUS (GOLDEN HAMSTER), 538 aa.	8.8E-158	
7546	cg43287561	468	ACTGTGCTCTGG AAGTTGGCATCA AT[gap]GAAGAT GGGCTCTGCCG CTGTGATT	T	gap	Ile (9717)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.4E-156	9 (9q34)

7547	cg43287561	553	GTTCTTTCTGG ATTGTTCTCAGG G[gap]G[ACAAAA GGCTGCCTGGTT TCTGTCA	gap	G	Val	Val (9718)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SWISSNEW-ACC:Q15526 SURFEIT LOCUS PROTEIN 1 - Homo sapiens (Human), 300 aa.	1.4E-156	9 (9q34)
7548	cg43298828	702	CCACTCAACTGG CTGGACACCATC A[C/gap]CTGGAT GGTGGTGACCAT GGGCAGC	C	gap	Val	End (9719)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92984 INTERFERON-INDUCED LEUCINE ZIPPER PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	1.1E-155	17
7549	cg43298828	703	CACTCAACTGGC TGGACACCATCA C[C/gap]TGGATG GTGGTGACCATG GGCAGCT	C	gap	Gln	Gln (9720)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:Q92984 INTERFERON-INDUCED LEUCINE ZIPPER PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	1.1E-155	17
7550	cg41629243	891	TCCTTGGCCTCC TTCTTGGCCAGC C[G/gap]CCGTGC GCGCTTCTCCTC GGCGTC	G	gap	Arg	Gly (9721)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O75229 R31449_3 - HOMO SAPIENS (HUMAN), 813 aa (fragment).	7.8E-155	19 (19p13.3)
7551	cg42713596	380	CTGTTGGCCGAA ATAGGGCTGAAG C[C/gap]TCTTTG GAGCGAGCTCA GAATCTCA	C	gap	Ser	Leu (9722)	FRAMES HIFT	UNCLAS SIFIED	Human Gene TREMBLNEW- ACC:AAD23902 ACTIVATION OF SENTRIN/SUMO PROTEIN AOS1 - HOMO SAPIENS (HUMAN), 346 aa.	3.1E-154	
7552	cg43981925	1805	TATACTGGAAGG TCTTGCTACCAA CTT[gap]GCCCCCT GAAGTGGTGCAC CAGAAAC	T	gap	Gln	Arg (9723)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:O00560 MELANOMA DIFFERENTIATION ASSOCIATED PROTEIN-9 - HOMO SAPIENS (HUMAN), 298 aa.	6.4E-154	8
7553	cg43060941	1196	TTTCCCTTTTCA CTAGATGCAGAG TT[gap]TTTTTTGA ACTTTTAACCTC ATGTT	T	gap	Asn	Thr (9724)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P70287 RETINOBLASTOMA BINDING PROTEIN 6 (PACT) - MUS MUSCULUS (MOUSE), 1587 aa (fragment).	4.9E-153	

7554	cg43060941	960	TCCTCTGGTGTCA TAGTCAGTTTTT [T/gap]GTCTCTAT TGGGAGTGAAGT CTTTA	gap	Lys	Lys (9725)	FRAMES HIFT	UNCLAS SIFIED	Human Gene SPTREMBL-ACC:P70287 RETINOBLASTOMA BINDING PROTEIN 6 (PACT) - MUS MUSCULUS (MOUSE), 1587 aa (fragment).	4.9E-153	
7555	cg43980820	1082	GATGTCGTGTG ACCCAGCTTGAC C[C/gap]TGGCGG ACCCACTAGTGT TGGACAC	gap	Arg	Arg (9726)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15024 MRNA (HA0800) FOR ORF - HOMO SAPIENS (HUMAN), 290 aa (fragment).	3.3E-150	3
7556	cg43258297	145	ATAGTCCATACA GTGTGGCTACTG C[C/gap]AAGGTC AGGATGGCCAG CAGACCCA	gap	Leu	Leu (9727)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB50866 DEOXYRIBONUCLEASE III (DNASE III) - HOMO SAPIENS (HUMAN), 304 aa.	3.8E-150	3
7557	cg43919239	576	AAAGGTGCGGC AGAGAGCCCCA GCT[G/gap]GGCA CTTGTTAACTCC TGAGGTCCA	gap	Pro	Gln (9728)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
7558	cg43919239	578	AGGTGCGGCAG AGAGCCCCAGCT GG[G/gap]CACTT GTAACTCCTGA GGTCCAGT	gap	Cys	Cys (9729)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P14207 FOLATE RECEPTOR BETA PRECURSOR (FR- BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP) - Homo sapiens (Human), 255 aa.	4.2E-150	
7559	cg43943351	418	TTGGGTGATATG CGGCTCCACAA G[G/gap]TGCTGA GCACCACGTGG CTCTGTTC	gap	Pro	Leu (9730)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa.	4.5E-150	17

7560	cg43943351	872	AGGTGGTCACTG TCAATGACAAAC G[C/gap]CCCCAG GCCCTTCAGTCG CTGAGCT	C	gap	Ala	Arg (9731)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13057 HYPOTHETICAL PROTEIN POV-2 - Homo sapiens (Human), 286 aa.	4.5E-150	17
7561	cg43925047	754	GTGTCCATGAAA CGGGAGCCACT GG[C/gap]CCACG GAGCCATCTTCA AAGCCAGT	C	gap	Ala	Pro (9732)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43730 BK390B3.1 (MANIC FRINGE PRECURSOR PROTEIN) - HOMO SAPIENS (HUMAN), 321 aa.	9.4E-150	
7562	cg43946935	793	AGCCTTATTCA GGTTATCTACTT TTT[gap]GGAAAT GCAGGAAGTTCC CACCTTG	T	gap	Gly	Glu (9733)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60671 CELL CYCLE CHECKPOINT PROTEIN HRAD1 - HOMO SAPIENS (HUMAN), 282 aa.	1.8E-149	
7563	cg43930377	1451	TACAAAAAGCTA GCATGGCTTCTT T[gap/A]AAAAAA ACAATATCCCAA ATAAAA	gap	A	Leu	Leu (9734)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment).	7.8E-149	4
7564	cg43930377	1459	GCTAGCATGGCT TCTTTAAAAAAA [gap/A]CAATATC CCAAATAAAATC AGAGTC	gap	A	Thr	Asn (9735)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43230 HYPOTHETICAL 33.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 290 aa (fragment).	7.8E-149	4
7565	cg43041577	1597	GAAATCTCAAAG GTCTGGTAAGAA G[G/gap]CAAGCC GCAACACAAAGT CTAAGTC	G	gap	Ala	Gln (9736)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45767 HYPOTHETICAL 34.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 299 aa (fragment).	2.7E-148	10
7566	cg43943919	802	TCGTAGACATGC TCTTGTGGGAT GTT[gap]CTCCG ACAGAGCATGAT ATAGGCC	T	gap	Thr	His (9737)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB46921 DA159A1.1 (NOVEL PROTEIN) - HOMO SAPIENS (HUMAN), 399 aa.	2.7E-148	X



7567	cg43985796	1698	GTTGACATCACT GTTGATGCTCTG G[G/gap]CCACGC CAGGGTACTGGA TCCTCAT	G	gap	Ala (9738)	Ala	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q60936 HYPOTHETICAL HEART PROTEIN - Mus musculus (Mouse), 298 aa (fragment).	9E-148	1
7568	cg43931669	138	GCCGGGGGAGC CGCCATCGGAG CGC[C/gap]AGGG GACAGAGCACA GGAAAGGGAC	C	gap	Arg (9739)	Gly	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99703 ATAXIN-2 RELATED PROTEIN - HOMO SAPIENS (HUMAN), 347 aa (fragment).	2.3E-148	
7569	cg43937734	827	CTGTGTCTTATG ATGGTGGCTCTG C[C/gap]AAGACC ATCCTGAATAAT GGGAAGA	C	gap	Lys	Arg (9740)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P07451 CARBONIC ANHYDRASE III (EC 4.2.1.1) (CARBONATE DEHYDRATASE III) - Homo sapiens (Human), 259 aa.	3.5E-148	8
7570	cg43947808	846	CCCTTTCATCCC TATGTGGAAC G[T/gap]GGTGGC AAGTGGGAGAAA CCATCAG	T	gap	Gly	Val (9741)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34076 CGI-81 PROTEIN - HOMO SAPIENS (HUMAN), 282 aa.	9.8E-148	18
7571	cg43961927	442	CCAGTCTCTCCC GGCGATGGTGG CG[C/gap]CGTTC TTGCCCTCTTC CCGGTCTG	C	gap	Arg	Arg (9742)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60828 JM26 PROTEIN, COMPLETE CDS (CLONE LLOXNC01U138D3 (BAYLOR COLLEGE)) - HOMO SAPIENS (HUMAN), 265 aa.	4E-145	
7572	cg43946394	247	AATCTGTAGCTT CCGGATACCGTA G[C/gap]CCACGG GCACCAAGCTTGG AAGCCC	C	gap	Gly	Ala (9743)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa.	2.8E-144	19
7573	cg43946394	586	TACGTGCTGGGT CTGTGGGGCCG TG[G/gap]CCCCG TGCCAGGCGA GCTCTTCTC	G	gap	Ala	Ala (9744)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa.	2.8E-144	19

7574	cg43946394	840	GGAGGATCACG CTGGCGCGGTTT TC[C/gap]TGGCG GGAGGCACCTG CCACAGGCC	C	gap	Gln (9745)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P29692 ELONGATION FACTOR 1-DELTA (EF-1- DELTA) - Homo sapiens (Human), 281 aa.	2.8E-144	19
7575	cg43983449	1418	TGCATGATGGAA ATGAGGCAGGAT G[G/gap]CAGAGC CAGTGCCAGCTG AGAACAC	G	gap	Ala (9746)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:OT6019 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 462 aa.	7.3E-144	
7576	cg44027658	375	GAAGAAAGTGCCC GTCCACGCACAG C[G/gap]AGGAGC TTCATGATTGTAT CCAAAA	G	gap	Arg (9747)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P48507 GLUTAMATE-CYSTEINE LIGASE REGULATORY SUBUNIT (EC 6.3.2.2) (GAMMA- GLUTAMYL CYSTEINE SYNTHETASE) (GAMMA-ECS) (GCS LIGHT CHAIN) - Homo sapiens (Human), 274 aa.	2E-143	1 (1p21)
7577	cg43998829	1037	AGGTGGTGGAC GGCCTGGAGAA GGC[C/gap]ATCT ACAAGGGCCCA GGCAGCGAAG	C	gap	Ser (9748)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P21964 CATECHOL O-METHYLTRANSFERASE, MEMBRANE-BOUND FORM (EC 2.1.1.6) (MB-COMT) [CONTAINS: CATECHOL O-METHYLTRANSFERASE, SOLUBLE FORM (S-COMT)] - Homo sapiens (Human), 271 aa.	2.1E-143	22 (22q11.2)
7578	cg43958563	1417	GAAAGCAGCTGA GATATAGTACAG G[G/gap]CACAAT GTGCTGGGCTC GGGCTCTT	G	gap	Pro (9749)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)

7579	cg43958563	1482	TTGAGAAGGTGC GGCGATCCAAA G[C/gap]CCCCCG GGGACTGCGTG TAGCCGCC	C	gap	Gly	Ala (9750)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P15927 REPLICATION PROTEIN A 32 KD SUBUNIT (RP-A) (RF-A) (REPLICATION FACTOR-A PROTEIN 2) - Homo sapiens (Human), 270 aa.	4.7E-142	1 (1p35)
7580	cg43919223	535	CACCTTATCCAG GACAGCTGTCTC T[A/gap]TGAGTG CTCACCCACCT GGGGCCC	A	gap	Tyr	Leu (9751)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P41439 FOLATE RECEPTOR GAMMA PRECURSOR (FR- GAMMA) (FOLATE RECEPTOR 3) - Homo sapiens (Human), 243 aa.	1.4E-140	11
7581	cg42921274	649	ACCAGAGTCTTT CAGGAGCCGGG GT[G/gap]CCAAG GCCAGAAATGTGG GTAATGAT	G	gap	Ala	Asp (9752)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD26417 HEMK HOMOLOG - HOMO SAPIENS (HUMAN), 338 aa.	5E-140	
7582	cg43260991	293	CGCCCCAACCC GCCCCATGCCG CGC[gap]GCCAC AGGAGCCAGG AGCCTGTGCG	gap	G	Pro	Arg (9753)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60949 TBC1 - MUS MUSCULUS (MOUSE), 1141 aa.	6.2E-140	
7583	cg43260991	301	ACCCGCCCATG CCGCGCCACCA GG[G/gap]AGCCA GGAGCCTGTGC GCAGGCCCA	G	gap	Ser	Ala (9754)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q60949 TBC1 - MUS MUSCULUS (MOUSE), 1141 aa.	6.2E-140	
7584	cg43292703	992	GCCACTCGAGC CAGATGCTTGT GT[gap]GICGGCG GAGGCCGCGCT GGTGTGACT	gap	G	Asp	Ala (9755)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99818 CHROMOSOME 12P13 SEQUENCE; HTGS PHASE 3, COMPLETE SEQUENCE - HOMO SAPIENS (HUMAN), 268 aa.	1.7E-139	

7585	cg43305515	1381	CTCAAGCATGTC GGGCCAGGGA AG[C/gap]CGAAG GCGGACATGAC CGGGCGCA	C	gap	Gly	Ala (9756)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O35297 SECRETED APOPTOSIS RELATED PROTEIN 1 - MUS MUSCULUS (MOUSE), 295 aa.	4.4E-139	4
7586	cg43935076	1655	GAACCGAGTCTC TCTTCTCTATTG [T/gap]TTCACCTC ACTGTAGAAGGT CATAA	T	gap	Lys	Asn (9757)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
7587	cg43935076	1697	AGGTCATAAATG CTTCCTCGGTGC T[G/gap]CCTCCG CCGCCCTGAAGTC CCGCTCT	G	gap	Gly	Gly (9758)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75937 SPF31 - HOMO SAPIENS (HUMAN), 264 aa.	1.5E-136	1
7588	cg43952219	1075	CAGTTTGCCAAA GAGCTCTACCAG A[T/gap]TTTTTTG GAGGCATAACAA TAGAAG	T	gap	Asn	Ile (9759)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa.	2.5E-136	X
7589	cg43952219	1081	GCCAAAGAGCTC TACCAGATTTTT [T/gap]GGAGGCA TAACAATAGAAG TATTGA	T	gap	Pro	Pro (9760)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O43736 INTEGRAL MEMBRANE PROTEIN 2A (E25 PROTEIN) - Homo sapiens (Human), 263 aa.	2.5E-136	X
7590	cg43994220	232	GCGGGCACCCAG GTTGCTCTGGAA GA[G/gap]CTTGA GGATGTGGTTCT CGATCACC	G	gap	Leu	Ser (9761)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
7591	cg43994220	282	CTGTTGCACTTT CCGGTATCCCG G[G/gap]CCACGG CAAGGTCCATCG GGGIGTA	G	gap	Ala	Ala (9762)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19

7592	cg4394220	787	TGGTGGAGTGCT TCAGGGAGCTG CC[gap/T]CCTGT GGAGAGGAAC ACTGGCATC	gap	T	Gly	Arg (9763)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O14593 DNA- BINDING PROTEIN RFXANK - Homo sapiens (Human), 260 aa.	5.8E-135	19
7593	cg43929878	1026	CCTGACTGAGGT GGACCGGCAGG GG[G/gap]CCCAC ATTGTTGGCTAC TTCTCCAA	G	gap	Ala	Pro (9764)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O02193 MALES- ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-) - Drosophila melanogaster (Fruit fly), 827 aa.	3.1E-134	
7594	cg43942432	530	AATGAGATTCTC CCAGCAACGGG AG[G/gap]CCAAG CCCTCCGCAGC CGAATAAT	G	gap	Ala	Ala (9765)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60573 CAP-BINDING PROTEIN 4EHP - HOMO SAPIENS (HUMAN), 245 aa.	5.3E-134	2
7595	cg43942432	802	AAGTGTAGTTGT ACTGCAGGGGAT G[C/gap]TCTGCC GGCCCAGGGAC AACAGCCT	C	gap	Glu	Asp (9766)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60573 CAP-BINDING PROTEIN 4EHP - HOMO SAPIENS (HUMAN), 245 aa.	5.3E-134	2
7596	cg43916993	1557	CAGGCTGTAAGC TCGCTGCAGATT G[G/gap]CGATGG CCTCATCATAGC TCTCCAT	G	gap	Ala	Ala (9767)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD33400 CARBOXY TERMINUS OF HSP70- INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	2.3E-133	16
7597	cg43918679	516	GTGAGCTGTACC TGCGGAGGAAC CG[C/gap]ATCCC CAGCCTGGCTGA GCTCTTCT	C	gap	Ile	Ser (9768)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3E-131	21
7598	cg43918679	845	CTGGACAGCGA GGAGGAGGCAA CCA[G/gap]CGGC GCCCAGGATGAA CGTGGCCTG	G	gap	Ser	Thr (9769)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:O43822 28.3 KD PROTEIN C21ORF2 (C21ORF- HUMF09G8.5) (YF5/A2) - Homo sapiens (Human), 256 aa.	3E-131	21

7599	cg43931621	2141	TGGATTCTCCCA CAAAGCCCGCCA GG[ <i>gap</i> ]AGGGAG CCCACGCCCCAG GGTCGCAC	G	gap	Leu (9770)	Leu	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O35139 FN54 - MUS MUSCULUS (MOUSE), 383 aa (fragment).	4.7E-131	5
7600	cg44007142	941	CCAGGCTGGCG TCGCTCTCTGTG TT[C/ <i>gap</i> ]CCGCT GCCGGGACTTA GCCGCCCTC	C	gap	Glu	Asn (9771)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34089 CGI-94 PROTEIN - HOMO SAPIENS (HUMAN), 253 aa.	3.1E-129	
7601	cg43950545	766	CTGCTACGAAT GTTTGGCGTAG G[C/ <i>gap</i> ]ACATCT CCTTGCCCTCT AGCTTTT	C	gap	Val	Val (9772)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30062 SUPPRESSOR OF G2 ALLELE OF SKP1 HOMOLOG - HOMO SAPIENS (HUMAN), 333 aa.	3.5E-129	13
7602	cg43972431	1944	GGGAGGGAGAT GGCATTCTTGTAG CA[C/ <i>gap</i> ]CCGGG GAGGGCGTTTCT GTGAACAC	C	gap	Val	Cys (9773)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD16888 CDC42 EFFECTOR PROTEIN 3 - HOMO SAPIENS (HUMAN), 254 aa.	7.1E-129	2
7603	cg43300586	252	AGTGGCTGCGG CGGGAAGATGG CGG[A/ <i>gap</i> ]GCTG CGCGTGCTCGTA GCTGTCAAG	A	gap	Glu	Gly (9774)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P38117 ELECTRON TRANSFER FLAVOPROTEIN BETA- SUBUNIT (BETA-ETF) - Homo sapiens (Human), 255 aa.	3.6E-128 (19q13.3)	19
7604	cg43054809	335	TTGCTCTTGGCT TTTGTGGCCTTG G[C/ <i>gap</i> ]ATCCAG CGTGCTCTGGG CATGAGTG	C	gap	Ala	Pro (9775)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15125 PHENYLALKYLAMINE BINDING PROTEIN - HOMO SAPIENS (HUMAN), 230 aa.	2E-127	X
7605	cg42891437	229	TTGAGCACGGAG CTCAGGTCCGGA G[G/ <i>gap</i> ]AACACC ATGGTGAGGAG GCCCAAGA	G	gap	Phe	Phe (9776)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75425 ORF3, SPLICEVARIANT_B - HOMO SAPIENS (HUMAN), 235 aa.	2.4E-127 7 (7q21)	

7606	cg43949081	933	GATTTGGACCAAC TGGACCAGCCAA G[C/gap]TTCAG CCAGTTACACTG AAAGTCT	gap	Lys	Asn (9777)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB44334 CYSTEINE CONJUGATE BETA-LYASE - FUGU RUBRIPES (JAPANESE PUFFERFISH) (TAKIFUGU RUBRIPES), 419 aa.	6.7E-127	
7607	cg43949081	149	GGAGCACCTTG GCCCTGGTCTTG GG[C/gap]CAGCA GACGCAGAAGC AGGGAGTGC	gap	Ala	Pro (9778)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19
7608	cg43949081	150	GAGCACCTTGGC CCTGGTCTTGG C[C/gap]AGCAGA CGCAGAAGCAG GGAGTGCA	gap	Leu	Leu (9779)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19
7609	cg43949081	178	CAGACGCAGAA GCAGGGAGTGC AGA[C/gap]CCCG GCAACACAGGTGT GTAGCCCCAG	gap	Ala	Val (9780)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19

7610	cg43949061	207	GGCAAAACAGGT GTGTAGCCACG GCG[G/gap]CTCA GATGCAGGTAAT CATACATGT	G	gap	Ser (9781)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19
7611	cg43949061	390	GATGTTGGCCTC GCGGAAGCAGG CC[C/gap]AGCAC CACAAACCCGGG CCTGGGGCT	C	gap	Leu (9782)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15102 PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE IB GAMMA SUBUNIT (EC 3.1.1.47) (PAF ACETYLHYDROLASE 29 KD SUBUNIT) (PAF-AH 29 KD SUBUNIT) (PAF-AH GAMMA SUBUNIT) - Homo sapiens (Human), 231 aa.	2.1E-125	19
7612	cg43975901	1076	AGCTAATGTGAA CCCTGGAGGAT GG[G/gap]CACCA GCCTCAGTGTTA AGGGCAGT	G	gap	Ala (9783)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD30288 GOODPASTURE ANTIGEN-BINDING PROTEIN (EC 2.7.1.37) - HOMO SAPIENS (HUMAN), 624 aa.	2.6E-125	
7613	cg43066224	733	CGGGAGGCTCC CACTGCACCTGT AG[G/gap]TGGCG CTCAGCGAGGG GGCTTAGGC	G	gap	His (9784)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14213 CYTOKINE RECEPTOR PRECURSOR - HOMO SAPIENS (HUMAN), 229 aa.	5.4E-125	19
7614	cg44002548	981	TGATGCATCAGG ACAGGGCTTTTG C[C/gap]ACTGCA CGCTTGAACCTC TCCGGAC	C	gap	Thr (9785)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45746 HYPOTHETICAL 49.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 454 aa.	1.1E-124	17
7615	cg44002548	1044	GTACCCTCTCAA CGATCCAGAAGT T[G/gap]CCACGG CTGCTAGTTGCG TCATCCA	G	gap	Pro (9786)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB45746 HYPOTHETICAL 49.4 KD PROTEIN - HOMO SAPIENS (HUMAN), 454 aa.	1.1E-124	17



7616	cg43934053	680	TTGGCACCTTCG GGCAAGGGGAG GG[G/gap]CTTGC AGCACCCCCAC CAGTAGGT	G	gap	Gly	Ala (9787)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD39005 RIP-LIKE KINASE - HOMO SAPIENS (HUMAN), 518 aa.	2E-120	
7617	cg43923128	2174	GAGTGGAGATG GGCAGAGGGCTC TGG[C/gap]CCCT GCTCCTCTGGCT TCTCAGCAG	C	gap	Gly	Gly (9788)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P70361 TERA - MUS MUSCULUS (MOUSE), 277 aa.	3.2E-120	1
7618	cg43963595	156	TCACACTCTCAC ACACACACACAC A[gap]/CJTGCCAC GCACATATCCAA GCTCCAA	gap	C	Met	Ser (9789)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75391 SPERM ACROSOMAL PROTEIN - HOMO SAPIENS (HUMAN), 293 aa.	8.5E-120	17
7619	cg43950398	1454	CTGCTTGGTGGC GGCTCGTGAAG GG[G/gap]CAAGG CCGAGAACTTC TGAATGT	G	gap	Ala	Ala (9790)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O75545 HYPOTHETICAL 26.0 KD PROTEIN - HOMO SAPIENS (HUMAN), 230 aa (fragment).	1.4E-119	1
7620	cg43994051	517	AATTCTGCAAAG AACATGGCTTTG C[C/gap]GGATGG TTTGAAACCTCT GCAAGG	C	gap	Gly	Asp (9791)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q13637 RAS- RELATED PROTEIN RAB-32 - Homo sapiens (Human), 225 aa.	9.7E-119	6
7621	cg43998873	188	CTCTCAGAATTC CTGACTGTCCGC A[G/gap]GTTCC AAATCCTCCAGC GCTTGAG	G	gap	Thr	Thr (9792)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB39895 GRIP1 PROTEIN - HOMO SAPIENS (HUMAN), 849 aa (fragment).	2E-118	

7622	cg43917206	972	GGACCAACAGG CAATATCAATCTT C[C/gap]TCCGGG CTTTAACTGATC TATTAGC	C	gap	Gly	Glu (9793)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P22081 PROTEIN-L- ISOASPARTATE(D-ASPARTATE) O- METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN-BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L- ISOASPARTYL/D- ASPARTYL METHYLTRANSFERASE) (L- ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) - Homo sapiens (Human), 226 aa.	6.9E-118	6
7623	cg43258389	1431	GCCACTTCTGCA GCCTGCCGTGT GG[C/gap]AAACT GGATGAAAGCAC ACTGCTGT	C	gap	Ala	Pro (9794)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q22412 T11G6.8 - CAENORHABDITIS ELEGANS, 658 aa.	1.6E-115	5
7624	cg43951899	460	GCAGGCGGTGA GCTGGGGCCG GCA[G/gap]GGGC GCGACAGTGC GGCGTGGTCG	G	gap	Leu	Cys (9795)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9
7625	cg43951899	463	GGCGGTGAGCT GGGGGCCCGCA GGG[G/gap]CGC GGACAGTGGG CGTGGTCGAAC	G	gap	Pro	Pro (9796)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q64322 NPDC-1 PROTEIN PRECURSOR - Mus musculus (Mouse), 332 aa.	3.3E-115	9
7626	cg43939521	1019	GTGAGCATGACC CCCATGTGCTCC T[G/gap]GCCGTG GCCAAGCTGTTT TGGAGTC	G	gap	Ala	Pro (9797)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q12381 PRE-MRNA SPLICING FACTOR - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 906 aa.	5.7E-114	
7627	cg43939521	588	AGCCCAAGATCT GTGCGAGGAGG CC[C/gap]TGCGG CACTATGAGGAC TTGCCCAA	C	gap	Leu	Cys (9798)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q12381 PRE-MRNA SPLICING FACTOR - SCHIZOSACCHAROMYCES POMBE (FISSION YEAST), 906 aa.	5.7E-114	

7628	cg43982971	501	GCGCCATTGAGT TCGGACAGCGG ATT[ <i>gap</i> ]CTCCA GGTGGCATCTCA AGCCTCCA	G	<i>gap</i>	Leu	Ser (9799)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P87765 VWV-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
7629	cg43982971	742	GCCCTACCCTGGC GCCCATGGAACC TTC[ <i>gap</i> ]CCGGTC AGCGGCCCGCA TGTCCTCC	C	<i>gap</i>	Pro	Pro (9800)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P87765 VWV-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
7630	cg43982971	744	CCTACCCTGGCC CCATGGAACCTC C[C[ <i>gap</i> ]GGTCAG CGGCCCGCATG TCCCCTCC	C	<i>gap</i>	Gly	Val (9801)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P87765 VWV-DOMAIN BINDING PROTEIN 2 - MUS MUSCULUS (MOUSE), 261 aa.	5.7E-114	
7631	cg43948724	1060	GGAGGAGGCCT GTCCCAATTCTG CC[C[ <i>gap</i> ]GCTCC ATGGAAAAGCGG GCTTGACT	C	<i>gap</i>	Pro	Arg (9802)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114 (16q21)	16 (16q21)
7632	cg43948724	1165	TTAATCCTTCTTT GTAATACCTTTCT A[ <i>gap</i> ]ATGTGACA TTTCTCTTCCCC TTAGA	A	<i>gap</i>	End	Tyr (9803)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114 (16q21)	16 (16q21)
7633	cg43948724	1166	TAATCCTTCTTTG TAATACCTTTCTA A[ <i>gap</i> ]TGTGACAT TTCTCTTCCCCT TAGAA	A	<i>gap</i>	Cys	Val (9804)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114 (16q21)	16 (16q21)

7634	cg43948724	1471	TGGAAGCATGTA GACTGTGCCAGA G[G/gap]CCAGAC CCACGGGCTCAT GCACCCC	G	gap	Gly	Ala (9805)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
7635	cg43948724	1502	CCCACGGGCTC ATGCACCCCTGA GC[C/gap]AGCAG GGCATCTTGGAA AAGGAACT	C	gap	Gln	Ser (9806)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
7636	cg43948724	800	CTGATGAGAGAC AGCGCATGCTG GT[gap/C]GCAGC GTAAGGACGAAC TCCTCCAG	gap	C	Cys	Ser (9807)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
7637	cg43948724	948	TGCGTCSAAGGA TGCTGGCTGCC GC[C/gap]GCCGA ACGGAGGCTTCA GAAGCAGC	C	gap	Pro	Arg (9808)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P26442 AUTOCRINE MOTILITY FACTOR RECEPTOR PRECURSOR (AMF RECEPTOR) (GP78) - Homo sapiens (Human), 323 aa.	9.9E-114	16 (16q21)
7638	cg43921344	959	GGGCCCTCGAAT GGTAAGAGGGG CT[G/gap]CCTGG GGGCCCATGGG TCTGGTAGA	G	gap	Gly	Gly (9809)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa.	2.3E-112	
7639	cg43921344	108	AGGCCAAGTGG GGAAGTGCAGG TGC[A/gap]CAAG AGAGCGCTTGAG GCTCTGGTC	A	gap	Val	Gly (9810)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa.	2.3E-112	

7640	cg43921344	228	CAGGGCACCGT GCACCATGGCT GG[C/gap]CCCTC TCGGTGGGAA GTAGCGTGC	C	gap	Gly	Ala (9811)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa.	2.3E-112	
7641	cg43921344	398	CTAGCGGGGG CAGTATGGGA GAG[C/gap]CCCT CCACGCAGCTG GCATTGATGT	C	gap	Gly	Gly (9812)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O88902 PROTEIN TYROSINE PHOSPHATASE TD14 (EC 3.1.3.48) - RATTUS NORVEGICUS (RAT), 1494 aa.	2.3E-112	
7642	cg43957889	325	GGGAGATGTTT GTGGCGGCTTG C[C/gap]TGCTCC AAGAAATGCGCTT TGCQCCTC	C	gap	Cys	Ala (9813)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O00577 COSMID 6E5 CDK4, SAS AND KIAA0167 GENES, COMPLETE CDS, AND OS9 - HOMO SAPIENS (HUMAN), 227 aa.	2.7E-111	12
7643	cg43960984	777	ATCTTTCCCAT CGACCTGGAGTC C[C/gap]TCTCGG GAACCTTAACCAT ACTTCTT	C	gap	Gly	Gly (9814)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q61712 DNAJ PROTEIN HOMOLOG MTJ1 - Mus musculus (Mouse), 552 aa.	8.6E-111	10
7644	cg4396282	298	AGAGCCCTGCT CCTGGCCATAG C[C/gap]AAATCC CTTGGGCCCAA GTCCTT	C	gap	Gly	Ala (9815)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:P97314 DOUBLE LIM PROTEIN-1 - MUS MUSCULUS (MOUSE), 193 aa.	2.9E-110	12
7645	cg43981416	385	CTGGATCCACGC CCCTGGCCCCG AG[G/gap]TCCTG CAGTCTTCGGG CCGCCCGT	G	gap	Asp	Asp (9816)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD45561 TRANSFERRIN RECEPTOR 2 ALPHA - HOMO SAPIENS (HUMAN), 801 aa.	1E-109	7
7646	cg43976845	137	GGGAGCGGCTG GGATGGCGCGT CCG[C/gap]GGCC CCGCGAGTACAA AGCGGGCGA	C	gap	Arg	Gly (9817)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34137 CGI-142 PROTEIN - HOMO SAPIENS (HUMAN), 203 aa.	3.4E-109	15

7647	cg43928772	1735	ACTAAAGGCGCT TTCCGCCATCAC C[C/gap]CCACTG GCATCTTCGCGG CCGGCCT	C	gap	Gly	Gly (9818)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q99627 HCOP9 - HOMO SAPIENS (HUMAN), 209 aa.	8.9E-109	2
7648	cg44913737	179	GGCAGGGGCAC TCAGTCCCTCCG CA[G/gap]GTTCT TAAGCCGTTCT CCAGGTCT	G	gap	Leu	Cys (9819)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q43633 BC-2 PROTEIN - HOMO SAPIENS (HUMAN), 222 aa.	2.4E-108	19
7649	cg44913737	229	TGCATCAGCATC AGCTAGGGCTGA G[G/gap]CTGCGG CCTCTGCTTTTT CCACCC	G	gap	Ala	Ala (9820)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q43633 BC-2 PROTEIN - HOMO SAPIENS (HUMAN), 222 aa.	2.4E-108	19
7650	cg44913737	237	CATCAGCTAGGG CTGAGGCTGCG GC[C/gap]TCTGC TTTTTCCACC AGCAGCCA	C	gap	Glu	Glu (9821)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q43633 BC-2 PROTEIN - HOMO SAPIENS (HUMAN), 222 aa.	2.4E-108	19
7651	cg43327495	1079	CTGAAAAGGTGT GATCAATTCCAA CTT/gap]GCACGG CGGCGGTGGTG AGGACGCA	T	gap	Gln	Arg (9822)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD34096 CGI-101 PROTEIN - HOMO SAPIENS (HUMAN), 209 aa.	5E-108	17
7652	cg42657906	195	TCATCAGGTGCT GAGGGGCCCGG GG[G/gap]CGCTG GGGCAAGGC AGAGTAGAG	G	gap	Pro	Pro (9823)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14919 NC2 ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 205 aa.	6.2E-108	11

7653	cg42857906	431	GCCGCCGCTGC CTGGCTTCGGC CC[C/gap]TGGG GCGCCCTTGTC CCATCCAT	C	gap	Arg (9824)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14919 NC2 ALPHA SUBUNIT - HOMO SAPIENS (HUMAN), 205 aa.	6.2E-108	11
7654	cg43286554	206	TGGCCTTCTCTC TTGGGGGCTTTG C[gap/C]TTCTCAT CCTCTTTGCTG TCAAAA	gap	C	Lys (9825)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q15527 SURFEIT LOCUS PROTEIN 2 - Homo sapiens (Human), 256 aa.	6.4E-108	9
7655	cg43942004	740	ATGGAGAGAGGT GTCATGGGCTGA G[C/gap]CTCCCA GTGGAAAAATCGC TTATATA	C	gap	Ser (9826)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107 5 (5q23)	
7656	cg43942004	741	TGGAGAGAGGT GTCATGGGCTGA GC[C/gap]TCCCA GTGGAAAAATCGC TTATATAC	C	gap	Ser (9827)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q99075 HEPARIN- BINDING EGF-LIKE GROWTH FACTOR PRECURSOR (HB-EGF) (HBEGF) (DIPHTERIA TOXIN RECEPTOR) (DT-R) - Homo sapiens (Human), 208 aa.	1E-107 5 (5q23)	
7657	cg43947512	344	AAGTCAGGTTCC ATTGGCAACTG C[C/gap]GAGTGG ATCGCGGAGCC CGTGCGGC	C	gap	Ser (9828)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:Q14197 DS-1 PROTEIN - Homo sapiens (Human), 206 aa.	2.1E-107	17
7658	cg42854459	95	AAAAACTATATG AGAAAGCTGGCA A[G/gap]CCCCAGT GAACCTCCTGGC CGGAGAG	G	gap	Gly (9829)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:AAD41342 HEPARANASE - HOMO SAPIENS (HUMAN), 543 aa.	3.5E-107	

7659	cg42923937	901	GCTGAGCACTTG CCTGTGGTCACG C[C/gap]TTTGAT GAGACGGACGA GGACAGGA	C	gap	Arg	Ser (9830)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O43378 R29893_1 - HOMO SAPIENS (HUMAN), 216 aa (fragment).	4.4E-107	
7660	cg43967668	248	CGCTTGTCGAAC CACTTGCCGTTG G[C/gap]CGCGCC TGACAGGACCG CGCAGTTC	C	gap	Ala	Pro (9831)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P05452 TETRAPECTIN PRECURSOR (TN) (PLASMINOGEN-KRINGLE 4 BINDING PROTEIN) - Homo sapiens (Human), 202 aa.	5.6E-107	3 (3p22)
7661	cg43969137	346	GGCTCATAGAAG ATGTGGCTGGTA G[C/gap]CTGCC TGGCCTAGGCC GCAGGAGA	C	gap	Ala	Leu (9832)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O08973 HYPOTHETICAL 33.5 KD PROTEIN - MUS MUSCULUS (MOUSE), 300 aa.	3.6E-105	17
7662	cg43981269	595	ACTCCTCCACG CCGAGGCGCAG GC[C/gap]GCCAT CAACGGCTACA CGGCAGCC	C	gap	Ala	Pro (9833)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q91579 RIBONUCLEOPROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 462 aa.	4.5E-105	
7663	cg44912062	504	AGCTGGCCGAG CTGGAGGGCCG CCA[G/gap]GAGG AGCTGCTGCGG GAGAACCTAG	G	gap	Glu	Arg (9834)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q15834 HEPATITIS DELTA ANTIGEN INTERACTING PROTEIN A - HOMO SAPIENS (HUMAN), 202 aa.	1.5E-104	11
7664	cg43989798	491	GCGACTATCTGC TGCGCGGTTACC G[C/gap]ATGCTG GGCGAGACGTG TGCGGACT	C	gap	Met	Cys (9835)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O60232 AUTOANTIGEN P27 - Homo sapiens (Human), 189 aa.	1.4E-103	



7665	cg43999798	654	CTCCCAAGCTCG GGAGCACCAGC TG[G/gap]CCTCA GCCTCAGAGCTC CCCCTGGG	gap	Ala	Pro (9836)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSNEW-ACC:O60232 AUTOANTIGEN P27 - Homo sapiens (Human), 199 aa.	1.4E-103	
7666	cg43947568	547	GCCTCGACACAA TTACCACAAAGT G[G/gap]CTCCCC TGGTGCAGTCCT TGTGTGC	gap	Ala	Leu (9837)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O60427 BC269730_2 - HOMO SAPIENS (HUMAN), 444 aa.	2.9E-103	11
7667	cg43250168	254	AGAGACCCGGC TTCGGCTTCATG GC[C/gap]GGCCT CCCGCAGGTGT CTGCCCCAGC	gap	Gly	Ala (9838)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to TREMBLNEW-ACC:CAB43382 HYPOTHETICAL 146.2 KD PROTEIN - HOMO SAPIENS (HUMAN), 1296 aa.	3.3E-102	2
7668	cg42885795	440	TAAGATGCTGTT TTCTGGCGTCTG C[C/gap]AAAATC ATAGACCACAGG GATCACC	gap	Gly	Ala (9839)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:O88310 INTELECTIN - MUS MUSCULUS (MOUSE), 313 aa.	4.2E-102	
7669	cg44032188	1169	TTCGGTCGTGAT GCCCTTCATGGT G[G/gap]CCTGCG TGCCCACTGGCA TGAACAC	gap	Ala	Ala (9840)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:Q23623 PUTATIVE QUEUINE TRNA- RIBOSYLTRANSFERASE (EC 2.4.2.29) (TRNA-GUANINE TRANSFERASE) TRANSGLYCOSYLASE (GUANINE INSERTION ENZYME) - Caenorhabditis elegans, 400 aa.	8.8E-102	19
7670	cg43999564	760	CCTTCTGGCTCA GTACGCGGGAC TG[G/gap]CGTAG CGCTCCTCGGCA CTCATCGC	gap	Arg	Arg (9841)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SWISSPROT-ACC:P49914 5- FORMYL-TETRAHYDROFOLATE CYCLO-LIGASE (EC 6.3.3.2) (5,10- METHENYL- TETRAHYDROFOLATE SYNTHETASE) (MTHFS) - Homo sapiens (Human), 202 aa.	2.8E-101	15

7671	cg44911139	757	AACTCAGTCGT TCTAAGGGCATT G[C/gap]CTAGCT GGAATTCTGTGA AATCCAG	C	gap	Ala	Ala (9842)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14499 SPLICING FACTOR - HOMO SAPIENS (HUMAN), 530 aa.	7.9E-101	14
7672	cg44911139	758	ACTCACGTCGTT CTAAGGGCATTG C[C/gap]TACGTG GAATTCTGTGAA ATCCAGT	C	gap	Tyr	Thr (9843)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Homologous to SPTREMBL-ACC:Q14499 SPLICING FACTOR - HOMO SAPIENS (HUMAN), 530 aa.	7.9E-101	14
7673	cg43941552	653	ACTTCAGATGG AATGCTCTCTGC A[G/gap]GCCAAG CCCGCAGTGCCT ACGTCTA	G	gap	Ala	Pto (9844)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	1.6E-100	
7674	cg43925214	916	GCGTGAAGGCG TTGGAGTCGAAG GA[G/gap]CGGGG ATCCGCCAGCAT CTGGAAGC	G	gap	Arg	Arg (9845)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD4480 BUP - HOMO SAPIENS (HUMAN), 195 aa.	4.3E-100	10
7675	cg43941550	531	CACCTCGCCACA CAGGGTGCTCAC G[G/gap]CCATGC CCAGGAAGGCC GGGTCCCC	G	gap	Ala	Ala (9846)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)

7676	cg43941550	553	ACGGCCATGCC CAGGAAGGCCG GGT[C/gap]CCCT CCGAGGGTGC TGAGCCTGCA	C	gap	Asp	Thr (9847)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
7677	cg43941550	556	GCCATGCCCGG GAAGGCCGGT CCC[C/gap]TCCG GAGGGTGCTGA GCCTGCATCT	C	gap	Gly	Gly (9848)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
7678	cg43941550	629	TAGACGTAGGCA CTGCGGGCTTG GC[C/gap]TGCAG AGAGCATTCCAT CTGGAAGT	C	gap	Gln	Gln (9849)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
7679	cg43941550	632	ACGTAGGCACTG CGGGCTTGCC TG[C/gap]AGAGA GCATTCCATCTG GAAGTTGT	C	gap	Leu	Leu (9850)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)

7680	cg43941550	649	TTGGCCTGCAGAG GAGCATTCCATC T[G/gap]GAAGTT GTGGACTTTTCT AGTGAGA	gap	Gln	Arg (9851)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
7681	cg43941550	729	TATCTTCATGAT GTAGCAGCAGGT G[C/gap]CAGGGG CTGGCTTGTAGG CGATCAG	gap	Gly	Ala (9852)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P11686 PULMONARY SURFACTANT-ASSOCIATED PROTEIN C PRECURSOR (SP-C) (SP5) (PULMONARY SURFACTANT- ASSOCIATED PROTEOLIPID SPL(VAL)) - Homo sapiens (Human), 197 aa.	5.5E-100	8 (8p21)
7682	cg43950149	925	TCACTTCTACTG TGGCAAATTTGC C[G/gap]CCTTCA CAGGCCCTTTCT TCATAGG	gap	Gly	Gly (9853)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa.	7.1E-100	12
7683	cg43950149	508	GCCAGATCTCAT TGGCCCGTCCGT A[G/gap]GGCTTC ATGGGAGGGTC ATAACCCG	gap	Pro	Pro (9854)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa.	7.1E-100	12
7684	cg43950149	560	GCAGAAGTAGAT GTCCCCCGCGTA G[G/gap]TGGCTG TGCCCTCCAGG GCAGCACG	gap	Thr	Thr (9855)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32098 HEME-BINDING PROTEIN - HOMO SAPIENS (HUMAN), 189 aa.	7.1E-100	12
7685	cg43926315	2128	GAAGGTGGTGCT GGTGGTGCAACT G[C/gap]TGGTTT TGGAGACAGTAC TGGAAAT	gap	Ala	Gln (9856)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD42873 NY-REN-37 ANTIGEN - HOMO SAPIENS (HUMAN), 173 aa (fragment).	1.2E-99	14

7686	cg43981133	416	GTGGTGGCCCT GATGCCCGAGG TGG[G/gap]CAGC CTGCAGCACGCA CGGGTGCTG	G	gap	Gly	Ala (9857)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75786 GANGLIOSIDE-INDUCED DIFFERENTIATION ASSOCIATED PROTEIN 1 - HOMO SAPIENS (HUMAN), 358 aa.	1.5E-99	20
7687	cg44026081	511	ACATGACCTGGC AGCGGGGCGG AG[G/gap]AGCTT CATCTCAAGG CCAGGAGG	G	gap	Ser	Ala (9858)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60736 KE03 PROTEIN - HOMO SAPIENS (HUMAN), 367 aa (fragment).	2.7E-97	
7688	cg43935925	786	TGACCAGGTCC GGATTTCGTCTG C[C/gap]TTCGGG ATGTTGTCTGAA GCATGAT	C	gap	Lys	Lys (9859)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34117 CGI-122 PROTEIN - HOMO SAPIENS (HUMAN), 185 aa.	4.6E-98	16
7689	cg43992729	691	CTCCACACTGCT GCAAGGCTGG GC[C/gap]ATATG TTGCTGGGAATT CCCTCCAC	C	gap	His	Ile (9860)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70303 CELL DEATH-INDUCING DNA FRAGMENTATION FACTOR, ALPHA SUBUNIT-LIKE EFFECTOR B (CELL DEATH ACTIVATOR CIDE-B) - MUS MUSCULUS (MOUSE), 219 aa.	2.6E-95	14
7690	cg43927693	514	GCAGCTGGCCC TGAAGTGGGCAT GG[C/gap]CCCCC ATCTTCTTTGGT GCCCCGACA	C	gap	Pro	Pro (9861)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22
7691	cg43927693	545	ATCTTCTTTGGT GCCCCGACAAATG G[G/gap]CTGGGC CTTGGTGGATCT CCTGCTG	G	gap	Gly	Ala (9862)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22

7692	cg43927693	552	TTGGTGCCCGAC AAATGGGCTGG GC[gap]TTGGT GGATCTCCTGCT GGTCAGTG	gap	Leu	Trp (9863)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22
7693	cg43927693	723	ACAACCATGGCT GGCGTGGGGA CG[gap]CGGCT GCCAGAGTGAGT GCCCGGCC	gap	Arg	Gly (9864)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P30536 PERIPHERAL-TYPE BENZODIAZEPINE RECEPTOR (PBR) (PKBS) (MITOCHONDRIAL BENZODIAZEPINE RECEPTOR) - Homo sapiens (Human), 169 aa.	5.3E-95	22
7694	cg43934685	664	TGAAAAATTGA TGTCAGTGAAGA G[C/gap]TTCCAG CCAGAAGAAAAT GAAATCG	gap	Leu	Phe (9865)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q15022 ORF - HOMO SAPIENS (HUMAN), 803 aa (fragment).	1.2E-94	17
7695	cg43950632	723	CTGCACAGATGG CGGCTATCAGGC C[C/gap]TTCCGG TTTTCTGCTCC TTCAGTA	gap	Lys	Lys (9866)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14805 RNA-BINDING PROTEIN REGULATORY SUBUNIT - HOMO SAPIENS (HUMAN), 189 aa.	2.3E-94	1
7696	cg43993152	1185	GACCCAGACCA GATTTCAACACA TG[gap]TTCC ATACAGGAAGGA CTGCTCTG	gap	Asn	Asn (9867)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD27746 CGI-37 PROTEIN - HOMO SAPIENS (HUMAN), 180 aa.	3.7E-94	
7697	cg42514925	538	CAAGGAACCCAA CAGTCTGCATGG A[A/gap]GGAGTC AGAGGGTTTGAT AAAGTGC	gap	Arg	Gly (9868)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q12915 IBD1 - HOMO SAPIENS (HUMAN), 204 aa (fragment).	2.3E-93	
7698	cg17948203	321	AGTTACAAGAGT AGTAGATGAACA A[C/gap]ACTAAA GGCGTTGCTTGA GTCCATG	gap	Thr	Asn (9869)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75660 DJ501N12.1 - HOMO SAPIENS (HUMAN), 247 aa (fragment).	3.8E-93	

7689	cg42807594	624	GGGAGCATCCC AAAGCATACTCG AA[G]gap]GCTCG AGCCAGGCAC ATGCCACAA	G	gap	Leu	Phe (9870)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34142 CGI-147 PROTEIN - HOMO SAPIENS (HUMAN), 179 aa.	3.8E-92	17
7700	cg43980242	952	GAGAACTGGG CCTGACCCGGAT TC[G]gap]GGACA GGAAC TGGTATG TGCAGCCC	G	gap	Arg	Arg (9871)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P26438 ADP-RIBOSYLATION FACTOR 6 - Homo sapiens (Human), Mus musculus (Mouse), and, 174 aa.	1.7E-91	14
7701	cg439830979	1216	GCCACCATGGG CCTGGCTGGAA GAG[C]gap]CAGA GTGAAAGGAAAAA TTTTCCCCT	C	gap	Ala	Ala (9872)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q19265 SIMILAR TO M. MUSCULUS MER5 AND OTHER AHPC/TSA PROTEINS - CAENORHABDITIS ELEGANS, 576 aa.	3.4E-90	9
7702	cg439830979	362	CTACGTGCTGTT CCTCGCCGACG AG[G]gap]AGTTC GACGTGGTAGTG TCCGACCA	G	gap	Glu	Ser (9873)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q19265 SIMILAR TO M. MUSCULUS MER5 AND OTHER AHPC/TSA PROTEINS - CAENORHABDITIS ELEGANS, 576 aa.	3.4E-90	9
7703	cg43983913	812	GGAGTCCACAAA CTCGTCACTCAT C[C]gap]TCCGGA GCTCGCGGCCA TAGCGCTG	C	gap	Arg	Arg (9874)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11
7704	cg43983913	925	CCATCCCTTCGT CGTCTCCGTCC C[C]gap]GCGGG TAGGAGCTGTGG CGACTCC	C	gap	Ala	Ala (9875)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14803 BCL-X/BCL-2 BINDING PROTEIN - HOMO SAPIENS (HUMAN), 168 aa (fragment).	5.1E-90	11

7705	cg43983527	1032	CGAGAGTCTGC GGCCCCGGTGC TCC[G/gap]GCTG CGATGAGATAAT ATTCGCTGA	G	gap	Gly	Ala (9876)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa.	6.5E-90	3 (11q23.3)
7706	cg43983527	1033	GAGAGTCTGCG GGCCCCGGTGC CCG[G/gap]CTGC GATGAGATAATA TTCGCTGAG	G	gap	Gly	Ala (9877)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa.	6.5E-90	3 (11q23.3)
7707	cg43983527	837	CAAAGAAGTGA ATACGTCTGCGA G[C/gap]TCTGCA AGGAGCGGCC CCTCCTGA	C	gap	Leu	Ser (9878)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47226 TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)] - Mus musculus (Mouse), 423 aa.	6.5E-90	3 (11q23.3)
7708	cg38719198	543	GCAGCAGGCGG ACGTGGTCGTG GCA[gap]A/GAAG TGACACAGCCAT CCTGGGTG	gap	A	Glu	Arg (9879)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43598 RCL (RCL) - HOMO SAPIENS (HUMAN), 174 aa.	1.3E-89	6
7709	cg43980642	625	CAGGCAGCATT AAACTTAAGCAG A[gap]A/GAGCTT AAAGCAGCGCCT GGGTAAG	gap	A	Glu	Glu (9880)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O93501 NO27 PROTEIN - XENOPUS LAEVIS (AFRICAN CLAWED FROG), 248 aa.	2.4E-89	1
7710	cg43950029	266	TTAGTTGTGTC TGCTAGGCTCTG C[C/gap]TCAGGG ATTTTGGAGTT CTTCTGG	C	gap	Arg	Ser (9881)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q17474 B0334.3A - CAENORHABDITIS ELEGANS, 623 aa.	3.9E-89	
7711	cg44927780	1406	ATAGAGAGGAAA CAACTTGAGGGA G[C/gap]TGGCGG CCATCAATGCAG AGTGCTG	C	gap	Ser	Thr (9882)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23368 ZC518.2 - CAENORHABDITIS ELEGANS, 1030 aa.	6.3E-89	4



7712	cg44927780	1544	AACGGACCGATC CACAGCCATGTT TTG/gap]CCAGAA GGCAGATGGCA GCTTGATC	G	gap	Ala	Glu (9883)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q23388 ZC518.2 - CAENORHABDITIS ELEGANS, 1030 aa.	6.3E-89	4
7713	cg43059113	425	CAAGAGGGCTG GCATTCTGGCT GGC/gap]CCTGG GCACCTCAGCAGT CGGTGCTT	C	gap	Gly	Gly (9884)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa.	7.4E-89	3
7714	cg43059113	747	AACAGCAGAGTT TTCACCTCCAGT G/G/gap]CTGGAG CCTGTGATTCAA AGAAGTC	G	gap	Ala	Ala (9885)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA78341 16G2 - HOMO SAPIENS (HUMAN), 382 aa.	7.4E-89	3
7715	cg43941586	401	TGGAAGACGGG GATAAGCGCTGT AA[G/gap]CTTCT GCTGGGGATAG GAATTCCTGG	G	gap	Leu	Phe (9886)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10589 BONE MARROW STROMAL ANTIGEN 2 (BST-2) - Homo sapiens (Human), 180 aa.	2.5E-88	19
7716	cg43960450	1711	GCTTCAAGATCA GCTCAAAAGCCT G/G/gap]CCAGAG GCACGTTTGTG ATTGCT	G	gap	Gly	Gly (9887)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55821 SCG10 PROTEIN (SUPERIOR CERVICAL GANGLION-10 PROTEIN) - Mus musculus (Mouse), 179 aa.	8.5E-88	8
7717	cg43026816	65	CAGTCTATGCCT GGCCCAGCGC AGC/gap]CCCAG GTCCAGGGGGG GTCTGGTTG	C	gap	Ala	Leu (9888)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O76103 R29425_1 - HOMO SAPIENS (HUMAN), 656 aa.	2.3E-87	
7718	cg43931874	484	CCTCTGTAATCA TCACTGGCCGCA A/G/gap]GTCCCG GATGTCCTCCTC GATGAGG	G	gap	Leu	Leu (9889)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54745 P65 PROTEIN - RATTUS NORVEGICUS (RAT), 613 aa.	2.4E-87	

7719	cg43931874	716	TCAGGCGAGCT GGGTCCCACTTG GGG[gap]CCTTC CCGGCGAATTG GTTACACAGG	G	gap	Gly (9890)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54745 P65 PROTEIN - RATTUS NORVEGICUS (RAT), 613 aa.	2.4E-87	
7720	cg43298131	436	GAGCTGTCCTG GTGAGGAACGC CC[C/gap]AGGCC CCGAGGCACCG GCCCCACGA	C	gap	Gln (9891)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB41450 CENTAURIN BETA2 - HOMO SAPIENS (HUMAN), 778 aa.	3.7E-87	
7721	cg43992520	1167	AGCTTCGGCCCC AGTTTGTAGTAG A[G/gap]GCGCCG CCCCACCTCACC CAGCCGG	G	gap	Ser (9892)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P25791 RHOMBOTIN-2 (CYSTEINE RICH PROTEIN TTG-2) (T- CELL TRANSLOCATION PROTEIN 2) (LIM-ONLY PROTEIN 2) - Homo sapiens (Human), 158 aa.	6E-87	11
7722	cg43946899	371	TTTGGCGGCCA TGTGCTTCCCGA A[G/gap]GTCCTC TCTGATGACATG AAGAAGC	G	gap	Val (9893)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P24001 NATURAL KILLER CELLS PROTEIN 4 PRECURSOR - Homo sapiens (Human), 234 aa.	6E-87	
7723	cg43946899	372	TTTGGCGGCCAT GTGCTTCCCGAA G[G/gap]TCCTCT CTGATGACATGA AGAAGCT	G	gap	Ser (9894)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P24001 NATURAL KILLER CELLS PROTEIN 4 PRECURSOR - Homo sapiens (Human), 234 aa.	6E-87	
7724	cg42529218	205	CCCCCGAGGCC AACCCCGCCGA CGG[C/gap]AGTG ACGCTGACGAG GACGATGAGG	C	gap	Val (9895)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35540 HEPATOMA-DERIVED GROWTH FACTOR, RELATED PROTEIN 2 - MUS MUSCULUS (MOUSE), 669 aa.	7.5E-87	
7725	cg43970868	663	ACACCGGGGAC ACTCTGGGCAGC GTC[gap]CTCCG GGGCTTCTTCAC CATCCGCA	C	gap	Ser (9896)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAA19508 Y39A1C.2 PROTEIN - CAENORHABDITIS ELEGANS, 1066 aa.	9.8E-87	12

7726	cg43918822	3295	ATTGTTCTCCAG GCGTAGCAAGG GG[G/gap]CCACC AGGCCACATTT GTATGGAG	G	gap	Ala (9897)	Ala (9897)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB04720 T08G5.5 PROTEIN - CAENORHABDITIS ELEGANS, 923 aa.	1.1E-86	15
7727	cg44018226	1715	AGGCTCCCAGG CTCCAGGAGCC GGG[G/gap]CTGA CGCTGTCAACC ACCAGGTAC	G	gap	Pro (9898)	Pro (9898)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD40106 PUTATIVE MEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 194 aa.	1.6E-86	
7728	cg44920099	591	TCTCCAGTCCCC ACCACCACGATC TTC[gap]TATCCG GGCTCCAGCA ACCAGAAG	C	gap	Glu (9899)	Arg (9899)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43224 HYPOTHETICAL 22.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 207 aa (fragment).	1.7E-86	
7729	cg44920099	772	CGATGTACATTG CCTGAGCGGCC TC[G/gap]CGTTG CAGCAGAGAGAT GCGCGTCC	G	gap	Arg (9900)	Arg (9900)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43224 HYPOTHETICAL 22.8 KD PROTEIN - HOMO SAPIENS (HUMAN), 207 aa (fragment).	1.7E-86	
7730	cg43995092	404	ATACTTGTCTGA GGGCCCTGAGG GC[C/gap]GATCA TCCAATCCAGTT GCAGTACT	C	gap	Arg (9901)	Asp (9901)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD18134 T41P - HOMO SAPIENS (HUMAN), 505 aa.	1.1E-85	8
7731	cg43934734	931	AACCACCTTATG TAGGGGCCGGG GA[G/gap]CCCTC CAAGGGCATTGA AGCACAGA	G	gap	Leu (9902)	Ser (9902)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.1E-84	20
7732	cg43934734	670	CGATGGGAGAC AGCGTCTTCTC CG[C/gap]CTTAG GCATCTCTGCGT ACGTCCTGC	C	gap	Ala (9903)	Arg (9903)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O14878 PUTATIVE ONCOGENE PROTEIN - HOMO SAPIENS (HUMAN), 157 aa (fragment).	7.1E-84	20



7739	cg43336199	689	CTCCCGGAGGA GGGCACCGTAG TTA[G/gap]CTCT CTGGCAGGCAG TGGTCATGAA	G	gap	Ala	Val (9910)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60894 MRNA ENCODING RAMP1 PRECURSOR - HOMO SAPIENS (HUMAN), 148 aa.	1.6E-79	2
7740	cg44024149	657	GAAGTCAACTGT GTGAGTGTGATA A[G/gap]GCTGCT GCCACCTGTTTT GCTAGAA	G	gap	Ala	Leu (9911)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P14555 PHOSPHOLIPASE A2, MEMBRANE ASSOCIATED PRECURSOR (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2- ACYLHYDROLASE) (GROUP II PHOSPHOLIPASE A2) - Homo sapiens (Human), 144 aa.	5.3E-79	1 (1p35)
7741	cg43250517	354	TCAGCATGGAAA CCTGGGAGAAA GG[C/gap]CTGTT CCTGAAGGTACA GCAGCCGG	C	gap	Ala	Pro (9912)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34037 CGI-41 PROTEIN - HOMO SAPIENS (HUMAN), 475 aa.	1.4E-78	
7742	cg43948675	367	GTGTCCCGTGTCT TGAATGCACCGC A[G/gap]GCAGCA CAAGTTCTCATA TCCTTGC	G	gap	Leu	Cys (9913)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	
7743	cg43948675	368	TGTCCCGTGTCT GAATGCACCGCA G[G/gap]CAGCAC AAGTTCTCATAT CCTTGCT	G	gap	Cys	Cys (9914)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O70454 G10 PROTEIN HOMOLOG - RATTUS NORVEGICUS (RAT), 144 aa.	7.8E-78	
7744	cg43304219	1236	TCTATCAGCAGA GACAGCTTCTTC T[G/gap]CAGTTC CTGCAAGTCCCT TGAGATA	G	gap	Gln	Arg (9915)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00323 HYPOTHETICAL 17.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 161 aa.	9.9E-78	16 (16p13.1 1)

7745	cg43936167	690	TTGCAGTCTGTT CCACAGTTTTGG CTT/gapTTTTTTTC TTTTCTTTTTTCT TTTCT	T	gap	Ser	Ala (9916)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	1.2E-77	20
7746	cg43936167	696	TCTGTTCCACAG TTTTGGCTTTTT TTT/gapCTTTTCTT TTTTCTTTTTCTT GTCA	T	gap	Lys	Lys (9917)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P09012 U1 SMALL NUCLEAR RIBONUCLEOPROTEIN A (U1 SNRNP A PROTEIN) - Homo sapiens (Human), 282 aa.	1.2E-77	20
7747	cg44936941	694	CTCGTGCTCTCT CATCTGCATCAA A/gapJTACCAA ACAGTTATTGCG TACCTTG	A	gap	Tyr	Tyr (9918)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:Q62630 SM-20 - RATTUS NORVEGICUS (RAT), 355 aa.	7E-77	1
7748	cg43931888	306	CAACGCCGAAC GCCTCCAGGA GGC/gapJCCACC TGGGAACCCCC GACCTGAAC	C	gap	Ala	Ala (9919)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:Q16192 ORF3 5' OF PD-ECGF/TP - HOMO SAPIENS (HUMAN), 157 aa.	1E-75	22
7749	cg43970034	870	ATTGTGCTGTTT TTCAGGCTTCTT TTT/gapJCTGAGT CAGCATCTTTTC TCIGGC	T	gap	Lys	Lys (9920)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:Q64362 FUSED TOES (FT1 PROTEIN) - MUS MUSCULUS (MOUSE), 292 aa.	1.3E-75	16
7750	cg43970034	871	TTGTGCTGTTCT TCAGGCTTCTTT TTT/gapJCTGAGT CAGCATCTTTTC TCTGGCT	T	gap	Lys	Lys (9921)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTRMBL- ACC:Q64362 FUSED TOES (FT1 PROTEIN) - MUS MUSCULUS (MOUSE), 292 aa.	1.3E-75	16
7751	cg44924517	65	CGGCTACCAGG AAGAGTCTGCCG AA[G/gapJGTGAA GGCCATGGACTT CATCACCT	G	gap	Val	End (9922)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34088 CGI-93 PROTEIN - HOMO SAPIENS (HUMAN), 291 aa.	1.6E-75	

7752	cg42897014	220	ACAAGGACCTCA AAGTCACAGCGC A[G/gap]CTTCTC CTGCTGCGCCC CTGCTGCC	G	gap	Leu	Cys (9923)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.7E-75	11 (11q13)
7753	cg42897014	234	GTCACAGCGCA GCTTCTCCTGCT GC[G/gap]CCCT GCTGCCAGGG GCAAGTGGT	G	gap	Ala	Gly (9924)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.7E-75	11 (11q13)
7754	cg42897014	449	CGGCGCCTGC GCCGCCCTTCTGC AC[G/gap]TGCGG GTCGTCGGGCG ACAGGTCCC	C	gap	Gln	Gln (9925)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.7E-75	11 (11q13)
7755	cg42897014	523	TGCGGCGGGC CCGGGCGTGC GTG[G/gap]CAGC GCCAGGAGCA GAATGCGACC	G	gap	Pro	His (9926)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15828 CYSTATIN M PRECURSOR (CYSTATIN E) - Homo sapiens (Human), 149 aa.	1.7E-75	11 (11q13)
7756	cg44909359	206	CATAGACGAGG GCAAGGCGGCG TCA[gap]GJCCAA GTTAATCAGATC AACACTGAG	gap	G	Thr	Ser (9927)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03700 INTEGRASE - Bacteriophage lambda, 356 aa.	4.1E-75	
7757	cg44909359	248	AACACTGAGCGA TGCAATCCGAGA G[G/gap]CAATAG CTGAAGGCCATA TAACAAC	G	gap	Ala	Gln (9928)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P03700 INTEGRASE - Bacteriophage lambda, 356 aa.	4.1E-75	
7758	cg43971400	386	GGAAAACATCCT TGTAATGCGACT A[G/gap]CAACCA AGGAACAAGAGA TGCAAGA	G	gap	Ala	Gln (9929)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15007 HYPOTHETICAL PROTEIN KIAA0105 - Homo sapiens (Human), 151 aa.	4.4E-75	6

7759	cg44012742	1302	GGAGCGCAACTA CTGCCGCCTGC GG[G/gap]AGGCT CTGCAGCCCTG CTTACCCA	G	gap	Glu	Arg (9930)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q20487 SIMILAR TO RAT TRG GENE PRODUCT. NCBI GI: 1109880 - CAENORHABDITIS ELEGANS, 2018 aa.	1.8E-74	
7760	cg43272466	1780	CAGTTCITGGTG GATGCAGTGAA C[C/gap]TTCGGC CTTGCTGTGAC CACATAC	C	gap	Gly	Val (9931)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O54860 CARBOXYPEPTIDASE X2 MUS MUSCULUS (MOUSE), 764 aa.	1.9E-74	10
7761	cg43969639	775	TCATCCCGGGCA GGAGAGGCTGT GG[C/gap]ACAT ACACCTGATTAT CAACAGCC	C	gap	Ala	Pro (9932)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME II - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
7762	cg43969639	776	CATCCCGGGCA GGAGAGGCTGT GG[C/gap]ACAT ACACCTGATTAT CAACAGCC	C	gap	Val	Val (9933)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q10166 HYPOTHETICAL 35.7 KD PROTEIN C26A3.11 IN CHROMOSOME II - Schizosaccharomyces pombe (Fission yeast), 322 aa.	2.3E-74	3
7763	cg43962490	395	GTCAGCTTCACC ATCATGGCGCAG A[G/gap]CTCATA GAGGACGAAGA CTCCGGGA	G	gap	Leu	Ser (9934)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD34049 CGI-54 PROTEIN - HOMO SAPIENS (HUMAN), 383 aa.	1.4E-73	2 (10q21)
7764	cg43981873	641	CCGAGGTGTGTT TGGTGGCCGGG GC[C/gap]GAGGT GGGATCCCGGG CACAGGCAG	C	gap	Arg	Glu (9935)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
7765	cg43981873	670	GTGGGATCCCG GGCACAGGCAG AGG[C/gap]CAGC CAGAGAAGAAGC CTGGCAGAC	C	gap	Gln	Ser (9936)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	



7766	cg43981873	671	TGGGATCCCGG GCACAGGCAGA GGC[C/gap]AGCC AGAGAAAGAAGCC TGGCAGACA	C	gap	Gln	Ser (9937)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45867 LSM4 PROTEIN - HOMO SAPIENS (HUMAN), 139 aa.	1.7E-73	
7767	cg43933021	645	CTCTGCTGGTCG ACGTGGCGTCT G[G/gap]CCGTTT GGCCGAGGGCT GCAAGTAC	G	gap	Pro	Gln (9938)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38508 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa.	2.8E-73	13
7768	cg43933021	653	GTCGACGTCGG CGTCTGGCCGTT TG[G/gap]CCGAG GGCTGCAAGTAC TCAGCGTA	G	gap	Ala	Ala (9939)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38508 DNAJ DOMAIN- CONTAINING PROTEIN MCJ - HOMO SAPIENS (HUMAN), 150 aa.	2.8E-73	13
7769	cg43271682	164	AGTCACTGCC CGCACCTGCGC CCTT[gap]CAGCC CCGCCAGCGC TTCTGCCGT	T	gap	End	Trp (9940)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:Q15728 MALIGNANT MELANOMA METASTASIS-SUPPRESSOR KISS-1 - Homo sapiens (Human), 145 aa.	1.3E-70	1
7770	cg43923124	261	TATAGAGGGCTG CTGTATTTCAG A[G/gap]CTAAGT CCTCCAGTTCTC GATTCAC	G	gap	Ala	Leu (9941)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:P70381 TERA - MUS MUSCULUS (MOUSE), 277 aa.	2.9E-70	
7771	cg42886021	457	CACAATGAAGTG AACCAGGAAGCTG G[G/gap]CAAGCC TGATTTTGAAGT CTCAAGA	G	gap	Gly	Ala (9942)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P55789 AUGMENTER OF LIVER REGENERATION (HERV1 PROTEIN) - Homo sapiens (Human), 125 aa.	1.4E-69	
7772	cg3003900	333	CGTGGGGGAGC GGGGGGCGCTG CGC[G/gap]GTCT TGGGCCTCTGCT GCAGCCCCGG	G	gap	Val	Ser (9943)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01178 OXYTOCIN- NEUROPHYSIN 1 PRECURSOR (OXYTOCIN-NEUROPHYSIN 1) - Homo sapiens (Human), 125 aa.	1.8E-69	20 (20p13)

7773	cg3003900	334	GTGCGGAGCG GGGGCCGCTGC GCG[G/gap]TCTT GGGCTCTGCT GCAGCCCGGA	G	gap	Val	Ser (9944)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P01178 OXYTOCIN- NEUROPHYSIN 1 PRECURSOR (OXYTOCIN-NEUROPHYSIN 1) - Homo sapiens (Human), 125 aa.	1.8E-69	20 (20p13)
7774	cg42921698	337	CCCCGCCACCT CCACAGGCGC AC[G/gap]CGCGC CAGCGGCAGGC GGTGCGGA	G	gap	Arg	Arg (9945)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19
7775	cg42921698	472	GGAAGGAACG CCCGGCCGCG CTC[C/gap]TCGC GGCCCCAGGAG CCTTGCTCCT	C	gap	Glu	Glu (9946)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19
7776	cg42921698	478	GAACGCCCGGC CCGCGCTCCTC GCG[G/gap]CCCC AGGAGCCTTGCT CCTTGCTGT	G	gap	Gly	Gly (9947)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19
7777	cg42921698	644	GCCGCGAATTCT CAGCACCGTGC CA[G/gap]GGCGG ATGCCCTCGGG CAGCGAGGA	G	gap	Pro	Leu (9948)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19
7778	cg42921698	646	CGCGAATTCTCA GCACCGTGCCA GG[G/gap]CGGAT GCCCTCGGCA GCGAGGACT	G	gap	Arg	Arg (9949)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19

7779	cg42921698	652	TTCTCAGCACCG TGCCAGGGCGG AT[G/gap]CCCTC GGGACGCGAGG ACTTGTTGGG	G	gap	Gly	Gly (9950)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P47929 GALECTIN-7 (HKL-14) - Homo sapiens (Human), 135 aa.	2.3E-69	19
7780	cg43266481	341	CTGAAAGAATAA TTCAATATTATG G[G/gap]CCCAGC CACCTGGGGCA GAAGATGG	G	gap	Pro	Pro (9951)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14264 ENVELOPE PROTEIN - HOMO SAPIENS (HUMAN), 564 aa.	5.3E-69	
7781	cg43930848	596	CAACGCGTTCAG GACCCCGGCGC GG[G/gap]CAGGG CGCCCACGAGC TGGCTGGCT	G	gap	Ala	Ala (9952)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O75817 RIBONUCLEASE P PROTEIN SUBUNIT P20 - HOMO SAPIENS (HUMAN), 140 aa.	7.9E-69	7 (7q21)
7782	cg42925004	580	AGCCACCCCTATC TCCATGGCTGTG G[C/gap]CCTTCA GGACTACATGGC CCCCGAC	C	gap	Ala	Ala (9953)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16674 MELANOMA DERIVED GROWTH REGULATORY PROTEIN PRECURSOR (MELANOMA INHIBITORY ACTIVITY) - Homo sapiens (Human), 131 aa.	1.6E-68	
7783	cg42925004	671	TCCTCTCCAAGC TGAAGGGCCGT GG[G/gap]CGGCT CTTCTGGGGAG GCAGCGTTC	G	gap	Arg	Gly (9954)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q16674 MELANOMA DERIVED GROWTH REGULATORY PROTEIN PRECURSOR (MELANOMA INHIBITORY ACTIVITY) - Homo sapiens (Human), 131 aa.	1.6E-68	
7784	cg44004331	524	GGCAAAAGCAAA CTTGAGGCGGTA G[G/gap]CCTCGG CCAGCAACAGG CTGATGTC	G	gap	Ala	Ala (9955)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB46628 HYPOTHETICAL 34.3 KD PROTEIN - HOMO SAPIENS (HUMAN), 288 aa.	7.1E-68	

7785	cg43958562	301	GCATGTTGTCCT CAGTCTGCTTTG C[A/gap]GCATCT AAAAATTTTCGT GCAGAAA	A	gap	Ala (9956)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33909 COLON CANCER- ASSOCIATED PROTEIN MIC1 - HOMO SAPIENS (HUMAN), 609 aa.	9.1E-68	18 (18q11)
7786	cg42831353	481	GCGGCTCCACA CGTACACCCAGCA TG[G/gap]CCATG AGGCCTGGCCC AGGAAGAAC	G	gap	Ala (9957)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD37863 PUTATIVE NADH OXIDOREDUCTASE COMPLEX I SUBUNIT - CAENORHABDITIS ELEGANS, 237 aa.	1.3E-67	22
7787	cg43980385	446	GGCAGGAACCG TCCTTATCATTG GG[gap/G]CAGAG AGCAGAAGGTG GCACAGCCC	gap	G	Pro (9958)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20
7788	cg43980385	452	AACCCTCCTTAT CATTGGGCAGAG A[gap/A]GCAGAA GGTGGCACAGC CCGCGCTG	gap	A	Phe (9959)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20
7789	cg43980385	463	ATCATTGGGCAG AGAGCAGAAGGT G[G/gap]CACAGC CCGCGCTGCAG CACTTGAG	G	gap	Ala (9960)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37641 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20

7780	cg43980385	469	GGGCAGAGAGC AGAAGGTGGCA CAG[C/gap]CCGC GCTGCAGCACTT GAGGTTGTC	gap	Gly	Ala (9961)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37841 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20
7791	cg43980385	555	AGTTCTGGTCAG CCTGGAGCTCG GG[G/gap]CACAC GCCAGTCTTCTC TGCTCCTG	gap	Cys	Cys (9962)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB37841 DJ461P17.6 (MAJOR EPIDIDYMIS-SPECIFIC PROTEIN E4 PRECURSOR, HE4, EPIDIDYMIS SECRETORY PROTEIN E4, WAP-TYPE (WHEY ACIDIC PROTEIN) 'FOUR- DISULFIDE CORE' DOMAIN PROTEIN) - HOMO SAPIENS (HUMAN), 124 aa.	1.5E-67	20
7792	cg43080742	299	AACTGGCCCGGT GTGGGAACCTG GC[C/gap]TGCCG GTCAGACCTCCA GGTGCGG	gap	Cys	Ala (9963)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P53603 FORMINOTRANSFERASE- CYCLODEAMINASE (FTCD) [INCLUDES: GLUTAMATE FORMINOTRANSFERASE (EC 2.1.2.5) (GLUTAMATE FORMYLTRANSFERASE) FORMINOTETRAHYDROFOLATE CYCLODEAMINASE (EC 4.3.1.4)] - Sus scrofa [Pig], 541 aa.	2.2E-66	21

7793	cg43080742	324	CTGCCGGTACAG CCTCCAGGTGG CG[gap]CCAAA GCCCTGGAGAT GGCGGTGTT	gap	Ala	Pro (9964)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P53603 FORMINOTRANSFERASE- CYCLODEAMINASE (FTCD) [INCLUDES: GLUTAMATE FORMINOTRANSFERASE (EC 2.1.2.5) (GLUTAMATE FORMYLTRANSFERASE) FORMINOTETRAHYDROFOLATE CYCLODEAMINASE (EC 4.3.1.4)] - Sus scrofa (Pig), 541 aa	2.2E-66	21
7794	cg44911411	438	GAATCTCGTGAC ATTGGCCACAG C[gap]TGAGCA AGACCTGTTCCC CGGCGCTG	gap	Leu	End (9965)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
7795	cg44911411	454	GGCCACAGCCT GAGCAAGACCTG TT[gap]CCCGG CCTGCCCCATCC CAGAAGGC	gap	Ser	Ser (9966)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
7796	cg44911411	553	CTGTGCAATTC AGTGGGCGCGA TG[gap]CGGGC TGCGGGCAAGC GTCACCCCTG	gap	Gly	Ala (9967)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q16553 RIG-E PRECURSOR - HOMO SAPIENS (HUMAN), 131 aa.	4.5E-66	
7797	cg43294227	351	CAGGCGCGGGG CCTGGCGGCCA AGG[gap]CCCC GGGGGCACGAG CGACGCGTAC	gap	Gly	Ala (9968)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment).	6.1E-66	8
7798	cg43294227	571	GCCTCGACAAGT TCCTGGGCCGC GC[gap]GAGGT GGACCTGCGGG ATCTGCACC	gap	Glu	Arg (9969)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment).	6.1E-66	8

7799	cg43294227	612	GATCTGCACCGC GACCAGGGCGG CA[G/gap]GAAGA CGCAGTGGTATA AGTTGAAA	G	gap	Arg (9970)	Arg (9970)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment).	6.1E-66	8
7800	cg43294227	613	ATCTGCACCGCG ACCAGGGCGG AG[G/gap]AAGAC GCAGTGGTATA GTTGAAAT	G	gap	Lys	Arg (9971)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment).	6.1E-66	8
7801	cg43294227	622	GCGACCAGGGC CGCAGGAAGAC GCA[G/gap]TGGT ATAAGTTGAAAT CCAAACCAG	G	gap	Trp	Gly (9972)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA74880 KIAA0857 PROTEIN - HOMO SAPIENS (HUMAN), 733 aa (fragment).	6.1E-66	8
7802	cg44010741	114	GAGCGGCGCG GAGCCTGCCCT GG[G/gap]CGCCA GGTGTTCGGG GTGCGGGTC	G	gap	Gly	Ala (9973)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O75380 NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A) - Homo sapiens (Human), 124 aa.	6.6E-65	5
7803	cg44010741	143	CAGGTGTTTCGG GGTGCGGGTCT CG[C/gap]CGACC GGGAGAAAGT CAGGCACAC	C	gap	Pro	Arg (9974)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O75380 NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A) - Homo sapiens (Human), 124 aa.	6.6E-65	5
7804	cg4272355	80	TCGCCTCTTCA TCCTGGCCTTG G[C/gap]ACCGGA GTGGAGTTCGTG CGCTTTA	C	gap	Thr	Pro (9975)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD45885 MULTISPANNING NUCLEAR ENVELOPE MEMBRANE PROTEIN NURIM - HOMO SAPIENS (HUMAN), 261 aa (fragment).	1.8E-64	

7805	cg44001502	188	AACGCTCTCACC GGGAGCCAGAG CTC/gap]CCATG CTTCTCTGCGCA ATATCCAT	C	gap	Ser (9976)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q14849 MLN64 MRNA - HOMO SAPIENS (HUMAN), 445 aa.	7.6E-64	
7806	cg43969715	585	GAGCTCGTCATG ATTGGCCAGGTG TIG/gap]CTCTGC AGTGGATACAGC TGTACGT	G	gap	Ala (9977)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60688 HYPOTHETICAL 13.6 KD PROTEIN - HOMO SAPIENS (HUMAN), 119 aa.	3.3E-63	22
7807	cg40360053	217	TCGCTCACTGGC TCCTCCGGCGG CA[G/gap]CTCGT GCTGAGGGAGC TCCTGGCTG	G	gap	Leu (9978)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O14598 TESTIS-SPECIFIC BASIC PROTEIN Y 1 - Homo sapiens (Human), 125 aa.	8.7E-63	
7808	cg43969918	999	ACGGATGTATAC CTGCTCCAGCTG TIG/gap]CCACTC GGCCATCTCTGT ATGTGAC	G	gap	Ala (9979)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P43331 SMALL NUCLEAR RIBONUCLEOPROTEIN SM D3 (SNRNP CORE PROTEIN D3) (SM-D3) - Homo sapiens (Human), 126 aa.	2.9E-62	22
7809	cg44017203	137	GATAGTGCTAGT GGAGGGCGCCC GC[C/gap]TGGCG ACGAGGCAGAG GCAGGCAGC	C	gap	Arg (9980)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	6E-62	11
7810	cg44017203	141	ATGCTAGTGGAG GGCGCCCGCCT GG[C/gap]GACGA GGCAGAGGCAG GCAGCAAGA	C	gap	Ala (9981)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60478 PUTATIVE SEVEN PASS TRANSMEMBRANE PROTEIN - HOMO SAPIENS (HUMAN), 399 aa.	6E-62	11
7811	cg43950850	465	CAAGATAATATC CAGCAAAAAA Algap/A]GGCCGT AATATAGAAAG CTGGCGA	gap	A	Phe (9982)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95298 NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I- B14.5B) (CI-B14.5B) - Homo sapiens (Human), 119 aa.	7.8E-62	11



7812	cg43329229	183	GCCCGTGCAG ATCGGCTGCTGA AA[G/gap]CCCGT GCCCTGAAGATC CGGAGGA	G	gap	Ala	Pro (9983)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83047 KIAA1095 PROTEIN - HOMO SAPIENS (HUMAN), 1098 aa (fragment).	5.4E-61	
7813	cg43329229	207	AGCCCGTGCCCT GAAGATCCGGG AG[G/gap]AGCGC AGCGTTATGACG ACCGACGA	G	gap	Glu	Ser (9984)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83047 KIAA1095 PROTEIN - HOMO SAPIENS (HUMAN), 1098 aa (fragment).	5.4E-61	
7814	cg40157055	196	GGACTGCTCGTG GCCGCGGCGT GG[C/gap]CGGCG CTGCGCTCTTGC TGGTCCAC	C	gap	Ala	Ala (9985)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O35675 M-DELTA-LIKE 3 GENE PRECURSOR - MUS MUSCULUS (MOUSE), 585 aa.	5.5E-61	
7815	cg43298020	237	TGGTGGATCACCT TCAATGTGGGTG TT[G/gap]GCCCG GCCTACATGAAC CAGAGAA	G	gap	Ala	Pro (9986)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa.	7E-61	
7816	cg43298020	238	GGTGGATCACCT CAATGTGGGTG G[G/gap]CCCGG CCTACATGAACC AGAGAAA	G	gap	Ala	Pro (9987)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa.	7E-61	
7817	cg43298020	245	CACCTCAATGTG GGTGTGGCCCA GG[C/gap]CTACA TGAACCCAGAGAA AGCTGGAC	C	gap	Ala	Ala (9988)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P78537 GCN5-LIKE PROTEIN 1 (RT14 PROTEIN) - Homo sapiens (Human), 125 aa.	7E-61	
7818	cg43285334	613	GATTGCTTCAT TAAACGCTTGGT TTC[gap]CCCGTTC CGGTCGTAGGC GGCCCCAGA	C	gap	Gly	Gly (9989)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.9E-60	1

7819	cg43285334	615	TTGCTTCATTAA ACGCTTGGTTCC [C/gap]GTTCCGG TCGTAGGCGGC CCAGATG	C	gap	Gly (9990)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20965 HSPC003 - HOMO SAPIENS (HUMAN), 125 aa.	1.9E-60	1
7820	cg43985327	248	GGGACCTCAGT GGACACTTCCGT GG[G/gap]CACTG CCAGCCGCCTG GGGGGCACA	G	gap	Pro (9991)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.1E-59	1
7821	cg43985327	255	CAGTGGACACTT CCGTGGGCACT GC[C/gap]AGCCG CCTGGGGGCA CATAGGATC	C	gap	Leu (9992)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.1E-59	1
7822	cg43985327	499	CTGGGGTCGTG CGGATCCCTGAG GC[C/gap]GCAGC TCGGGTGAATC TCATCCAA	C	gap	Arg (9993)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O00488 ZINC FINGER PROTEIN - HOMO SAPIENS (HUMAN), 116 aa.	2.1E-59	1
7823	cg43278994	422	GGCCCATACCCT GCCAGCCCGCA CA[G/gap]CTCCT CTGCTCCCCCG ACAGCGTG	G	gap	Cys (9994)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83030 KIAA1078 PROTEIN - HOMO SAPIENS (HUMAN), 856 aa (fragment).	3E-59	19
7824	cg43278994	572	GCGGTTGTTCA CCTTGCCCGCCA G[G/gap]CAGCAG TGTGATAGGCA TTGIGGA	G	gap	Cys (9995)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:BAA83030 KIAA1078 PROTEIN - HOMO SAPIENS (HUMAN), 856 aa (fragment).	3E-59	19
7825	cg43976473	761	TGGGATGCGATG GAGCTGCCATAG G[C/gap]CATAGC CACATTGGCCAT TGGGTCC	C	gap	Pro (9996)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q35946 HYPOTHETICAL 14.9 KD PROTEIN - RATTUS NORVEGICUS (RAT), 137 aa.	3.5E-59	11

7826	cg43939569	807	AGCCTTTTCTAC TATCACCGGCAC C[C/gap]GGTCCG GGTATTTCTTTC GGATCTT	C	gap	Arg (9997)	Arg (9997)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD32455 GANGLIOSIDE EXPRESSION FACTOR 2 HOMOLOG - HOMO SAPIENS (HUMAN), 117 aa.	3.5E-59	17
7827	cg44011422	729	GAGAAGATGCAC GAGGGTGACGA GG[G/gap]CCCTG GCCACCACCAT AGCCAGGC	G	gap	Gly (9998)	Ala (9998)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM-BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
7828	cg44011422	737	GCACGAGGGTG ACGAGGGCCCT GGC[C/gap]ACCA CCATAAGCCAGG CCTCGGGGA	C	gap	His (9999)	Thr (9999)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM-BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
7829	cg44011422	765	CACCATAAGCCA GGCCTCGGGGA GG[G/gap]CACCC CCTAAGACCACA GTGGCCAA	G	gap	Gly (10000)	Ala (10000)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06702 CALGRANULIN B (MIGRATION INHIBITORY FACTOR- RELATED PROTEIN 14) (MRP-14) (P14) (LEUKOCYTE L1 COMPLEX HEAVY CHAIN) (S100 CALCIUM-BINDING PROTEIN A9) - Homo sapiens (Human), 114 aa.	4.4E-59	1 (1q12)
7830	cg44937260	130	TCCGAGCAGTC GCCGAGATCGTC G[G/gap]CCGCCA GGGTTGTAAAT TAAAGCA	G	gap	Gly (10001)	Ala (10001)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q94140 MEX-3 - CAENORHABDITIS ELEGANS, 415 aa.	4.4E-59	

7831	cg44914411	669	AGGCCCGCTCC GGAGAGCCCCG GAC[C/gap]TGAC GGGTGCCCAATAC TAGCCAGCG	C	gap	Arg	Ser (10002)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O60777 DJ186O1.1 - HOMO SAPIENS (HUMAN), 124 aa (fragment).	7.2E-59	22
7832	cg44915744	243	AAGATTCGAGCG AAATATCCCGAC A[G/gap]GGTTCC GGTGATTGTGGA AAAGGTC	G	gap	Arg	Arg (10003)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:O08765 GANGLIOSIDE EXPRESSION FACTOR 2 (GEF-2) - Homo sapiens (Human), and Rattus norvegicus (Rat), 117 aa.	1.9E-58	16
7833	cg42717343	380	TCTCTACTGATG TTGAGACAGTCT C[C/gap]TCCGGC TTTCTGGAAGAA TTCACGTG	C	gap	Ser	Pro (10004)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P15267 KIDNEY ANDROGEN- REGULATED PROTEIN PRECURSOR (KAP) - Homo sapiens (Human), and Mus musculus (Mouse), 121 aa.	1.9E-58	
7834	cg43253299	428	GGAAAGCTCCTT CTGGACGAATGT C[C/gap]ATCGTT AAGAACCTGCAG AACCTGG	C	gap	Ile	Ser (10005)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:P06307 PROCHOLECYSTOKININ PRECURSOR (CCK) - Homo sapiens (Human), 115 aa.	4.6E-57	3
7835	cg43962116	616	CTGCAGGTCAAA TAGACAGTCCGA A[G/gap]GCACTG ACGATGCAGTAC ATGGTCT	G	gap	Ala	Ala (10006)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15763 CYTOPLASMIC DYNEIN LIGHT CHAIN (T-COMPLEX TESTIS- SPECIFIC PROTEIN 1 HOMOLOG) (PROTEIN CW-1) - Homo sapiens (Human), and Bos taurus (Bovine), 113 aa.	5.9E-57	6
7836	cg43962116	617	TGCAGGTCAAAT AGACAGTCCGAA G[G/gap]CACTGA CGATGCAGTACA TGGTCTT	G	gap	Ala	Ala (10007)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q15763 CYTOPLASMIC DYNEIN LIGHT CHAIN (T-COMPLEX TESTIS- SPECIFIC PROTEIN 1 HOMOLOG) (PROTEIN CW-1) - Homo sapiens (Human), and Bos taurus (Bovine), 113 aa.	5.9E-57	6

7837	cg43934461	580	GAGGTGGATGC CGGCCCTAGCA CTG[gap]CCCT GGCCCTCATACT GGCTTCAGC	G	gap	Ala (10008)	Ala (10008)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33392 BREAST CANCER ASSOCIATED GENE 1 PROTEIN - HOMO SAPIENS (HUMAN), 606 aa.	8.8E-57	3
7838	cg43919432	1237	CTTGGATTCTG CAGTCCAGTAA C[gap]TCCGGC GGCGCTCACTCT GCTCCAA	C	gap	Arg (10009)	Ser (10009)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
7839	cg43919432	459	TCTTGTGCTCCA TAATCTGCTGGA G[gap]TGGTGC CCAGCATAGTCT GGCTTGG	C	gap	Gln (10010)	His (10010)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
7840	cg43919432	537	CACCAAGGACAT CTGACACCATGT A[gap]GGGGCC AGCCAGCCCCAC CAAGGGAG	G	gap	Pro (10011)	Pro (10011)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
7841	cg43919432	540	CAAGGACATCTG ACACCATGTAGG G[gap]CGCAGC CAGCCCACCAAG GGAGTGC	G	gap	Arg (10012)	Arg (10012)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O17066 F23F1.5 PROTEIN - CAENORHABDITIS ELEGANS, 322 aa.	1.2E-56	15
7842	cg43991184	51	CGGACCTCACCA AGCACCGGCGC AC[gap]CACAC GGCGGAGAAAG CCTACCGCT	G	gap	His (10013)	Thr (10013)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment).	2E-56	1

7843	cg43991184	67	CCGGCGCACGC ACACGGGCGAG AAG[C/gap]CCTA CCGCTGCGAACT GTGCGGCAA	C	gap	Pro	Pro (10014)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment).	2E-56	1
7844	cg43991184	69	GGCGCACGCAC ACGGGCGAGAA GCC[C/gap]TACC GCTGCGAACTGT GCGGCAAGC	C	gap	Tyr	Thr (10015)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment).	2E-56	1
7845	cg43991184	93	CCTACCGCTGCG AACTGTGCGGCA A[G/gap]CGGTTT ACGTGCGTGTC AATCTCA	G	gap	Arg	Gly (10016)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:Q29294 ZINC FINGER PROTEIN - SUS SCROFA (PIG), 138 aa (fragment).	2E-56	1
7846	cg44011808	666	CACCATCTCCAG CAGTCCGTGCG CA[G/gap]CCGCT TCTGAAAAGGCG GCCTCCAA	G	gap	Gly	Gly (10017)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:O95178 NADH-UBIQUINONE OXIDOREDUCTASE AGGG SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-AGGG) (CI-AGGG) - Homo sapiens (Human), 105 aa.	2.5E-56	
7847	cg43999272	171	ATCGCGGACGG AAGATGGCGTCC GC[C/gap]ACCCG TCTCATCCAGCG GCTGCGGA	C	gap	Thr	Pro (10018)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD05427 NADH-UBIQUINONE OXIDOREDUCTASE B14.5A SUBUNIT - HOMO SAPIENS (HUMAN), 113 aa.	3.2E-56	19
7848	cg43999272	290	CAGCCTCCTCCC AAGCTCCCTGTG G[G/gap]TCCTAG CCACAAGCTCTC CAACAAT	G	gap	Gly	Val (10019)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD05427 NADH-UBIQUINONE OXIDOREDUCTASE B14.5A SUBUNIT - HOMO SAPIENS (HUMAN), 113 aa.	3.2E-56	19

7849	cg42697199	304	ATGTTGATGTAG ACTTTGCCATCT TC/gapJTTGGGC GGGGCTGCGGC GTGGGCGT	C	gap	Glu	Lys (10020)	FRAMES HIPT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB43303 HYPOTHETICAL 13.5 KD PROTEIN - HOMO SAPIENS (HUMAN), 131 aa (fragment).	1.1E-55	19
7850	cg43935092	198	GCGTTCAGACCA ACTCCTGGATAT G/gap/GJAGCTCA ACCTTCAACAAG ACTACAC	gap	G	Ser	Glu (10021)	FRAMES HIPT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD26992 VAMP5-LIKE PROTEIN HOMO SAPIENS (HUMAN), 116 aa.	1.8E-55	2
7851	cg44018498	1102	TAGCCTGTCTAC CATGAAATCAAT G/gap/CATCAG CCATCATAGGGT CCACCGG	G	gap	Ala	Ala (10022)	FRAMES HIPT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45970 HYPOTHETICAL 43.5 KD PROTEIN - ARABIDOPSIS THALIANA (MOUSE-EAR CRESS), 392 aa.	1.8E-55	15
7852	cg43269198	618	AGCATTGCCATT CCAGACCAGGG TG/gap/JCTGTG CCCATGTACAGG CGGGACAG	G	gap	Ala	Ala (10023)	FRAMES HIPT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB41301 DJ598C15.1.1 (NOVEL PROTEIN) (ISOFORM 1) - HOMO SAPIENS (HUMAN), 162 aa (fragment).	1.8E-55	20
7853	cg43917989	763	CCCCTCTGGCCA TGGGCATGCTTG CT/gap/JGGGGCC GCCACGGGTGC TGCTCTTG	T	gap	Gly	Gly (10024)	FRAMES HIPT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD23762 EVECTIN-1 - RATTUS NORVEGICUS (RAT), 223 aa.	2.3E-55	11
7854	cg43916991	719	CCCTTCTTGTC CTGCAGCGTGTG G/gap/JTCATTT GACCCCGTGAC CCGGAGC	G	gap	Gly	Val (10025)	FRAMES HIPT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD33400 CARBOXY TERMINUS OF HSP70-INTERACTING PROTEIN - HOMO SAPIENS (HUMAN), 303 aa.	3E-55	16
7855	cg43129880	187	CTGGACACTGTG GAAGTGCTGAAA G/gap/JAATTCA GAAAGCCCAAGGA GGTCAAG	C	gap	Ala	Glu (10026)	FRAMES HIPT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAC33104 I-1 RECEPTOR CANDIDATE PROTEIN - HOMO SAPIENS (HUMAN), 1504 aa.	1.1E-54	3

7856	cg43957773	453	CGTAGAGCAACT GCAATCGCTCTG G[G/gap]CCTGGG CCTGGACAGGA CGGAGACC	G	gap	Ala	Ala (10027)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SPTREMBL- ACC:O43914 DNAX ACTIVATION PROTEIN 12 - HOMO SAPIENS (HUMAN), 113 aa.	3.3E-54	19
7857	cg43123055	468	AGCTGCAGTCGC TGGTCCCTCAGG G[gap]GJAGGTGT GGGAGCTGTC CCCAATGG	gap	G	Ser	Ser (10028)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P08949 NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN B] - Homo sapiens (Human), 121 aa.	8.8E-54	2
7858	cg43123055	495	GGTGCGGGAG CTGTCCCAATG GG[G/gap]ATGGG CTGGAAGGCTCC AGACTCTT	G	gap	Ser	Ser (10029)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P08949 NEUROMEDIN B-32 PRECURSOR [CONTAINS: NEUROMEDIN B] - Homo sapiens (Human), 121 aa.	8.8E-54	2
7859	cg43969772	707	CAGATTCGTAGT CAGCATAAGTTC T[G/gap]CCTTCT GGCCTCTTGGTA GGCTGTA	G	gap	Gly	Gly (10030)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
7860	cg43969772	728	TTCTGCCCTTCTG GCCTCTTGGTAG G[C/gap]TGTACC AGCAAAATGGTG TGAGACA	C	gap	Gln	His (10031)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q14259 ENHANCER OF RUDIMENTARY HOMOLOG - Homo sapiens (Human), and Mus musculus (Mouse), 104 aa.	4.9E-53	14
7861	cg43047973	270	CCTGGCGAGCG CTCTGGGCTGGT GC[C/gap]ACCGG GTGATCTCCTAC CGGGGCCA	C	gap	Gly	Ala (10032)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSPROT- ACC:Q02080 MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2) - Homo sapiens (Human), 365 aa.	1.9E-51	19



7862	cg42803443	120	CGCGGCAGCCA GAGCGCTGGTC CGC[G/gap]CAGG TTGGCCAGCAGC GGCGGCACC	gap	Arg	Ala (10033)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:CAB45012 573K1.15 (MM17M1-8 (NOVEL 7 TRANSMEMBRANE RECEPTOR (RHODOPSIN FAMILY) (OLFACTORY RECEPTOR LIKE PROTEIN)) - MUS MUSCULUS (MOUSE), 309 aa (fragment).	1.9E-51	
7863	cg43511776	96	TTTTCTAGTTAAG TCCCAAGGTGTC [A/gap]ACGACAA TGAGGAGGGTTT CTTCAG	gap	Asn	Thr (10034)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa.	3.1E-51	4
7864	cg44341684	96	TTTTCTAGTTAAG TCCCAAGGTGTC [A/gap]ACGACAA TGAGGAGGGTTT CTTCAG	gap	Asn	Thr (10035)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to SWISSNEW- ACC:P02675 FIBRINOGEN BETA CHAIN PRECURSOR - Homo sapiens (Human), 491 aa.	3.1E-51	4
7865	cg43924435	847	GTAGGACCTTCT GCCACTGGGCA AG[C/gap]TCCGC CTGCCGCATGGA ATGCAGTT	gap	Glu	Asp (10036)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD20971 HSPC009 - HOMO SAPIENS (HUMAN), 106 aa.	2.8E-50	17
7866	cg44010855	598	CACTGCCTGCAC CCCAAGCTGCAG A[G/gap]CACCAA GCGCTTCATCA GTGGTAC	gap	Ser	Thr (10037)	FRAMES HIFT	UNCLAS SIFIED	Human Gene Similar to TREMBLNEW- ACC:AAD38944 NJAC PROTEIN - HOMO SAPIENS (HUMAN), 99 aa.	5.8E-50	5
7867	cg43298240	375	CAACCAGCAATG AAGGTGAAGATG C[G/gap]GGGGG GGCAGGTCCCG GGACGGGTT	gap	Arg	Ala (10038)	FRAMES HIFT	water_ch annel	Human Gene Similar to SWISSPROT- ID:O14520 AQUAPORIN-7 LIKE (AQUAPORIN ADIPOSE) (AQPAP) - HOMO SAPIENS (HUMAN), 342 aa.	4.9E-65	

**WHAT IS CLAIMED IS:**

1. An isolated polynucleotide selected from the group consisting of:
  - a) a nucleotide sequence comprising one or more polymorphic sequences  
5 selected from the group consisting of SEQ ID NOS:1 - 7867;
  - b) a fragment of said nucleotide sequence, provided that the fragment  
includes a polymorphic site in said polymorphic sequence;
  - c) a complementary nucleotide sequence comprising a sequence  
10 complementary to one or more of said polymorphic sequences selected  
from the group consisting of SEQ ID NOS:1-7867; and
  - d) a fragment of said complementary nucleotide sequence, provided that the  
fragment includes a polymorphic site in said polymorphic sequence.
2. The polynucleotide of claim 1, wherein said polynucleotide sequence is DNA.  
15
3. The polynucleotide of claim 1, wherein said polynucleotide sequence is RNA.
4. The polynucleotide of claim 1, wherein said polynucleotide sequence is between  
about 10 and about 100 nucleotides in length.  
20
5. The polynucleotide of claim 1, wherein said polynucleotide sequence is between  
about 10 and about 90 nucleotides in length.
6. The polynucleotide of claim 1, wherein said polynucleotide sequence is between  
25 about 10 and about 75 nucleotides in length.
7. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and  
about 50 bases in length.
- 30 8. The polynucleotide of claim 1, wherein said polynucleotide is between about 10 and  
about 40 bases in length.

9. The polynucleotide of claim 1, wherein said polynucleotide is between about 15 and about 30 bases in length.
10. The polynucleotide of claim 1, wherein said polymorphic site includes a nucleotide other than the nucleotide listed in Table 1, column 5 for said polymorphic sequence.
11. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes a nucleotide other than the complement of the nucleotide listed in Table 1, column 5 for the complement of said polymorphic sequence.
12. The polynucleotide of claim 1, wherein said polymorphic site includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
13. The polynucleotide of claim 1, wherein the complement of said polymorphic site includes the complement of the nucleotide listed in Table 1, column 6 for said polymorphic sequence.
14. An isolated allele-specific oligonucleotide that hybridizes to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is selected from the group consisting of:
- a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867 provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence;
  - b) a nucleotide sequence that is a fragment of said polymorphic sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;
  - c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867, provided that the complementary nucleotide sequence includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and

- d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

5 15. The oligonucleotide of claim 14, wherein the oligonucleotide does not hybridize under stringent conditions to a second polynucleotide selected from the group consisting of:

- 10 a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867, wherein said polymorphic sequence includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence;
- b) a nucleotide sequence that is a fragment of any of said nucleotide sequences;
- 15 c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867, wherein said polymorphic sequence includes the complement of the nucleotide listed in Table 1, column 5; and
- 20 d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

25 16. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 51 bases in length.

17. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 10 and about 40 bases in length.

30 18. The oligonucleotide of claim 15, wherein the oligonucleotide is between about 15 and about 30 bases in length.

19. A method of detecting a polymorphic site in a nucleic acid, the method comprising:

a) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS:

1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and

b) determining whether said nucleic acid and said oligonucleotide hybridize; whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphic site in said nucleic acid.

20. The method of claim 19, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

21. The method of claim 19, wherein said oligonucleotide is between about 10 and about 51 bases in length.

22. The method of claim 19, wherein said oligonucleotide is between about 10 and about 40 bases in length.

23. A method of detecting the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a nucleic acid from said subject;

b) contacting said nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5; and

c) determining whether said nucleic acid and said oligonucleotide hybridize; whereby hybridization of said oligonucleotide to said nucleic acid sequence indicates the presence of the polymorphism in said subject.

24. A method of determining the relatedness of a first and second nucleic acid, the method comprising:

a) providing a first nucleic acid and a second nucleic acid;

b) contacting said first nucleic acid and said second nucleic acid with an oligonucleotide that hybridizes to a polymorphic sequence selected from the group consisting of SEQ ID NOS: 1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5;

c) determining whether said first nucleic acid and said second nucleic acid hybridize to said oligonucleotide; and

d) comparing hybridization of said first and second nucleic acids to said oligonucleotide, wherein hybridization of first and second nucleic acids to said nucleic acid indicates the first and second subjects are related.

25. The method of claim 24, wherein said oligonucleotide does not hybridize to said polymorphic sequence when said polymorphic sequence includes the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or when the complement of the polymorphic sequence includes the complement of the nucleotide recited in Table 1, column 5 for said polymorphic sequence.

26. The method of claim 24, wherein the oligonucleotide is between about 10 and about 51 bases in length.

27. The method of claim 24, wherein the oligonucleotide is between about 10 and about 40 bases in length.

28. The method of claim 24, wherein the oligonucleotide is between about 15 and about 30 bases in length.

29. An isolated polypeptide comprising a polymorphic site at one or more amino acid residues, wherein the protein is encoded by a polynucleotide selected from the group

consisting of polymorphic sequences SEQ ID NOS:1-7867, or their complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

30. The polypeptide of claim 29, wherein said polypeptide is translated in the same open reading frame as is a wild type protein whose amino acid sequence is identical to the amino acid sequence of the polymorphic protein except at the site of the polymorphism.

31. The polypeptide of claim 29, wherein the polypeptide encoded by said polymorphic sequence, or its complement, includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence, or the complement includes the complement of the nucleotide listed in Table 1, column 6.

32. An antibody that binds specifically to a polypeptide encoded by a polynucleotide comprising a nucleotide sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1-7867, or its complement, provided that the polymorphic sequence includes a nucleotide other than the nucleotide recited in Table 1, column 5 for said polymorphic sequence, or the complement includes a nucleotide other than the complement of the nucleotide recited in Table 1, column 5.

33. The antibody of claim 32, wherein said antibody binds specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

34. The antibody of claim 32, wherein said antibody does not bind specifically to a polypeptide encoded by a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

35. A method of detecting the presence of a polypeptide having one or more amino acid residue polymorphisms in a subject, the method comprising  
a) providing a protein sample from said subject;

b) contacting said sample with the antibody of claim 34 under conditions that allow for the formation of antibody-antigen complexes; and  
c) detecting said antibody-antigen complexes,  
whereby the presence of said complexes indicates the presence of said polypeptide.

5

36. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

10

a) providing a subject suffering from a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement; and

15

b) administering to the subject an effective therapeutic dose of a second nucleic acid comprising the polymorphic sequence, provided that the second nucleic acid comprises the nucleotide present in the wild type allele, thereby treating said subject.

20

37. The method of claim 36, wherein the second nucleic acid sequence comprises a polymorphic sequence which includes the nucleotide listed in Table 1, column 5 for said polymorphic sequence.

25

38. A method of treating a subject suffering from, at risk for, or suspected of, suffering from a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

30

a) providing a subject suffering from a pathology associated with aberrant expression of a polymorphic sequence selected from the group consisting of polymorphic sequences SEQ ID NOS:1 - 7867, or its complement; and

b) administering to the subject an effective therapeutic dose of a polypeptide,

wherein said polypeptide is encoded by a polynucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7867, provided that said polymorphic



sequence includes the nucleotide listed in Table 1, column 6 for said polymorphic sequence.

39. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a first nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement; and

b) administering to the subject an effective dose of the antibody of claim 34, thereby treating said subject.

40. A method of treating a subject suffering from, at risk for, or suspected of suffering from, a pathology ascribed to the presence of a sequence polymorphism in a subject, the method comprising:

a) providing a subject suffering from, at risk for, or suspected of suffering from, a pathology associated with aberrant expression of a nucleic acid comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or its complement; and

b) administering to the subject an effective dose of an oligonucleotide comprising a polymorphic sequence selected from the group consisting of SEQ ID NOS:1 - 7867, or by a polynucleotide comprising a nucleotide sequence that is complementary to any one of polymorphic sequences SEQ ID NOS:1 - 7867, provided that said polymorphic sequence includes the nucleotide listed in Table 1, column 5 or Table 1, column 6 for said polymorphic sequence, thereby treating said subject.

41. An oligonucleotide array, comprising one or more oligonucleotides hybridizing to a first polynucleotide at a polymorphic site encompassed therein, wherein the first polynucleotide is chosen from the group consisting of:

a) a nucleotide sequence comprising one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867;

b) a nucleotide sequence that is a fragment of any of said nucleotide sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence;

c) a complementary nucleotide sequence comprising a sequence complementary to one or more polymorphic sequences selected from the group consisting of SEQ ID NOS:1 - 7867; and

d) a nucleotide sequence that is a fragment of said complementary sequence, provided that the fragment includes a polymorphic site in said polymorphic sequence.

42. The array of claim 41, wherein said array comprises about 10 oligonucleotides.

43. The array of claim 41, wherein said array comprises about 100 oligonucleotides.

44. The array of claim 41, wherein said array comprises about 1000 oligonucleotides.

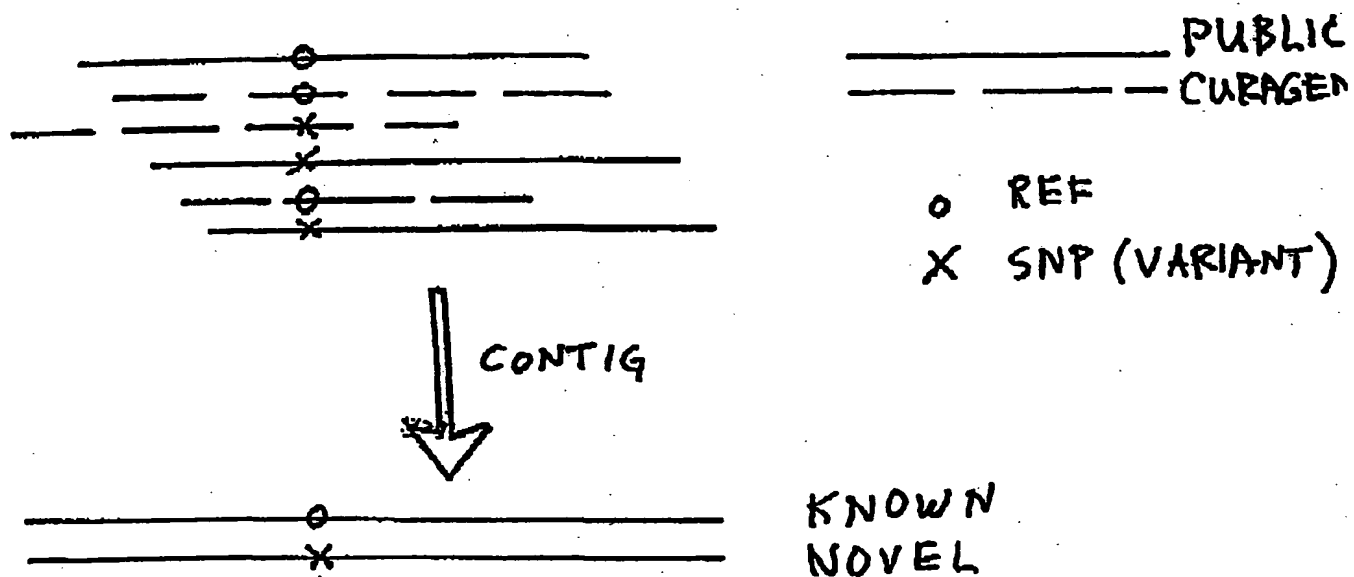


FIG. 1

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Shimkets, Richard A.  
Leach, Martin

<120> Nucleic Acids Containing Single  
Nucleotide Polymorphisms and Methods of Use Thereof

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<140> not yet assigned

<141> 2000-12-28

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&lt;223&gt; Accession number cg43065549

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gagtcctggg gtcctgtgat ctgggtgccgg tcagagcagt caaggagggg a

51

&lt;210&gt; 173

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43065549

&lt;400&gt; 173

cgggtcagagc agtcaaggag gggaccctgg ggctgacccc agcagtgtca g

51

&lt;210&gt; 174

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43018621

&lt;400&gt; 174

cggacaacct ggagctgaag aagctagtat acctctactt gatgaattac g

51

&lt;210&gt; 175

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43924995

&lt;400&gt; 175

caaaatggca gatgaatttc acagttcgct atgaaactac aaataaaaact t

51

&lt;210&gt; 176

&lt;211&gt; 51

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51

<210> 191

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51

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<210> 229  
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51

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43329663

&lt;400&gt; 233

ctcgagaggc caaccagag aaattcaaca gccgctttcg gaataagatg t

51

&lt;210&gt; 234

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43151490

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51

&lt;210&gt; 235

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51

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&lt;221&gt; allele

&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg44929725

&lt;400&gt; 236

atgtccttac cacaccatgg aaattcaaag ttgccaaaca gctggccagt g

51

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&lt;223&gt; single nucleotide polymorphism

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&lt;222&gt; (0)...(0)

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51

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&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

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&lt;223&gt; Accession number cg44929725

&lt;400&gt; 238

ctgaagtgga cccacacat tttgagaagc gcttcctaaa gaggatccgt g

51

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&lt;223&gt; single nucleotide polymorphism

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&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg44929725

&lt;400&gt; 239

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51

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51

&lt;210&gt; 365

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

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&lt;223&gt; Accession number cg43918944

&lt;400&gt; 366

tcttggagag tcttgatttc cagcctagca ttgcaaagcg atacattgac c

51

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&lt;223&gt; single nucleotide polymorphism

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&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43918944

&lt;400&gt; 367

aaatgatcag tgctaacatc ttccgtacac ttcctccaag tgataaccga g

51

&lt;210&gt; 368

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51

&lt;210&gt; 493

&lt;211&gt; 51

&lt;212&gt; DNA

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&lt;223&gt; single nucleotide polymorphism

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&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg1408914

&lt;400&gt; 493

cccccaaaat gctgatgagc tttatttcag agaggaacat catctecttt c

51

&lt;210&gt; 494

&lt;211&gt; 51

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51

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&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg21138682

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&lt;223&gt; Accession number cg44005525

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51

&lt;210&gt; 554

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&lt;212&gt; DNA

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&lt;223&gt; single nucleotide polymorphism

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&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43921266

&lt;400&gt; 554

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51

&lt;210&gt; 555

&lt;211&gt; 51

&lt;212&gt; DNA

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&lt;223&gt; Accession number cg43929067

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51

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&lt;223&gt; Accession number cg43947011

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51

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&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature



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51

&lt;210&gt; 621

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

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51

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&lt;223&gt; single nucleotide polymorphism

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51

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&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

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&lt;223&gt; Accession number cg43968854

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51

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&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43947129

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51

&lt;210&gt; 746

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43927276

&lt;400&gt; 746

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51

&lt;210&gt; 747

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

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&lt;223&gt; Accession number cg43957632

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51

&lt;210&gt; 748

&lt;211&gt; 51

&lt;212&gt; DNA

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&lt;220&gt;

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&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43957632

&lt;400&gt; 748

gctcggagcc cgggtgggga tagcacgca gcccctggcc gcagcgcggg g

51

&lt;210&gt; 749

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg43950796

&lt;400&gt; 749

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51

&lt;210&gt; 750

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&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; allele

&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

&lt;222&gt; (0)...(0)

&lt;223&gt; Accession number cg44001387

&lt;400&gt; 750

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51

&lt;210&gt; 751

&lt;211&gt; 51

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

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&lt;222&gt; (26)...(0)

&lt;223&gt; single nucleotide polymorphism

&lt;221&gt; misc\_feature

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&lt;223&gt; Accession number cg43917229

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51

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51

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51

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